

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
4 September 2003 (04.09.2003)

PCT

(10) International Publication Number
WO 03/072720 A2(51) International Patent Classification⁷:**C12N**

Street, #3, San Carlos, CA 94070 (US). FOUCHIER, Ronaldus, Adrianus, Maria [NL/NL]; Essenburgsingel 44a, NL-3021 AR Rotterdam (NL). VAN DEN HOGEN, Bernadetta, Gerarda [NL/NL]; Essenburgsingel 44a, NL-3021 AR Rotterdam (NL). OSTERHAUS, Albertus, Dominicus, Marcellinus, Erasmus [NL/NL]; Dr. Breveestraat 16, NL-3981 CH Bunnik (NL).

(21) International Application Number:

PCT/US03/05276

(22) International Filing Date: 21 February 2003 (21.02.2003)

(25) Filing Language:

English

(26) Publication Language:

English

(74) Agents: CORUZZI, Laura, A. et al.; Pennie & Edmonds LLP, 1155 Avenue of the Americas, New York, NY 10036 (US).

(30) Priority Data:

60/358,934 21 February 2002 (21.02.2002) US

(71) Applicants (for all designated States except US): MED-IMMUNE VACCINES, INC. [US/US]; 35 W. Watkins Mill Road, Gaithersburg, MD 20878 (US). VIRONOVATrIVE BV [NL/NL]; P.O. Box 1738, NL-3000 DR Rotterdam (NL).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(72) Inventors; and

(75) Inventors/Applicants (for US only): HALLER, Aurelia [AT/US]; 313 Hillview Avenue, Redwood City, CA 94062 (US). TANG, Roderick [MY/US]; 730 Chestnut

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),

[Continued on next page]

(54) Title: RECOMBINANT PARAINFLUENZA VIRUS EXPRESSION SYSTEMS AND VACCINES COMPRISING HETEROLOGOUS ANTIGENS DERIVED FROM METAPNEUMOVIRUS

Human 1 NSWKVILIFSLILITPQHGLKESVYLEPESCTTIEGYLSVLRTG-MYTRVFTILEVGDVENLTC 60
M ++ ++ L+ P ++B-Y ESGCST-T GY SVLRTGWYTRNFV LE+G+VEN+TC
Turkey 1 MDVRICLILLPLISNPSSCCTQSTYBESCTVTRGKYSVLATGNTYINVNLYQNVENLTC 60

Human 61 ADGPSLKLTKELDLSGALRELRTVSDADQANRQEQLIEPNSRGPVFLGLAIALGVATAAAVTA 120
DGPRLI TEL LTKXALREL+IVSADQ-A+B ++ +P+ RKFVQIAALGVATAAAVTA
Turkey 61 NDGPSLKLTKELDLSGALRELRTVSDADQAKESRLLSFRRRFVFLGLAIALGVATAAAVTA 120

Human 121 GVIAIAKTRILLESVTIAKGALKKTTNEAVSTLGNQGVVLATAVAKRELKDPSRNLTTRAINRKY 180
GVA+AKTRILLESVTIAKGALKKTTNEAVSTLGNQGVVLATAVAKRELKDPSRNLTTRAINRKY
Turkey 121 GVIAIAKTRILLESVTIAKGALKKTTNEAVSTLGNQGVVLATAVAKRELKDPSRNLTTRAINRKY 180

Human 181 KEDIAIDLGKAASPSFQFNRFLPFLVNRVQFQSDNAGITPAISLDINTDAELARAV6NMPTSAQQ 240
KC+IAD-KNA-SQ Q NRRPF+LNVRQFSD+AGIT A+SDIOMTD ET RA++ MPFS+GQ
Turkey 181 KCNIAIDLGKAASPSFQFNRFLPFLVNRVQFQSDNAGITPAISLDINTDAELARAV6NMPTSAQQ 240

Human 241 IKLMLBTRGVTRRNGFGFLIGUVGSSVYMVQLPPIPGVQIDTPCWIVKAAPSGCGKKKHYA 300
I LML NRAMVRKKGFLIGUVGSSVYMVQLPPIPGVQIDTPCWIVKAAPSGCGKKKHYA
Turkey 241 ISMLMLBTRGVTRRNGFGFLIGUVGSSVYMVQLPPIPGVQIDTPCWIVKAAPSGCGKKKHYA 300

Human 301 CILREDDQGKWCNAGSTVYYPNENKEDETGRDHVFCDTAGINVBQSKHECNINISTNNYP 360
C+LREDDQGKWCNAGSTVYYPN+ DCE E+D+PCDTAGINVB+ ++CH NIST+ YP
Turkey 301 CILREDDQGKWCNAGSTVYYPNENKEDETGRDHVFCDTAGINVBQSKHECNINISTNNYP 360

Human 361 -CKVSTGRHPISMVALSPLGVLVACYKGVSIGSISGSNVRGVIKEQNLKGCSYITNQDAUTTYI 420
CKVSTGRHP+SMVAL+PLG LV+CY+ VSCBISGS+VOLIKQ LGC++I S +ADP+T+I
Turkey 361 CKVSTGRHPVSMVAL+PLG LV+CY+ VSCBISGS+VOLIKQ LGC++I S +ADP+T+I

Human 421 DNTTVYQLSKVVGEGEHRVKGPRVSSFPVCFEDQFVVALDQVFFESIENSQALWDQSNSRI 480
DNTTVYQLSKV GEQ IKG PV ++F+P+ FPFEDQFVVALDQVFFESI- SQ L+D+SN +
Turkey 421 DNTTVYQLSKVVGEGEHRVKGPRVSSFPVCFEDQFVVALDQVFFESIENSQALWDQSNSRI 480

Human 481 LSSAKGNTGFIIVIIILIAVLGSTMILSVFVII--IEKTKPTGAPPELSGVTMNGFT 536
L + X G I I++ +LQ +L ++ ++KTK P P +G ++ ++
Turkey 481 LGADAKSKAGIAIAIVLVLGIFPLLAIVYCCSRVRAKTK-PHDYPATGHSMAVY 537

(57) Abstract: The present invention relates to recombinant bovine parainfluenza virus (bPIV) cDNA or RNA which may be used to express heterologous gene products in appropriate host cell systems and/or to rescue negative strand RNA recombinant viruses that express, package, and/or present the heterologous gene product. In particular, the heterologous gene products include gene product of another species of PIV or from another negative strand RNA virus, including but not limited to, influenza virus, respiratory syncytial virus, human metapneumovirus and avian pneumovirus. The chimeric viruses and expression products may advantageously be used in vaccine formulations including vaccines against a broad range of pathogens and antigens.

WO 03/072720 A2**BEST AVAILABLE COPY**



European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

Published:

- *without international search report and to be republished upon receipt of that report*

5

**RECOMBINANT PARAINFLUENZA VIRUS EXPRESSION
SYSTEMS AND VACCINES COMPRISING HETEROLOGOUS ANTIGENS
DERIVED FROM METAPNEUMOVIRUS**

This application claims priority to U.S. Provisional Patent Application No. 60/358,934, filed February 21, 2002, which is incorporated by reference herein in its entirety.

10 Copending and co-assigned U.S. Patent Application ___, filed on even date herewith, listing Ronaldus Fouchier, Bernadetta van den Hoogen, Albertus Osterhaus, Aurelia Haller, and Roderick Tang as Inventors, entitled "METAPNEUMOVIRUS STRAINS AND THEIR USE IN VACCINE FORMULATIONS AND AS VECTORS FOR EXPRESSION OF ANTIGENIC SEQUENCES", is incorporated herein by reference in its entirety.

15

1. INTRODUCTION

The present invention relates to recombinant parainfluenza virus (PIV) cDNA or RNA that may be used to express heterologous gene products in appropriate host cell systems and/or to rescue negative strand RNA recombinant viruses that express, package, and/or present the heterologous gene product. In particular, the present invention encompasses vaccine preparations comprising chimeric PIV expressing a heterologous gene product, wherein the heterologous gene product is preferably an antigenic peptide or polypeptide. In one embodiment, the PIV vector of the invention expresses one, two, or three heterologous gene products that may be encoded by the same or different viruses. In a preferred embodiment, the heterologous sequence encodes a heterologous gene product that is an antigenic polypeptide from another species of PIV or from another negative strand RNA virus, including but not limited to, influenza virus, respiratory syncytial virus (RSV), mammalian metapneumovirus, and avian pneumovirus. The vaccine preparations of the invention encompass multivalent vaccines, including bivalent and trivalent vaccine preparations. The multivalent vaccines of the invention may be administered in the form of one PIV vector expressing each heterologous antigenic sequence or two or more PIV vectors

each encoding different heterologous antigenic sequences. The vaccine preparations of the invention can be administered alone or in combination with other vaccines, prophylactic agents, or therapeutic agents.

5

2. BACKGROUND OF THE INVENTION

Parainfluenza viral infection results in serious respiratory tract disease in infants and children. (Tao *et al.*, 1999, Vaccine 17: 1100-08). Infectious parainfluenza viral infections account for approximately 20% of all hospitalizations of pediatric patients that suffer from 10 respiratory tract infections worldwide. *Id.* An effective antiviral therapy is not available to treat PIV related diseases, and a vaccine to prevent PIV infection has not yet been approved.

PIV is a member of the genus respirovirus (PIV1, PIV3) or rubulavirus (PIV2, PIV4) of the paramyxoviridae family. PIV is made up of two structural modules: (1) an internal ribonucleoprotein core, or nucleocapsid, containing the viral genome, and (2) an outer, 15 roughly spherical lipoprotein envelope. Its genome consists of a single strand of negative sense RNA, that is approximately 15,456 nucleotides in length and encodes at least eight polypeptides. These proteins include the nucleocapsid structural protein (NP, NC, or N depending on the genera), the phosphoprotein (P), the matrix protein (M), the fusion glycoprotein (F), the hemagglutinin-neuraminidase glycoprotein (HN), the large polymerase 20 protein (L), and the C and D proteins of unknown function. *Id.*

The parainfluenza nucleocapsid protein (NP, NC, or N) contains two domains within each protein unit. These domains include: an amino-terminal domain, that comprises nearly two-thirds of the molecule and interacts directly with the RNA, and a carboxyl-terminal domain, that lies on the surface of the assembled nucleocapsid. A hinge is thought to exist 25 at the junction of these two domains, thereby imparting some flexibility on this protein (see Fields *et al.* (ed.), 1991, FUNDAMENTAL VIROLOGY, 2nd ed, Raven Press, New York, incorporated by reference herein in its entirety). The matrix protein (M) is apparently involved in viral assembly, and it interacts with both the viral membrane and the nucleocapsid proteins. The phosphoprotein (P) is subject to phosphorylation and has been 30 implicated in transcription regulation, methylation, phosphorylation and polyadenylation. Produced initially as an inactive precursor, the fusion glycoprotein (F) is cleaved upon

translation to produce two disulfide linked polypeptides. The active F protein interacts with the viral membrane where it facilitates penetration of the parainfluenza virion into host cells by promoting the fusion of the viral envelope with the host cell plasma membrane. *Id.* The 5 glycoprotein, hemagglutinin-neuraminidase (HN) protrudes from the envelope and imparts hemagglutinin and neuraminidase activities on the virus. HN has a strongly hydrophobic amino terminus that functions to anchor the HN protein into the lipid bilayer. *Id.* Finally, the large polymerase protein (L) plays an important role in both transcription and replication.

Id.

10 Bovine parainfluenza virus was first isolated in 1959 from calves showing signs of shipping fever. It has since been isolated from normal cattle, aborted fetuses, and cattle exhibiting signs of respiratory disease (Breker-Klassen *et al.*, 1996, Can. J. Vet. Res. 60: 228-236. *See also* Shibuta, 1977, Microbiol. Immunol. 23 (7), 617-628). Human and bovine PIV3 share neutralizing epitopes but show distinct antigenic properties. Significant 15 differences exist between the human and bovine viral strains in the HN protein. In fact, a bovine strain induces some neutralizing antibodies to hPIV infection while a human strain seems to induce a wider spectrum of neutralizing antibodies against human PIV3 (Van Wyke Coelingh *et al.*, 1990, J. Virol. 64:3833-3843).

20 The replication of all negative-strand RNA viruses, including PIV, is complicated by the absence of the cellular machinery that is required to replicate RNA. Additionally, the negative-strand genome must be transcribed into a positive-strand (mRNA) copy before translation can occur. Consequently, the genomic RNA alone cannot synthesize the required RNA-dependent RNA polymerase upon entry into the cell. The L, P and N proteins must enter the host cell along with the genomic RNA.

25 It is hypothesized that most or all of the viral proteins that transcribe PIV mRNA also carry out the replication of the genome. The mechanism that regulates the alternative uses (*i.e.*, transcription or replication) of the same complement of proteins has not been clearly identified, but the process appears to involve the abundance of free forms of one or more of the nucleocapsid proteins. Directly following penetration of the virus, transcription is 30 initiated by the L protein using the negative-sense RNA in the nucleocapsid as a template.

Viral RNA synthesis is regulated such that it produces monocistronic mRNAs during transcription.

Following transcription, virus genome replication is the second essential event in infection by negative-strand RNA viruses. As with other negative-strand RNA viruses, virus genome replication in PIV is mediated by virus-specified proteins. The first products of replicative RNA synthesis are complementary copies (*i.e.*, plus-polarity) of the PIV genomic RNA (cRNA). These plus-stranded copies (anti-genomes) differ from the plus-stranded mRNA transcripts in the structure of their termini. Unlike the mRNA transcripts, the anti-
10 genomic cRNAs are not capped or methylated at the 5' termini, and they are not truncated nor polyadenylated at the 3' termini. The cRNAs are coterminal with their negative strand templates and contain all the genetic information in the complementary form. The cRNAs serve as templates for the synthesis of PIV negative-strand viral genomes (vRNAs).

The bPIV negative strand genomes (vRNAs) and antigenomes (cRNAs) are
15 encapsidated by nucleocapsid proteins; the only unencapsidated RNA species are viral mRNAs. Replication and transcription of bPIV RNA occurs in the cytoplasm of the host cell. Assembly of the viral components appears to take place at the host cell plasma membrane where the mature virus is released by budding.

20 **2.1. PARAMYXOVIRUS**

Classically, as devastating agents of disease, paramyxoviruses account for many animal and human deaths worldwide each year. The Paramyxoviridae form a family within the order of Mononegavirales (negative-sense single stranded RNA viruses), consisting of the sub-families Paramyxovirinae and Pneumovirinae. The latter sub-family is at present
25 taxonomically divided in the genera Pneumovirus and Metapneumovirus (Pringle, 1999, Arch. Virol. 144/2, 2065-2070). Human respiratory syncytial virus (hRSV), a species of the Pneumovirus genus, is the single most important cause of lower respiratory tract infections during infancy and early childhood worldwide (Domachowske, & Rosenberg, 1999, Clin. Microbiol. Rev. 12(2): 298-309). Other members of the Pneumovirus genus include the
30 bovine and ovine respiratory syncytial viruses and pneumonia virus of mice (PVM).

In the past decades several etiological agents of mammalian disease, in particular of respiratory tract illnesses (RTI), in particular of humans, have been identified (Evans, In: Viral Infections of Humans, Epidemiology and Control. 3th ed. (ed. Evans, A.S) 22-28
5 (Plenum Publishing Corporation, New York, 1989)). Classical etiological agents of RTI with mammals are respiratory syncytial viruses belonging to the genus Pneumovirus found with humans (hRSV) and ruminants such as cattle or sheep (bRSV and/or oRSV). In human RSV differences in reciprocal cross neutralization assays, reactivity of the G proteins in immunological assays and nucleotide sequences of the G gene are used to define two hRSV
10 antigenic subgroups. Within the subgroups the amino acid sequences show 94 % (subgroup A) or 98% (subgroup B) identity, while only 53% amino acid sequence identity is found between the subgroups. Additional variability is observed within subgroups based on monoclonal antibodies, RT-PCR assays and RNase protection assays. Viruses from both subgroups have a worldwide distribution and may occur during a single season. Infection
15 may occur in the presence of pre-existing immunity and the antigenic variation is not strictly required to allow re-infection. See, for example Sullender, 2000, Clinical Microbiology Reviews 13(1): 1-15; Collins et al. Fields Virology, ed. B.N. Knipe, Howley, P.M. 1996, Philadelphia: Lippencott-Raven. 1313-1351; Johnson et al., 1987, (Proc Natl Acad Sci USA, 84(16): 5625-9; Collins, in The Paramyxoviruses, D.W. Kingsbury, Editor. 1991, Plenum
20 Press: New York. p. 103-153.

Another classical Pneumovirus is the pneumonia virus of mice (PVM), in general only found with laboratory mice. However, a proportion of the illnesses observed among mammals can still not be attributed to known pathogens.

25 **2.2. RSV INFECTIONS**

Respiratory syncytial virus (RSV) is the leading cause of serious lower respiratory tract disease in infants and children (Feigen et al., eds., 1987, In: Textbook of Pediatric Infectious Diseases, WB Saunders, Philadelphia at pages 1653-1675; New Vaccine Development, Establishing Priorities, Vol. 1, 1985, National Academy Press, Washington
30 DC at pages 397-409; and Ruuskanen *et al.*, 1993, Curr. Probl. Pediatr. 23:50-79). The yearly epidemic nature of RSV infection is evident worldwide, but the incidence and severity

of RSV disease in a given season vary by region (Hall, 1993, *Contemp. Pediatr.* 10:92-110). In temperate regions of the northern hemisphere, it usually begins in late fall and ends in late spring. Primary RSV infection occurs most often in children from 6 weeks to 2 years of age
5 and uncommonly in the first 4 weeks of life during nosocomial epidemics (Hall *et al.*, 1979, *New Engl. J. Med.* 300:393-396). Children at increased risk for RSV infection include, but are not limited to, preterm infants (Hall *et al.*, 1979, *New Engl. J. Med.* 300:393-396) and children with bronchopulmonary dysplasia (Groothuis *et al.*, 1988, *Pediatrics* 82:199-203), congenital heart disease (MacDonald *et al.*, *New Engl. J. Med.* 307:397-400), congenital or
10 acquired immunodeficiency (Ogra *et al.*, 1988, *Pediatr. Infect. Dis. J.* 7:246-249; and Pohl *et al.*, 1992, *J. Infect. Dis.* 165:166-169), and cystic fibrosis (Abman *et al.*, 1988, *J. Pediatr.* 113:826-830). The fatality rate in infants with heart or lung disease who are hospitalized with RSV infection is 3%-4% (Navas *et al.*, 1992, *J. Pediatr.* 121:348-354).

RSV infects adults as well as infants and children. In healthy adults, RSV causes
15 predominantly upper respiratory tract disease. It has recently become evident that some adults, especially the elderly, have symptomatic RSV infections more frequently than had been previously reported (Evans, A.S., eds., 1989, *Viral Infections of Humans. Epidemiology and Control*, 3rd ed., Plenum Medical Book, New York at pages 525-544). Several epidemics also have been reported among nursing home patients and
20 institutionalized young adults (Falsey, A.R., 1991, *Infect. Control Hosp. Epidemiol.* 12:602-608; and Garvie *et al.*, 1980, *Br. Med. J.* 281:1253-1254). Finally, RSV may cause serious disease in immunosuppressed persons, particularly bone marrow transplant patients (Hertz *et al.*, 1989, *Medicine* 68:269-281).

Treatment options for established RSV disease are limited. Severe RSV disease of
25 the lower respiratory tract often requires considerable supportive care, including administration of humidified oxygen and respiratory assistance (Fields *et al.*, eds, 1990, *Fields Virology*, 2nd ed., Vol. 1, Raven Press, New York at pages 1045-1072).

While a vaccine might prevent RSV infection, and/or RSV-related disease, no vaccine is yet licensed for this indication. A major obstacle to vaccine development is
30 safety. A formalin-inactivated vaccine, though immunogenic, unexpectedly caused a higher and more severe incidence of lower respiratory tract disease due to RSV in immunized

infants than in infants immunized with a similarly prepared trivalent parainfluenza vaccine (Kim et al., 1969, Am. J. Epidemiol. 89:422-434; and Kapikian *et al.*, 1969, Am. J. Epidemiol. 89:405-421). Several candidate RSV vaccines have been abandoned and others
5 are under development (Murphy et al., 1994, Virus Res. 32:13-36), but even if safety issues are resolved, vaccine efficacy must also be improved. A number of problems remain to be solved. Immunization would be required in the immediate neonatal period since the peak incidence of lower respiratory tract disease occurs at 2-5 months of age. The immaturity of the neonatal immune response together with high titers of maternally acquired RSV antibody
10 may be expected to reduce vaccine immunogenicity in the neonatal period (Murphy et al., 1988, J. Virol. 62:3907-3910; and Murphy et al., 1991, Vaccine 9:185-189). Finally, primary RSV infection and disease do not protect well against subsequent RSV disease (Henderson et al., 1979, New Engl. J. Med. 300:530-534).

Currently, the only approved approach to prophylaxis of RSV disease is passive
15 immunization. Initial evidence suggesting a protective role for IgG was obtained from observations involving maternal antibody in ferrets (Prince, G.A., Ph.D. diss., University of California, Los Angeles, 1975) and humans (Lambrecht *et al.*, 1976, J. Infect. Dis. 134:211-217; and Glezen et al., 1981, J. Pediatr. 98:708-715). Hemming et al. (Morell *et al.*, eds., 1986, Clinical Use of Intravenous Immunoglobulins, Academic Press, London at
20 pages 285-294) recognized the possible utility of RSV antibody in treatment or prevention of RSV infection during studies involving the pharmacokinetics of an intravenous immune globulin (IVIG) in newborns suspected of having neonatal sepsis. In this study, it was noted that one infant, whose respiratory secretions yielded RSV, recovered rapidly after IVIG infusion. Subsequent analysis of the IVIG lot revealed an unusually high titer of RSV
25 neutralizing antibody. This same group of investigators then examined the ability of hyperimmune serum or immune globulin, enriched for RSV neutralizing antibody, to protect cotton rats and primates against RSV infection (Prince et al., 1985, Virus Res. 3:193-206; Prince et al., 1990, J. Virol. 64:3091-3092; Hemming et al., 1985, J. Infect. Dis. 152:1083-1087; Prince et al., 1983, Infect. Immun. 42:81-87; and Prince et al., 1985, J.
30 Virol. 55:517-520). Results of these studies indicate that IVIG may be used to prevent RSV infection, in addition to treating or preventing RSV-related disorders.

- Recent clinical studies have demonstrated the ability of this passively administered RSV hyperimmune globulin (RSV IVIG) to protect at-risk children from severe lower respiratory infection by RSV (Groothius et al., 1993, New Engl. J. Med. 329:1524-1530; and 5 The PREVENT Study Group, 1997, Pediatrics 99:93-99). While this is a major advance in preventing RSV infection, this treatment poses certain limitations in its widespread use. First, RSV IVIG must be infused intravenously over several hours to achieve an effective dose. Second, the concentrations of active material in hyperimmune globulins are insufficient to treat adults at risk or most children with compromised cardiopulmonary function. 10 Third, intravenous infusion necessitates monthly hospital visits during the RSV season. Finally, it may prove difficult to select sufficient donors to produce a hyperimmune globulin for RSV to meet the demand for this product. Currently, only approximately 8% of normal donors have RSV neutralizing antibody titers high enough to qualify for the production of hyperimmune globulin.
- 15 One way to improve the specific activity of the immunoglobulin would be to develop one or more highly potent RSV neutralizing monoclonal antibodies (MAbs). Such MAbs should be human or humanized in order to retain favorable pharmacokinetics and to avoid generating a human anti-mouse antibody response, as repeat dosing would be required throughout the RSV season. Two glycoproteins, F and G, on the surface of RSV have been 20 shown to be targets of neutralizing antibodies (Fields et al., 1990, *supra*; and Murphy et al., 1994, *supra*).
- A humanized antibody directed to an epitope in the A antigenic site of the F protein of RSV, SYNAGIS®, is approved for intramuscular administration to pediatric patients for prevention of serious lower respiratory tract disease caused by RSV at recommended 25 monthly doses of 15 mg/kg of body weight throughout the RSV season (November through April in the northern hemisphere). SYNAGIS® is a composite of human (95%) and murine (5%) antibody sequences. See, Johnson et al., 1997, J. Infect. Diseases 176:1215-1224 and U.S. Patent No. 5,824,307, the entire contents of which are incorporated herein by reference. The human heavy chain sequence was derived from the constant domains of human IgG1 30 and the variable framework regions of the VH genes of Cor (Press et al., 1970, Biochem. J. 117:641-660) and Cess (Takashi et al., 1984, Proc. Natl. Acad. Sci. USA 81:194-198). The

human light chain sequence was derived from the constant domain of C and the variable framework regions of the VL gene K104 with J -4 (Bentley et al., 1980, Nature 288:5194-5198). The murine sequences derived from a murine monoclonal antibody, Mab 5 1129 (Beeler et al., 1989, J. Virology 63:2941-2950), in a process which involved the grafting of the murine complementarity determining regions into the human antibody frameworks.

2.3. AVIAN PNEUMOVIRUSES

- 10 Respiratory disease caused by an avian pneumovirus (APV) was first described in South Africa in the late 1970s (Buys et al., 1980, Turkey 28:36-46) where it had a devastating effect on the turkey industry. The disease in turkeys was characterized by sinusitis and rhinitis and was called turkey rhinotracheitis (TRT). The European isolates of APV have also been strongly implicated as factors in swollen head syndrome (SHS) in 15 chickens (O'Brien, 1985, Vet. Rec. 117:619-620). Originally, the disease appeared in broiler chicken flocks infected with Newcastle disease virus (NDV) and was assumed to be a secondary problem associated with Newcastle disease (ND). Antibody against European APV was detected in affected chickens after the onset of SHS (Cook et al., 1988, Avian Pathol. 17:403-410), thus implicating APV as the cause.
- 20 Avian pneumovirus (APV) also known as turkey rhinotracheitis virus (TRTV), the aetiological agent of avian rhinotracheitis, an upper respiratory tract infection of turkeys (Giraud et al., 1986, Vet. Res. 119:606-607), is the sole member of the recently assigned Metapneumovirus genus, which, as said was until now not associated with infections, or what is more, with disease of mammals. Serological subgroups of APV can be 25 differentiated on the basis of nucleotide or amino acid sequences of the G glycoprotein and neutralization tests using monoclonal antibodies that also recognize the G glycoprotein. However, other differences in the nucleotide and amino acid sequences can be used to distinguish serological subgroups of APV. Within subgroups A, B and D, the G protein shows 98.5 to 99.7% aa sequence identity within subgroups while between the subgroups 30 only 31.2- 38% aa identity is observed. See for example Collins et al., 1993, Avian Pathology, 22: p. 469-479; Cook et al., 1993, Avian Pathology, 22: 257-273;

Bayon-Auboyer et al., J Gen Virol, 81(Pt 11): 2723-33; Seal, 1998, Virus Res, 58(1-2): 45-52; Bayon-Auboyer et al., 1999, Arch Virol, 144(6): 91-109; Juhasz, et al., 1994, J Gen Virol, 75(Pt 11): 2873-80.

5 A further serotype of APV is provided in WO00/20600, incorporated by reference herein, which describes the Colorado isolate of APV and compared it to known APV or TRT strains with in vitro serum neutralization tests. First, the Colorado isolate was tested against monospecific polyclonal antisera to recognized TRT isolates. The Colorado isolate was not neutralized by monospecific antisera to any of the TRT strains. It was, however, neutralized
10 by a hyperimmune antiserum raised against a subgroup A strain. This antiserum neutralized the homologous virus to a titre of 1:400 and the Colorado isolate to a titer of 1: 80. Using the above method, the Colorado isolate was then tested against TRT monoclonal antibodies. In each case, the reciprocal neutralization titer was <10. Monospecific antiserum raised to the Colorado isolate was also tested against TRT strains of both subgroups. None of the
15 TRT strains tested were neutralized by the antiserum to the Colorado isolate.

The Colorado strain of APV does not protect SPF chicks against challenge with either a subgroup A or a subgroup B strain of TRT virus. These results suggest that the Colorado isolate may be the first example of a further serotype of avian pneumovirus (See, Bayon-Auboyer et al., 2000, J. Gen. Vir. 81:2723-2733).

20 The avian pneumovirus is a single stranded, non-segmented RNA virus that belongs to the sub-family Pneumovirinae of the family Paramyxoviridae, genus metapneumovirus (Cavanagh and Barrett, 1988, Virus Res. 11:241-256; Ling et al., 1992, J. Gen. Virol. 73:1709-1715; Yu et al., 1992, J. Gen. Virol. 73:1355-1363). The Paramyxoviridae family is divided into two sub-families: the Paramyxovirinae and Pneumovirinae. The subfamily
25 Paramyxovirinae includes, but is not limited to, the genera: Paramyxovirus, Rubulavirus, and Morbillivirus. Recently, the sub-family Pneumovirinae was divided into two genera based on gene order, and sequence homology, i.e. pneumovirus and metapneumovirus (Naylor et al., 1998, J. Gen. Virol., 79:1393-1398; Pringle, 1998, Arch. Virol. 143:1449-1159). The pneumovirus genus includes, but is not limited to, human respiratory
30 syncytial virus (hRSV), bovine respiratory syncytial virus (bRSV), ovine respiratory syncytial virus, and mouse pneumovirus. The metapneumovirus genus includes, but is not

limited to, European avian pneumovirus (subgroups A and B), which is distinguished from hRSV, the type species for the genus pneumovirus (Naylor et al., 1998, J. Gen. Virol., 79:1393-1398; Pringle, 1998, Arch. Virol. 143:1449-1159). The US isolate of APV
5 represents a third subgroup (subgroup C) within metapneumovirus genus because it has been found to be antigenically and genetically different from European isolates (Seal, 1998, Virus Res. 58:45-52; Senne et al., 1998, In: Proc. 47th WPDC, California, pp. 67-68).

Electron microscopic examination of negatively stained APV reveals pleomorphic, sometimes spherical, virions ranging from 80 to 200 nm in diameter with long filaments
10 ranging from 1000 to 2000 nm in length (Collins and Gough, 1988, J. Gen. Virol. 69:909-916). The envelope is made of a membrane studded with spikes 13 to 15 nm in length. The nucleocapsid is helical, 14 nm in diameter and has 7 nm pitch. The nucleocapsid diameter is smaller than that of the genera Paramyxovirus and Morbillivirus, which usually have diameters of about 18 nm.

15 Avian pneumovirus infection is an emerging disease in the USA despite its presence elsewhere in the world in poultry for many years. In May 1996, a highly contagious respiratory disease of turkeys appeared in Colorado, and an APV was subsequently isolated at the National Veterinary Services Laboratory (NVSL) in Ames, Iowa (Senne et al., 1997, Proc. 134th Ann. Mtg., AVMA, pp. 190). Prior to this time, the United States and Canada
20 were considered free of avian pneumovirus (Pearson et al., 1993, In: Newly Emerging and Re-emerging Avian Diseases: Applied Research and Practical Applications for Diagnosis and Control, pp. 78-83; Hecker and Myers, 1993, Vet. Rec. 132:172). Early in 1997, the presence of APV was detected serologically in turkeys in Minnesota. By the time the first confirmed diagnosis was made, APV infections had already spread to many farms. The
25 disease is associated with clinical signs in the upper respiratory tract: foamy eyes, nasal discharge and swelling of the sinuses. It is exacerbated by secondary infections. Morbidity in infected birds can be as high as 100%. The mortality can range from 1 to 90% and is highest in six to twelve week old pouls.

Avian pneumovirus is transmitted by contact. Nasal discharge, movement of
30 affected birds, contaminated water, contaminated equipment; contaminated feed trucks and load-out activities can contribute to the transmission of the virus. Recovered turkeys are

thought to be carriers. Because the virus is shown to infect the epithelium of the oviduct of laying turkeys and because APV has been detected in young pouls, egg transmission is considered a possibility.

5 A significant portion of human respiratory disease is caused by members of the viral sub-families Paramyxovirinae and Pneumovirinae, there still remains a need for an effective vaccine to confer protection against a variety of viruses that result in respiratory tract infection.

10 Citation or discussion of a reference herein shall not be construed as an admission that such is prior art to the present invention.

3. SUMMARY OF THE INVENTION

The present invention relates to recombinant parainfluenza virus cDNA and RNA that may be engineered to express heterologous or non-native gene products, in particular, to 15 express antigenic polypeptides and peptides. In one embodiment, the present invention relates to recombinant bovine or human parainfluenza viruses which are engineered to express heterologous antigens or immunogenic and/or antigenic fragments of heterologous antigens. In another embodiment of the invention, the recombinant bovine or human 20 parainfluenza viruses are engineered to express sequences that are non-native to the PIV genome, including mutated PIV nucleotide sequences. In particular, the invention relates to recombinant Kansas-strain bovine parainfluenza type 3 virus as well as cDNA and RNA molecules coding for the same. The present invention also relates to recombinant PIV that contain modifications that result in chimeric viruses with phenotypes more suitable for use in vaccine formulations.

25 The present invention provides for the first time a chimeric PIV formulated as a vaccine that is able to confer protection against various viral infections, in particular, viruses that result in respiratory tract infections. In a specific embodiment, the present invention provides a vaccine that is able to confer protection against parainfluenza, influenza, or respiratory syncytial viral infection. The present invention provides for the first time a 30 vaccine that is able to confer protection against metapneumovirus infection in a mammalian host.

In accordance with the present invention, a recombinant virus is one derived from a bovine parainfluenza virus or a human parainfluenza virus that is encoded by endogenous or native genomic sequences or non-native genomic sequences. In accordance with the 5 invention, a non-native sequence is one that is different from the native or endogenous genomic sequence due to one or more mutations, including, but not limited to, point mutations, rearrangements, insertions, deletions, etc. to the genomic sequence that may or may not result in a phenotypic change.

In accordance with the present invention, a chimeric virus of the invention is a 10 recombinant bPIV or hPIV which further comprises one or more heterologous nucleotide sequences. In accordance with the invention, a chimeric virus may be encoded by a nucleotide sequence in which heterologous nucleotide sequences have been added to the genome or in which nucleotide sequences have been replaced with heterologous nucleotide sequences.

The present invention also relates to engineered recombinant parainfluenza viruses 15 and viral vectors that encode combinations of heterologous sequences which encode gene products, including but not limited to, genes from different strains of PIV, influenza virus, respiratory syncytial virus, mammalian metapneumovirus (e.g., human metapneumovirus), avian pneumovirus, measles, mumps, other viruses, pathogens, cellular genes, tumor 20 antigens, or combinations thereof. Furthermore, the invention relates to engineered recombinant parainfluenza viruses that contain a nucleotide sequence derived from a metapneumovirus in combination with a nucleotide sequence derived from a respiratory syncytial virus, and further in combination with a nucleotide sequence derived from a human 25 parainfluenza virus. The invention also encompasses recombinant parainfluenza vectors and viruses that are engineered to encode genes from different species and strains of the parainfluenza virus, including the F and HN genes of human PIV3.

In one embodiment, the PIV vector of the invention is engineered to express one or 30 more heterologous sequences, wherein the heterologous sequences encode gene products that are preferably antigenic gene products. In a preferred embodiment, the PIV vector of the invention expresses one, two or three heterologous sequences that encode antigenic polypeptides and peptides. In some embodiments, the heterologous sequences are derived

from the same virus or from different viruses. In a preferred embodiment, the heterologous sequences encode heterologous gene products that are antigenic polypeptides from another species of PIV, such as a human PIV, a mutant strain of PIV, or from another negative strand 5 RNA virus, including but not limited to, influenza virus, respiratory syncytial virus (RSV), mammalian metapneumovirus (*e.g.*, human metapneumovirus (hMPV)), and avian pneumovirus. In one embodiment, the heterologous sequence encodes an immunogenic and/or antigenic fragment of a heterologous gene product.

In a preferred embodiment, the recombinant PIV is a bovine PIV type 3, or an 10 attenuated human PIV type 3. In one embodiment, the sequences encoding fusion (F) protein, hemagglutinin (HN) glycoprotein, or other non-essential genes of the PIV genome are deleted and are substituted by heterologous antigenic sequences. In yet another embodiment, the PIV genome contains mutations or modifications, in addition to the 15 heterologous nucleotide sequences, that result in a chimeric virus having a phenotype that is more suitable for use in vaccine formulations, *e.g.*, an attenuated phenotype or a phenotype with enhanced antigenicity.

In a specific embodiment, the heterologous nucleotide sequence to be inserted into the PIV genome is derived from the nucleotide sequences encoding a F protein, a G protein or an HN protein. In certain embodiments, the nucleotide sequence to be inserted encodes a 20 chimeric F protein, a chimeric G protein or a chimeric HN protein. In a specific embodiment, the F protein comprises an ectodomain of a F protein of a metapneumovirus, a transmembrane domain of a F protein of a parainfluenza virus, and a luminal domain of a F protein of a parainfluenza virus. In certain embodiments, the nucleotide sequence to be inserted encodes a F protein, wherein the transmembrane domain of the F protein is deleted 25 so that a soluble F protein is expressed.

In another specific embodiment, the invention provides a chimeric virus comprising a PIV genome comprising a heterologous nucleotide sequence derived from a metapneumovirus. In a specific embodiment, the PIV virus is a Kansas-strain bovine parainfluenza type 3 virus. In other embodiments, the PIV virus is a human parainfluenza 30 virus with an attenuated phenotype. In yet other embodiments, the invention provides a chimeric bovine parainfluenza virus type 3/human parainfluenza virus engineered to contain

human parainfluenza F and HN genes in a bovine parainfluenza backbone. The chimeric virus may further comprise a heterologous nucleotide sequence derived from a metapneumovirus, and/or further comprise a heterologous nucleotide sequence derived from
5 a respiratory syncytial virus.

In certain embodiments, the virus of the invention comprises heterologous nucleotide sequences derived from at least two different genes of a metapneumovirus. In a specific embodiment, the heterologous sequence is derived from a metapneumovirus, e.g., avian pneumovirus and human metapneumovirus. More specifically, the heterologous sequence is
10 derived from an avian pneumovirus, including avian pneumovirus type A, B, C or D, preferably C.

The present invention also provides vaccine preparations and immunogenic compositions comprising chimeric PIV expressing one or more heterologous antigenic sequences. In a specific embodiment, the present invention provides multivalent vaccines,
15 including bivalent and trivalent vaccines. The multivalent vaccines of the invention may be administered in the form of one PIV vector expressing each heterologous antigenic sequence or two or more PIV vectors each encoding different heterologous antigenic sequences. In one embodiment, the vaccine preparation of the invention comprises chimeric PIV expressing one, two or three heterologous polypeptides, wherein the heterologous
20 polypeptides can be encoded by sequences derived from one strain of the same virus, different strains of the same virus, or different viruses. Preferably, the heterologous antigenic sequences are derived from a negative strand RNA virus, including but not limited to, influenza virus, parainfluenza virus, respiratory syncytial virus (RSV), mammalian metapneumovirus (e.g., human metapneumovirus (hMPV)), and avian pneumovirus (APV).
25 The heterologous antigenic sequences include, but are not limited to, sequences that encode human parainfluenza virus F or HN protein, F protein of RSV, HA protein of influenza virus type A, B, and C, and F protein of human MPV and avian pneumovirus. More preferably, the vaccine preparation of the invention comprises attenuated chimeric viruses that are viable and infectious. In a preferred embodiment, the recombinant PIV is a bovine PIV type
30 3, or an attenuated strain of human PIV.

In one embodiment, the vaccine preparation comprises the chimeric virus of the present invention, wherein the F, HN, or some other nonessential genes of the PIV genome have been substituted or deleted. In a preferred embodiment, the vaccine preparation of the 5 present invention is prepared by engineering a strain of PIV with an attenuated phenotype in an intended host. In another preferred embodiment, the vaccine preparation of the present invention is prepared by engineering an attenuated strain of PIV.

In another embodiment, the heterologous nucleotide sequence is added to the complete PIV genome. In certain embodiments, the PIV genome is engineered so that the 10 heterologous sequences are inserted at position one, two, three, four, five or six, so that the heterologous sequences are expressed as the first, second, third, fourth, fifth, or sixth gene of the viral genome. In specific embodiments, the heterologous sequence is inserted at position one, two, or three of the viral genome. In certain embodiments, the intergenic region between the end of the coding sequence of an inserted heterologous gene and the start of the 15 coding sequence of the downstream gene is altered to a desirable length, resulting in enhanced expression of the heterologous sequence or enhanced growth of the chimeric virus. Alternatively, the intergenic region is altered to a desirable length, with a potential to alter the expression of the heterologous sequence or growth of the recombinant or chimeric virus, e.g., attenuated phenotype. In some embodiments, both the position of the insertion and the 20 length of the intergenic region flanking a heterologous nucleotide sequence are engineered to select a recombinant or chimeric virus with desirable levels of expression of the heterologous sequence and desirable viral growth characteristics.

In certain embodiments, the invention provides a vaccine formulation comprising the recombinant or chimeric virus of the invention and a pharmaceutically acceptable excipient. 25 In specific embodiments, the vaccine formulation of the invention is used to modulate the immune response of a subject, such as a human, a primate, a horse, a cow, a sheep, a pig, a goat, a dog, a cat, a rodent or a subject of avian species. In a more specific embodiment, the vaccine is used to modulate the immune response of a human infant or a child. In another embodiment, the present invention relates to vaccine formulations for veterinary uses. The 30 vaccine preparation of the invention can be administered alone or in combination with other vaccines or other prophylactic or therapeutic agents.

3.1. CONVENTIONS AND ABBREVIATIONS

	cDNA	complementary DNA
5	CPE	cytopathic effects
	L	large protein
	M	matrix protein (lines inside of envelope)
	F	fusion glycoprotein
10	HN	hemagglutinin-neuraminidase glycoprotein
	N, NP or NC	nucleoprotein (associated with RNA and required for polymerase activity)
	P	phosphoprotein
	MOI	multiplicity of infection
15	NA	neuraminidase (envelope glycoprotein)
	PIV	parainfluenza virus
	bPIV	bovine parainfluenza virus
	bPIV3	bovine parainfluenza virus type 3
	^{hPIV}	human parainfluenza virus
20	hPIV3	human parainfluenza virus type 3
	bPIV/hPIV or b/h PIV	recombinant bPIV with hPIV sequences
	b/h PIV3 or bPIV3/hPIV3	recombinant bPIV type 3 with hPIV type 3 sequences
25	nt	nucleotide
	RNP	ribonucleoprotein
	rRNP	recombinant RNP
	vRNA	genomic virus RNA
	cRNA	antigenomic virus RNA
30	hMPV	human metapneumovirus

	APV	avian pneumovirus
	position	when position is used regarding engineering any virus, it refers to the position of the gene of the viral genome to be transcribed. For example, if a gene is located at position one, it is the first gene of the viral genome to be transcribe; if a gene is located at position two, it is the second gene of the viral genome to be transcribed.
5		
10	position 1 of bPIV3, b/h PIV3 and derivatives thereof	nucleotide position 104 of the genome, or alternatively, the position of the first gene of the viral genome to be transcribed
15	position 2 of bPIV3, b/h PIV3 and derivatives thereof	nucleotide position 1774 of the genome, or alternatively the position between the first and the second open reading frame of the native parainfluenza virus, or alternatively, the position of the second gene of the viral genome to be transcribed
20	position 3 of bPIV3, b/h PIV3 and derivatives thereof	nucleotide position 3724 of the genome, or alternatively the position between the second and the third open reading frame of the native parainfluenza virus, or alternatively, the position of the third gene of the viral genome to be transcribed.
25	position 4 of bPIV3, b/h PIV3 and derivatives thereof	nucleotide position 5042 of the genome, or alternatively the position between the third and the fourth open reading frame of the native parainfluenza virus, or alternatively, the position of the fourth gene of the viral genome to be transcribed.
30	position 5 of bPIV3, b/h PIV3 and derivatives thereof	nucleotide position 6790 of the genome, or alternatively the position between the fourth and the fifth open reading frame of the native parainfluenza virus, or alternatively, the position of the fifth gene of the viral genome to be transcribed.
	position 6 of bPIV3, b/h PIV3 and derivatives thereof	nucleotide position 8631 of the genome, or alternatively the position between the fifth and the sixth open reading frame of the native parainfluenza virus, or alternatively, the position of the sixth gene of the viral genome to be transcribed.

4. DESCRIPTION OF FIGURES

Figure 1. Pairwise alignments of the amino acid sequence of the F protein of the human metapneumovirus with different F proteins from different avian pneumoviruses.

- 5 Identical amino acids between the two sequences are indicated by the one-letter-symbol for the amino acid. Conserved amino acid exchanges between the two amino acid sequences are indicated by a "+" sign, and a space indicates a non-conserved amino acid exchange. A) Alignment of the human metapneumoviral F protein with the F protein of an avian pneumovirus isolated from Mallard Duck (85.6% identity in the ectodomain). B) Alignment 10 of the human metapneumoviral F protein with the F protein of an avian pneumovirus isolated from Turkey (subgroup B; 75% identity in the ectodomain).

Figure 2. PCR fragments from nt 5255 to nt 6255 derived from three different isolates of the b/h PIV3 chimeric virus were amplified. The resulting 1 kb DNA fragments 15 were digested with enzymes specific for the F gene of human PIV3. These enzymes do not cut in the corresponding fragment of bovine PIV3. The 1% agarose gel shows the undigested fragment (lanes 2,5, and 6) and the SacI or BgIII digested fragments (lanes 4, 6 and lanes 9, 10, and 11, respectively). The sample in lane 10 is undigested, however, upon a repeat of digestion with BgIII, this sample was cut (data not shown). Lanes 1 and 8 show a 20 DNA size marker.

Figure 3. PCR fragments from nt 9075 to nt 10469 derived from three different isolates of the b/h PIV3 chimeric virus were amplified. The resulting 1.4kb DNA fragments were digested with enzymes specific for the L gene of bovine PIV3. These enzymes do not 25 cut in the corresponding fragment of human PIV3. The 1% agarose gel shows the undigested 1.4 kb fragment (lanes 2, 5, and 8). The smaller DNA fragments produced by digestion with BamH1 and PvuII are shown in lanes 3, 4, 6, 7, 9, and 10). Lane 1 shows a DNA size marker.

30 Figure 4. Six constructs, including the bPIV3/hPIV3 vector and b/h PIV3 vectored RSV F or G cDNA, are demonstrated. The bovine PIV3 F gene and HN gene are deleted

and replaced with human PIV3 F and HN gene respectively. The RSV F or G genes are cloned into either position 1 or position 2. All RSV genes are linked to the bPIV3 N-P intergenic region with the exception of RSV F1* (N-N), which is followed by the shorter
5 bPIV3 N gene stop/N gene start sequences.

Figure 5. b/h PIV3 vectored RSV F or G gene displayed a positional effect. (A) is a Western blot analysis of chimeric virus-infected cell lysates. F protein was detected using monoclonal antibodies (MAbs) against the RSV F protein, and G protein was detected using 10 polyclonal antibodies (PAbs) against the RSV G protein. A 50 kDa band representing the F₁ fragment was detected in cells infected with all chimeric viruses as well as wild-type RSV. There was a greater accumulation of a 20 kDa F fragment in infected cell lysates of chimeric viruses compared to wild-type RSV. The experiment was done at MOI of 0.1, except that in lane 1, b/h PIV3 vectored RSV F1* N-N infections were repeated at a higher MOI of 1.0.
15 Both the immature and glycosylated forms of RSV G protein that migrated at approximately 50 kDa and 90 kDa were detected. (B) is a Northern blot analysis, which showed that the mRNA transcription correlated with the result of the protein expression demonstrated in Figure 5A. Equal amounts of total RNA were separated on 1% agarose gels containing 1% formaldehyde and transferred to nylon membranes. The blots were hybridized with
20 digoxigenin (DIG)-UTP-labeled riboprobes synthesized by in vitro transcription using a DIG RNA labeling kit. (C) is growth curves of chimeric viruses comprising b/h PIV3 vectored RSV F or G protein in Vero cells. Vero cells were grown to 90% confluence and infected at an MOI of 0.01. The infected monolayers were incubated at 37°C. Virus titers for each time point harvest were determined by TCID₅₀ assays, which were performed by inspecting
25 visually for CPE following incubation at 37°C for 6 days.

Figure 6. The b/h PIV3 vectored enhanced green fluorescence protein (eGFP) constructs. The eGFP gene is introduced into the b/h PIV3 vector sequentially between all genes of PIV3 (only position 1, 2, 3, and 4 are shown here). The eGFP gene was linked to
30 the bPIV3 N-P intergenic region. The b/h GFP 1 construct harbors the eGFP gene cassette in the 3' most proximal position of the b/h PIV3 genome. The b/h GFP 2 construct contains

the eGFP gene cassette between the N and P genes. The b/h GFP 3 construct contains the eGFP gene cassette between the P and M gene, and the b/h GFP4 construct contains the eGFP gene between M and F of b/h PIV3.

5

Figure 7. Positional effect of enhanced green fluorescence protein (eGFP) insertions in the b/h PIV3 genome. (A) shows the amount of green cells produced upon infecting Vero cells with b/h PIV3 vectored eGFP 1, 2, and 3 at MOI 0.1 and MOI 0.01 for 20 hours. The green cells were visualized by using a fluorescent microscope. (B) is a Western blot analysis 10 of infected cell lysates. The blots were probed with a GFP MAb as well as a PIV3 PAb. PIV3 antibody was also used to show that the blots had same volume loading. (C) is growth curves of b/h PIV3 vectored GFP constructs (at position 1, 2, and 3) in Vero cells.

15

Figure 8. Constructs of b/h PIV3 vectored RSV F gene with different intergenic regions. The three constructs, RSV F1* N-N, RSV F2 N-P, and RSV F1 N-P are the same as the RSV F* (N-N), RSV F2, and RSV F1 in Figure 4 respectively. The distance between the N gene start sequence and the N gene translation start codon in RSV F1* N-N is only 10 nucleotides (nts) long. In contrast, this distance is 86 nts long in RSV F2 construct. RSV F1* N-N also uses the N gene start sequence rather than the P gene start sequence as is done 20 in RSV F2 construct.

25

Figure 9. The length and/or nature of the intergenic region downstream of the inserted RSV gene has an effect on virus replication. (A) Western blot analysis of RSV F protein expression in chimeric viruses. Blots were probed with monoclonal antibodies against the RSV F protein. F1 protein levels expressed by RSV F1 construct and measured at 24 and 48 hours post-infection were close to the levels observed for RSV F2 construct, but much higher than those of RSV F1* N-N construct. (B) is multicycle growth curves comparing the kinetics of virus replication of RSV F1, RSV F1*N-N and RSV F2 constructs in Vero cells at an MOI of 0.1. Virus titers for each time point harvest were determined by 30 plaque assays, which were performed by immunostaining with RSV polyclonal antisera for quantification after 5 days of incubation.

Figure 10. Constructs of trivalent b/h PIV3 vectored RSV F and hMPV F. Two virus genomes, each comprising a chimeric b/h PIV3 vector and a first heterologous sequences derived from a metapneumovirus F gene and a second heterologous sequence derived from respiratory syncytial virus F gene, are shown here. Virus with either of the constructs has been amplified in Vero cells. The engineered virus as described can be used as a trivalent vaccine against the parainfluenza virus infection, metapneumovirus infection and the respiratory syncytial virus infection.

Figure 11. A construct harboring two RSV F genes. This construct can be used to determine virus growth kinetics, for RSV F protein production, and replication and immunogenicity in hamsters.

Figure 12. The chimeric b/h PIV3 vectored hMPV F constructs. The F gene of human metapneumovirus (hMPV) was inserted in position 1 or position 2 of the b/h PIV3 genome. The hMPV F gene cassette harbored the bPIV3 N-P intergenic region.

Figure 13. Immunoprecipitation and replication assays of b/h PIV3 vectored hMPV F gene (at position 2). (A) shows the immunoprecipitation of hMPV F protein using guinea pig or human anti-hMPV antiserum. A specific band migrating at approximately 80 kDa was observed in the lysates of b/h PIV3 vectored hMPV F2. This size corresponds to the F precursor protein, F₀. Non-specific bands of different sizes were also observed in the b/h PIV3 and mock control lanes. (B) shows growth curves that were performed to determine the kinetics of virus replication of b/h PIV3/hMPV F2 and compare it to those observed for b/h PIV3 and b/h PIV3/RSV F2 in Vero cells at an MOI of 0.1. (C) is growth curves that were performed to determine the kinetics of virus replication of b/h PIV3/hMPV F1 and compare it to those observed for b/h PIV3/hMPV F2 and b/h PIV3 in Vero cells at an MOI of 0.01.

Figure 14. A chimeric b/h PIV3 vectored soluble RSV F gene construct. This construct comprises a single copy of the soluble RSV F gene, a version of the RSV F gene

lacking the transmembrane and cytosolic domains. The advantage of this construct would be the inability of the soluble RSV F to be incorporated into the virion genome.

5

Figure 15. Immunostained b/h PIV3/hMPV F1 and b/h PIV3/hMPV F2. (A) the b/h PIV3/hMPV F1 virus were diluted and used to infect subconfluent Vero cells. Infected cells were overlayed with optiMEM media containing gentamycin and incubated at 35°C for 5 days. Cells were fixed and immunostained with guinea pig anti-hMPV sera. Expression of hMPV F is visualized by specific color development in the presence of the AEC substrate system. (B) the b/h PIV3/hMPV F2 virus were diluted and used to infect Vero cells. Infected cells were overlayed with 1% methyl cellulose in EMEM/L-15 medium (JRH Biosciences; Lenexa, KS). Cells were incubated, fixed and then immunostained with anti-hMPV guinea pig sera. The anti-hMPV guinea pig serum is specific for hMPV 001 protein.

10

15

Figure 16. Virion fractionation of b/h PIV3 vectored RSV genes on sucrose gradients. These series experiments investigate whether the RSV proteins were incorporated into the b/h PIV3 virion. (A) shows control gradient of free RSV F (generated in baculovirus and C-terminally truncated). Majority of free RSV F was present in fractions 3, 4, 5, and 6. (B) shows that the biggest concentration of RSV virions was observed in fractions 10, 11 and 12. The RSV fractions were probed with RSV polyclonal antiserum as well as RSV F MAb. The fractions that contained the greatest amounts of RSV virions also showed the strongest signal for RSV F, suggesting that the RSV F protein co-migrated and associated with RSV virion. The last figure on (B) also shows that the fractions 10, 11 and 12 displayed the highest virus titer by plaque assay. (C) The b/h PIV3 virions may be more pleiomorphic and thus the spread of the peak fractions containing b/h PIV3 virions was more broad. (D) Sucrose gradient fractions of b/h PIV3/RSV F2 were analyzed with both a PIV polyclonal antiserum and an RSV F MAb. The fractions containing most of the virions were fractions 11, 12, 13 and 14, as shown by Western using the PIV3 antiserum. Correspondingly, these were also the fractions that displayed the highest amounts of RSV F protein. Some free RSV F was also present in fractions 5 and 6. Fractions 11, 12, 13 and 14 displayed the peak virus titers. (E) The fractions containing the most virions of b/h

PIV3/RSV G2 (9, 10, 11 and 12) also showed the strongest signal for RSV G protein. Again, these were the fractions with the highest virus titers.

5

5. DESCRIPTION OF THE INVENTION

The present invention relates to recombinant parainfluenza cDNA and RNA constructs, including but not limited to, recombinant bovine and human PIV cDNA and RNA constructs, that may be used to express heterologous or non-native sequences.

In accordance with the present invention, a recombinant virus is one derived from a
10 bovine parainfluenza virus or a human parainfluenza virus that is encoded by endogenous or native genomic sequences or non-native genomic sequences. In accordance with the invention, a non-native sequence is one that is different from the native or endogenous genomic sequence due to one or more mutations, including, but not limited to, point mutations, rearrangements, insertions, deletions, etc. to the genomic sequence that may or
15 may not result in a phenotypic change.

In accordance with the present invention, a chimeric virus of the invention is a recombinant bPIV or hPIV which further comprises one or more heterologous nucleotide sequences. In accordance with the invention, a chimeric virus may be encoded by a nucleotide sequence in which heterologous nucleotide sequences have been added to the
20 genome or in which nucleotide sequences have been replaced with heterologous nucleotide sequences. These recombinant and chimeric viruses and expression products may be used as vaccines suitable for administration to humans or animals. For example, the chimeric viruses of the invention may be used in vaccine formulations to confer protection against pneumovirus, respiratory syncytial virus, parainfluenza virus, or influenza virus infection.
25

In one embodiment, the invention relates to PIV cDNA and RNA constructs that are derived from human or bovine PIV variants and are engineered to express one, two, or three heterologous sequences, preferably heterologous genes encoding foreign antigens and other products from a variety of pathogens, cellular genes, tumor antigens, and viruses. In particular, the heterologous sequences are derived from morbillivirus or a negative strand
30 RNA virus, including but not limited to, influenza virus, respiratory syncytial virus (RSV), mammalian metapneumovirus (e.g., human metapneumovirus variants A1, A2, B1, and B2),

and avian pneumovirus subgroups A, B, C and D. The mammalian MPVs can be a variant A1, A2, B1 or B2 mammalian MPV. However, the mammalian MPVs of the present invention may encompass additional variants of MPV yet to be identified, and are not limited to variants A1, A2, B1, or B2. In another embodiment of the invention, the heterologous sequences are non-native PIV sequences, including mutated PIV sequences. In some embodiments, the heterologous sequences are derived from the same or from different viruses.

In a specific embodiment, the virus of the invention is a recombinant PIV comprising heterologous nucleotide sequences derived from human metapneumovirus or avian pneumovirus. The heterologous sequences to be inserted into the PIV genome include, but are not limited to, the sequences encoding the F, G and HN genes of human metapneumovirus variants A1, A2, B1 or B2, sequences encoding the F, G and HN genes of avian pneumovirus type A, B, C or D, and immunogenic and/or antigenic fragments thereof.

In certain embodiments, the heterologous nucleotide sequence is added to the viral genome. In alternative embodiments, the heterologous nucleotide sequence is exchanged for an endogenous nucleotide sequence. The heterologous nucleotide sequence may be added or inserted at various positions of the PIV genome, e.g., at position 1, 2, 3, 4, 5, or 6. In a preferred embodiment, the heterologous nucleotide sequence is added or inserted at position

1. In another preferred embodiment, the heterologous nucleotide sequence is added or inserted at position 2. In even another preferred embodiment, the heterologous nucleotide sequence is added or inserted at position 3. Inserting or adding heterologous nucleotide sequences at the lower-numbered positions of the virus generally results in stronger expression of the heterologous nucleotide sequence compared to insertion at higher-

numbered positions. This is due to a transcriptional gradient that occurs across the genome of the virus. However, virus replication efficiency must also be considered. For example, in the b/h PIV3 chimeric virus of the invention, insertion of a heterologous gene at position 1 delays replication kinetics *in vitro* and to a lesser degree also *in vivo* (see section 8, example 3 and Figure 5 as well as section 26, example 21). Therefore, inserting heterologous nucleotide sequences at lower-numbered positions is the preferred embodiment of the invention if strong expression of the heterologous nucleotide sequence is desired. Most

preferably, a heterologous sequence is inserted at position 2 of a b/h PIV3 genome if strong expression of the heterologous sequence is desired. (See section 5.1.2. *infra* and section 8, example 3).

5 In some other embodiments, the recombinant or chimeric PIV genome is engineered such that the intergenic region between the end of the coding sequence of the heterologous gene and the start of the coding sequence of the downstream gene is altered. In yet some other embodiments, the virus of the invention comprises a recombinant or chimeric PIV genome engineered such that the heterologous nucleotide sequence is inserted at a position
10 selected from the group consisting of positions 1, 2, 3, 4, 5, and 6, and the intergenic region between the heterologous nucleotide sequence and the next downstream gene is altered. Appropriate assays may be used to determine the best mode of insertion (*i.e.*, which position to insert, and the length of the intergenic region) to achieve appropriate levels of gene expression and viral growth characteristics. For detail, *see* Section 5.1.2., *infra*.

15 In certain embodiments, the chimeric virus of the invention contains two different heterologous nucleotide sequences. The different heterologous nucleotide sequences may be inserted at various positions of the PIV genome. In a preferred embodiment, one heterologous nucleotide sequence is inserted at position 1 and another heterologous nucleotide sequence is added or inserted at position 2 or 3. In other embodiments of the
20 invention, additional heterologous nucleotide sequences are inserted at higher-numbered positions of the PIV genome. In accordance with the present invention, the position of the heterologous sequence refers to the order in which the sequences are transcribed from the viral genome, *e.g.*, a heterologous sequence at position 1 is the first gene sequence to be transcribed from the genome.

25 In certain embodiments of the invention, the heterologous nucleotide sequence to be inserted into the genome of the virus of the invention is derived from a negative strand RNA virus, including but not limited to, influenza virus, parainfluenza virus, respiratory syncytial virus, mammalian metapneumovirus, and avian pneumovirus. In a specific embodiment of the invention, the heterologous nucleotide sequence is derived from a human
30 metapneumovirus. In another specific embodiment, the heterologous nucleotide sequence is

derived from an avian pneumovirus. More specifically, the heterologous nucleotide sequence of the invention encodes a F, G or SH gene or a portion thereof of a human or avian metapneumovirus. In specific embodiments, a heterologous nucleotide sequences can be any 5 one of SEQ ID NO:1 through SEQ ID NO:5, SEQ ID NO:14, and SEQ ID NO:15 (see Table 16). In certain specific embodiments, the nucleotide sequence encodes a protein of any one of SEQ ID NO:6 through SEQ ID NO:13, SEQ ID NO:16, and SEQ ID NO:17 (see Table 16). In certain specific embodiments, the nucleotide sequence encodes a protein of any one of SEQ ID NO: 314 through 389.

10 In specific embodiments of the invention, a heterologous nucleotide sequence of the invention is derived from a type A avian pneumovirus. In other specific embodiments of the invention, a heterologous nucleotide sequence of the invention is derived from a type B avian pneumovirus. In even other specific embodiments of the invention, a heterologous nucleotide sequence of the invention is derived from a type C avian pneumovirus.

15 Phylogenetic analyses show that type A and type B are more closely related to each other than they are to type C (Seal, 2000, Animal Health Res. Rev. 1(1):67-72). Type A and type B are found in Europe whereas type C was first isolated in the U.S.

In another embodiment of the invention, the heterologous nucleotide sequence encodes a chimeric polypeptide, wherein the ectodomain contains antigenic sequences 20 derived from a virus other than the strain of PIV from which the vector backbone is derived, and the trans membrane and luminal domains are derived from PIV sequences. The resulting chimeric virus would impart antigenicity of the negative strand RNA virus of choice and would have an attenuated phenotype.

25 In a specific embodiment of the invention, the heterologous nucleotide sequence encodes a chimeric F protein. Particularly, the ectodomain of the chimeric F protein is the ectodomain of a metapneumovirus, so that a human metapneumovirus or avian pneumovirus, and the transmembrane domain as well as the luminal domain are the transmembrane and luminal domains of a parainfluenza virus, such as a human or a bovine parainfluenza virus. While not bound by any theory, insertion of a chimeric F protein may further attenuate the 30 virus in an intended host but retain the antigenicity of the F protein attributed by its ectodomain.

The chimeric viruses of the invention may be used in vaccine formulations to confer protection against various infections, including but not limited to, pneumovirus infection, respiratory syncytial virus infection, parainfluenza virus infection, influenza virus infection, or a combination thereof. The present invention provides vaccine preparations comprising chimeric PIV expressing one or more heterologous antigenic sequences, including bivalent and trivalent vaccines. The bivalent and trivalent vaccines of the invention may be administered in the form of one PIV vector expressing each heterologous antigenic sequences or two or more PIV vectors each encoding different heterologous antigenic sequences.

5 Preferably, the heterologous antigenic sequences are derived from a negative strand RNA virus, including but not limited to, influenza virus, parainfluenza virus, respiratory syncytial virus (RSV), mammalian metapneumovirus (e.g., human metapneumovirus) and avian pneumovirus. Thus, the chimeric virions of the present invention may be engineered to create, e.g., anti-human influenza vaccine, anti-human parainfluenza vaccine, anti-human

10 RSV vaccine, and anti-human metapneumovirus vaccine. Preferably, the vaccine preparation of the invention comprises attenuated chimeric viruses that are viable and infectious. The vaccine preparation of the invention can be administered alone or in combination with other vaccines or other prophylactic or therapeutic agents.

15 The present invention also relates to the use of viral vectors and chimeric viruses to formulate vaccines against a broad range of viruses and/or antigens including tumor antigens. The viral vectors and chimeric viruses of the present invention may be used to modulate a subject's immune system by stimulating a humoral immune response, a cellular immune response or by stimulating tolerance to an antigen. As used herein, a subject refers to a human, a primate, a horse, a cow, a sheep, a pig, a goat, a dog, a cat, a rodent and a member

20 of avian species. When delivering tumor antigens, the invention may be used to treat subjects having disease amenable to immune response mediated rejection, such as non-solid tumors or solid tumors of small size. It is also contemplated that delivery of tumor antigens by the viral vectors and chimeric viruses described herein will be useful for treatment subsequent to removal of large solid tumors. The invention may also be used to treat

25 subjects who are suspected of having cancer.

30

The invention may be divided into the following stages solely for the purpose of description and not by way of limitation: (a) construction of recombinant cDNA and RNA templates; (b) expression of heterologous gene products using recombinant cDNA and RNA templates; and ©) rescue of the heterologous genes in recombinant virus particles.

5.1. CONSTRUCTION OF THE RECOMBINANT cDNA AND RNA

The present invention encompasses recombinant or chimeric viruses encoded by viral vectors derived from the genomes of parainfluenza virus, including both bovine 10 parainfluenza virus and mammalian parainfluenza virus. In accordance with the present invention, a recombinant virus is one derived from a bovine parainfluenza virus or a mammalian parainfluenza virus that is encoded by endogenous or native genomic sequences or non-native genomic sequences. In accordance with the invention, a non-native sequence is one that is different from the native or endogenous genomic sequence due to one or more 15 mutations, including, but not limited to, point mutations, rearrangements, insertions, deletions etc. to the genomic sequence that may or may not result a phenotypic change. The recombinant viruses of the invention encompass those viruses encoded by viral vectors derived from the genomes of parainfluenza virus, including both bovine and mammalian 20 parainfluenza virus, and may or may not, include nucleic acids that are non-native to the viral genome. In accordance with the present invention, a viral vector which is derived from the genome of a parainfluenza virus is one that contains a nucleic acid sequence that encodes at least a part of one ORF of a parainfluenza virus.

The present invention also encompasses recombinant viruses comprising a viral vector derived from a bovine and/or mammalian PIV genome which contains sequences 25 which result in a virus having a phenotype more suitable for use in vaccine formulations, e.g., attenuated phenotype or enhanced antigenicity. The mutations and modifications can be in coding regions, in intergenic regions and in the leader and trailer sequences of the virus.

In accordance with the present invention, the viral vectors of the invention are derived from the genome of a mammalian parainfluenza virus, in particular a human parainfluenza 30 virus (hPIV). In particular embodiments of the invention, the viral vector is derived from the genome of a human parainfluenza virus type 3. In accordance with the present invention,

these viral vectors may or may not include nucleic acids that are non-native to the viral genome.

In accordance with the present invention, the viral vectors of the inventions are
5 derived from the genome of a bovine parainfluenza virus (bPIV). In particular embodiments of the invention, the viral vector is derived from the genome of bovine parainfluenza virus type 3. In accordance to the present invention, these viral vectors may or may include nucleic acids that are non-native to the viral genome.

In accordance with the invention, a chimeric virus is a recombinant bPIV or hPIV
10 which further comprises a heterologous nucleotide sequence. In accordance with the invention, a chimeric virus may be encoded by a nucleotide sequence in which heterologous nucleotide sequence have been added to the genome or in which endogenous or native nucleotide sequence have been replaced with heterologous nucleotide sequence. In accordance with the invention, the chimeric viruses are encoded by the viral vectors of the
15 invention which further comprise a heterologous nucleotide sequence. In accordance with the present invention, a chimeric virus is encoded by a viral vector that may or may not include nucleic acids that are non-native to the viral genome. In accordance with the invention, a chimeric virus is encoded by a viral vector to which heterologous nucleotide sequences have been added, inserted or substituted for native or non-native sequences.

20 A chimeric virus may be of particular use for the generation of recombinant vaccines protecting against two or more viruses (Tao et al., J. Virol. 72, 2955-2961; Durbin et al., 2000, J. Virol. 74, 6821-6831; Skiadopoulos et al., 1998, J. Virol. 72, 1762-1768 (1998); Teng et al., 2000, J. Virol. 74, 9317-9321). For example, it can be envisaged that a hPIV or bPIV virus vector expressing one or more proteins of another negative strand RNA virus,
25 e.g., MPV, or a RSV vector expressing one or more proteins of MPV will protect individuals vaccinated with such vector against both virus infections. A similar approach can be envisaged for other paramyxoviruses. Attenuated and replication-defective viruses may be of use for vaccination purposes with live vaccines as has been suggested for other viruses. (See, PCT WO 02/057302, at pp. 6 and 23, incorporated by reference herein).

30 In accordance with the present invention the heterologous to be incorporated into the viral vectors encoding the recombinant or chimeric viruses of the invention include

sequences obtained or derived from different strains of metapneumovirus, strains of avian pneumovirus, and other negative strand RNA viruses, including, but not limited to, RSV, PIV, influenza virus and other viruses, including morbillivirus.

- 5 In certain embodiments of the invention, the chimeric or recombinant viruses of the invention are encoded by viral vectors derived from viral genomes wherein one or more sequences, intergenic regions, termini sequences, or portions or entire ORF have been substituted with a heterologous or non-native sequence. In certain embodiments of the invention, the chimeric viruses of the invention are encoded by viral vectors derived from
10 viral genomes wherein one or more heterologous sequences have been added to the vector.

A specific embodiment of the present invention is a chimeric virus comprising a backbone encoded by nucleotide sequences derived from a parainfluenza virus genome. In a preferred embodiment, the PIV genome is derived from bovine PIV, such as the Kansas strain of bPIV3, or from human PIV. In a preferred embodiment, the PIV genome is derived
15 from the Kansas strain of bPIV3, in which bovine parainfluenza virus nucleotide sequences have been substituted with heterologous sequences or in which heterologous sequences have been added to the complete bPIV genome. A further specific embodiment of the present invention is a chimeric virus comprising a backbone encoded by nucleotide sequences derived from human parainfluenza virus type 3 genome, in which human parainfluenza virus
20 nucleotide sequences have been substituted with heterologous sequences or in which heterologous sequences have been added to the complete hPIV genome. An additional specific embodiment of the present invention is a chimeric virus comprising a backbone encoded by nucleotide sequences derived from bovine parainfluenza virus genome, such as the Kansas strain of bPIV3, in which (a) the bovine parainfluenza virus F gene and HN gene
25 have been substituted with the F gene and the HN gene of the human parainfluenza virus (bPIV/hPIV), and in which (b) heterologous sequences have been added to the complete bPIV genome.

The present invention also encompasses chimeric viruses comprising a backbone encoded by nucleotide sequences derived from the bPIV, the hPIV, or the bPIV/hPIV
30 genome containing mutations or modifications, in addition to heterologous sequences, that result in a chimeric virus having a phenotype more suitable for use in vaccine formulations,

e.g., attenuated phenotype or enhanced antigenicity. In accordance with this particular embodiment of the invention, a heterologous sequence in the context of a bovine PIV3 backbone may be any sequence heterologous to bPIV3.

- 5 Another specific embodiment of the present invention is a chimeric virus comprising a backbone encoded by nucleotide sequences derived from human PIV 1, 2, or 3 in which hPIV nucleotide sequences have been substituted with heterologous sequences or in which heterologous sequences have been added to the complete hPIV genome, with the proviso that the resulting chimeric virus is not a chimeric hPIV3 in which the hemagglutinin-
10 neuraminidase and fusion glycoproteins have been replaced by those of hPIV1. The present invention also encompasses chimeric viruses, comprising a backbone encoded by nucleotide sequences derived from a hPIV genome, containing mutations or modifications, in addition to heterologous sequences, that result in a chimeric virus having a phenotype more suitable for use in vaccine formulations, e.g., attenuated phenotype or enhanced antigenicity.
15 Heterologous gene coding sequences flanked by the complement of the viral polymerase binding site/promoter, e.g., the complement of 3'-PIV virus terminus of the present invention, or the complements of both the 3'- and 5'-PIV virus termini may be constructed using techniques known in the art. The resulting RNA templates may be of the negative-polarity and can contain appropriate terminal sequences that enable the viral RNA-
20 synthesizing apparatus to recognize the template. Alternatively, positive-polarity RNA templates, that contain appropriate terminal sequences which enable the viral RNA-synthesizing apparatus to recognize the template, may also be used. Recombinant DNA molecules containing these hybrid sequences can be cloned and transcribed by a DNA-directed RNA polymerase, such as bacteriophage T7 polymerase, T3 polymerase, the SP6
25 polymerase or a eukaryotic polymerase such as polymerase I and the like, for the *in vitro* or *in vivo* production of recombinant RNA templates that possess the appropriate viral sequences and that allow for viral polymerase recognition and activity.

In one embodiment, the PIV vector of the invention expresses one, two, or three heterologous sequences, encoding antigenic polypeptides and peptides. In some 30 embodiments, the heterologous sequences are derived from the same virus or from different viruses. In certain embodiments, more than one copy of the same heterologous nucleotide

sequences are inserted in the genome of a bovine parainfluenza virus, human parainfluenza virus, or bPIV/hPIV chimeric vector. In a preferred embodiment, two copies of the same heterologous nucleotide sequences are inserted to the genome of the virus of the invention.

- 5 In some embodiments, the heterologous nucleotide sequence is derived from a metapneumovirus, such as human metapneumovirus or an avian pneumovirus. In specific embodiments, the heterologous nucleotide sequence derived from a metapneumovirus is a F gene of the metapneumovirus. In other specific embodiments, the heterologous nucleotide sequence derived from a metapneumovirus is a G gene of the metapneumovirus. In some
10 other embodiments, the heterologous nucleotide sequence is derived from a respiratory syncytial virus. In specific embodiments, the heterologous nucleotide sequence derived from respiratory syncytial virus is a F gene of the respiratory syncytial virus. In other specific embodiments, the heterologous nucleotide sequence derived from respiratory syncytial virus is a G gene of the respiratory syncytial virus. When one or more heterologous nucleotide
15 sequences are inserted, the position of the insertion and the length of the intergenic region of each inserted copy can be manipulated and determined by different assays according to section 5.1.2. *infra*.

- In certain embodiments, rescue of the chimeric virus or expression products may be achieved by reverse genetics in host cell systems where the host cells are transfected with
20 chimeric cDNA or RNA constructs. The RNA templates of the present invention are prepared by transcription of appropriate DNA sequences with a DNA-directed RNA polymerase. The RNA templates of the present invention may be prepared either *in vitro* or *in vivo* by transcription of appropriate DNA sequences using a DNA-directed RNA polymerase such as bacteriophage T7 polymerase, T3 polymerase, the SP6 polymerase, or a
25 eukaryotic polymerase such as polymerase I. In certain embodiments, the RNA templates of the present invention may be prepared either *in vitro* or *in vivo* by transcription of appropriate DNA sequences using a plasmid-based expression system as described in Hoffmann *et al.*, 2000, Proc. Natl. Acad. Sci. USA 97:6108-6113 or the unidirectional RNA polymerase I-polymerase II transcription system as described in Hoffmann and Webster, 2000, J. Gen.
30 Virol. 81:2843-2847. The resulting RNA templates of negative-polarity would contain appropriate terminal sequences that would enable the viral RNA-synthesizing apparatus to

recognize the template. Alternatively, positive-polarity RNA templates that contain appropriate terminal sequences and enable the viral RNA-synthesizing apparatus to recognize the template may also be used. Expression from positive polarity RNA templates may be
5 achieved by transfection of plasmids having promoters that are recognized by the DNA-dependent RNA polymerase. For example, plasmid DNA, encoding positive RNA templates under the control of a T7 promoter, can be used in combination with the vaccinia virus or fowlpox T7 system.

Bicistronic mRNAs can be constructed to permit internal initiation of translation of
10 viral sequences and to allow for the expression of foreign protein coding sequences from the regular terminal initiation site, or vice versa. Alternatively, a foreign protein may be expressed from an internal transcriptional unit in which the transcriptional unit has an initiation site and polyadenylation site. In another embodiment, the foreign gene is inserted into a PIV gene such that the resulting expressed protein is a fusion protein.

15 In certain embodiments, the invention relates to trivalent vaccines comprising a virus of the invention. In specific embodiments, the virus used for a trivalent vaccine is a chimeric bovine parainfluenza type 3/human parainfluenza type 3 virus containing a first heterologous nucleotide sequence derived from a metapneumovirus, such as human metapneumovirus or avian pneumovirus, and a second heterologous nucleotide sequence derived from respiratory
20 syncytial virus. In an exemplary embodiment, such a trivalent vaccine would be specific to (a) the gene products of the F gene and the HN gene of the human parainfluenza virus; (b) the protein encoded by the heterologous nucleotide sequence derived from a metapneumovirus; and (c) the protein encoded by the heterologous nucleotide sequence derived from a respiratory syncytial virus. In a specific embodiment, the first heterologous nucleotide sequence is the F gene of the respiratory syncytial virus and is inserted in position
25 1, and the second heterologous nucleotide sequence is the F gene of the human metapneumovirus and is inserted in position 3. Many more combinations are encompassed by the present invention and some are shown by way of example in Table 1. For other combinations the F or G gene of an avian pneumovirus could be used. Further, nucleotide sequences encoding chimeric F proteins could be used (see *supra*). In some less preferred
30

embodiments, the heterologous nucleotide sequence can be inserted at higher-numbered positions of the viral genome.

5

Table 1. Exemplary arrangements of heterologous nucleotide sequences in the viruses used for trivalent vaccines.

	<u>Combination</u>	<u>Position 1</u>	<u>Position 2</u>	<u>Position 3</u>
	1	F-gene of hMPV	F-gene of RSV	-
10	2	F-gene of RSV	F-gene of hMPV	-
	3	-	F-gene of hMPV	F-gene of RSV
	4	-	F-gene of RSV	F-gene of hMPV
	5	F-gene of hMPV	-	F-gene of RSV
	6	F-gene of RSV	-	F-gene of hMPV
	7	G-gene of hMPV	G-gene of RSV	-
	8	G-gene of RSV	G-gene of hMPV	-
	9	-	G-gene of hMPV	G-gene of RSV
	10	-	G-gene of RSV	G-gene of hMPV
15	11	G-gene of hMPV	-	G-gene of RSV
	12	G-gene of RSV	-	G-gene of hMPV
	13	F-gene of hMPV	G-gene of RSV	-
	14	G-gene of RSV	F-gene of hMPV	-
	15	-	F-gene of hMPV	G-gene of RSV
	16	-	G-gene of RSV	F-gene of hMPV
	17	F-gene of hMPV	-	G-gene of RSV
	18	G-gene of RSV	-	F-gene of hMPV
	19	G-gene of hMPV	F-gene of RSV	-
20	20	F-gene of RSV	G-gene of hMPV	-
	21	-	G-gene of hMPV	F-gene of RSV
	22	-	F-gene of RSV	G-gene of hMPV
	23	G-gene of hMPV	-	F-gene of RSV
	24	F-gene of RSV	-	G-gene of hMPV

In some other embodiments, the intergenic region between a heterologous sequence and the start of the coding sequence of the downstream gene can be altered. For example, each gene listed on Table 1 may have a desirable length of the intergenic region. In an exemplary embodiment, a trivalent vaccine comprises a b/h PIV3 vector with a F gene of respiratory syncytial virus inserted at position 1, an altered intergenic region of 177 nucleotides (originally 75 nucleotides to the downstream N gene start codon AUG), and a F gene of human metapneumovirus inserted at position 3 with its natural intergenic region.

Many more combinations are encompassed by the present invention, as each insertion of a heterologous nucleotide sequence may be manipulated according to section 5.1.2., *infra*.

In a broader embodiment, the expression products and chimeric virions of the present
5 invention may be engineered to create vaccines against a broad range of pathogens, including viral antigens, tumor antigens and auto antigens involved in autoimmune disorders. One way to achieve this goal involves modifying existing PIV genes to contain foreign sequences in their respective external domains. Where the heterologous sequences are epitopes or
10 antigens of pathogens, these chimeric viruses may be used to induce a protective immune response against the disease agent from which these determinants are derived.

One approach for constructing these hybrid molecules is to insert the heterologous nucleotide sequence into a DNA complement of a PIV genome, *e.g.*, a hPIV, a bPIV, or a bPIV/hPIV, so that the heterologous sequence is flanked by the viral sequences required for viral polymerase activity; *i.e.*, the viral polymerase binding site/promoter, hereinafter referred
15 to as the viral polymerase binding site, and a polyadenylation site. In a preferred embodiment, the heterologous coding sequence is flanked by the viral sequences that comprise the replication promoters of the 5' and 3' termini, the gene start and gene end sequences, and the packaging signals that are found in the 5' and/or the 3' termini. In an alternative approach, oligonucleotides encoding the viral polymerase binding site, *e.g.*, the
20 complement of the 3'-terminus or both termini of the virus genomic segment can be ligated to the heterologous coding sequence to construct the hybrid molecule. The placement of a foreign gene or segment of a foreign gene within a target sequence was formerly dictated by the presence of appropriate restriction enzyme sites within the target sequence. However, recent advances in molecular biology have lessened this problem greatly. Restriction enzyme
25 sites can readily be placed anywhere within a target sequence through the use of site-directed mutagenesis (*e.g.*, see, for example, the techniques described by Kunkel, 1985, Proc. Natl. Acad. Sci. U.S.A. 82;488). Variations in polymerase chain reaction (PCR) technology, described *infra*, also allow for the specific insertion of sequences (*i.e.*, restriction enzyme sites) and also allow for the facile construction of hybrid molecules. Alternatively, PCR
30 reactions could be used to prepare recombinant templates without the need of cloning. For example, PCR reactions could be used to prepare double-stranded DNA molecules

containing a DNA-directed RNA polymerase promoter (e.g., bacteriophage T3, T7 or SP6) and the hybrid sequence containing the heterologous gene and the PIV polymerase binding site. RNA templates could then be transcribed directly from this recombinant DNA. In yet 5 another embodiment, the recombinant RNA templates may be prepared by ligating RNAs specifying the negative polarity of the heterologous gene and the viral polymerase binding site using an RNA ligase.

In addition, one or more nucleotides can be added at the 3' end of the HN gene in the untranslated region to adhere to the "Rule of Six" which may be important in successful virus 10 rescue. The "Rule of Six" applies to many paramyxoviruses and requires that the number of nucleotides of an RNA genome be a factor of six to be functional. The addition of nucleotides can be accomplished by techniques known in the art such as using a commercial mutagenesis kits like the QuikChange mutagenesis kit (Stratagene). After addition of the appropriate number of nucleotides, the correct DNA fragment, for example, a DNA fragment 15 of the hPIV3 F and HN gene, can then be isolated upon digestion with the appropriate restriction enzyme and gel purification. Sequence requirements for viral polymerase activity and constructs that may be used in accordance with the invention are described in the subsections below.

Without being bound by theory, several parameters affect the rate of replication of the 20 recombinant virus and the level of expression of the heterologous sequence. In particular, the position of the heterologous sequence in bPIV, hPIV, b/h PIV and the length of the intergenic region that flanks the heterologous sequence determine rate of replication and expression level of the heterologous sequence.

In certain embodiments, the leader and or trailer sequence of the virus are modified 25 relative to the wild type virus. In certain more specific embodiments, the lengths of the leader and/or trailer are altered. In other embodiments, the sequence(s) of the leader and/or trailer are mutated relative to the wild type virus.

The production of a recombinant virus of the invention relies on the replication of a 30 partial or full-length copy of the negative sense viral RNA (vRNA) genome or a complementary copy thereof (cRNA). This vRNA or cRNA can be isolated from infectious virus, produced upon in-vitro transcription, or produced in cells upon transfection of nucleic

acids. Second, the production of recombinant negative strand virus relies on a functional polymerase complex. Typically, the polymerase complex of pneumoviruses consists of N, P, L and possibly M2 proteins, but is not necessarily limited thereto.

5 Polymerase complexes or components thereof can be isolated from virus particles, isolated from cells expressing one or more of the components, or produced upon transfection of specific expression vectors.

Infectious copies of MPV can be obtained when the above mentioned vRNA, cRNA, or vectors expressing these RNAs are replicated by the above mentioned polymerase
10 complex 16 (Schnell *et al.*, 1994, EMBO J 13: 4195-4203; Collins *et al.*, 1995, PNAS 92: 11563-11567; Hoffmann *et al.*, 2000, PNAS 97: 6108-6113; Bridgen *et al.*, 1996, PNAS 93: 15400-15404; Palese *et al.*, 1996, PNAS 93: 11354-11358; Peeters *et al.*, 1999, J.Virol. 73: 5001-5009; Durbin *et al.*, 1997, Virology 235: 323-332).

The invention provides a host cell comprising a nucleic acid or a vector according to
15 the invention. Plasmid or viral vectors containing the polymerase components of PIV (presumably N, P, L and M2, but not necessarily limited thereto) are generated in prokaryotic cells for the expression of the components in relevant cell types (bacteria, insect cells, eukaryotic cells). Plasmid or viral vectors containing full-length or partial copies of the PIV genome will be generated in prokaryotic cells for the expression of viral nucleic acids *in vitro*
20 or *in vivo*. The latter vectors may contain other viral sequences for the generation of chimeric viruses or chimeric virus proteins, may lack parts of the viral genome for the generation of replication defective virus, and may contain mutations, deletions or insertions for the generation of attenuated viruses.

Infectious copies of PIV (being wild type, attenuated, replication-defective or
25 chimeric) can be produced upon co-expression of the polymerase components according to the state-of-the-art technologies described above.

In addition, eukaryotic cells, transiently or stably expressing one or more full-length or partial PIV proteins can be used. Such cells can be made by transfection (proteins or nucleic acid vectors), infection (viral vectors) or transduction (viral vectors) and may be
30 useful for complementation of mentioned wild type, attenuated, replication-defective or chimeric viruses.

... HETEROLOGOUS GENE SEQUENCES TO BE INSERTED

The present invention encompass engineering recombinant bovine or human parainfluenza viruses to express one or more heterologous sequences, wherein the 5 heterologous sequences encode gene products or fragments of gene products that are preferably antigenic and/or immunogenic. As used herein, the term "antigenic" refers to the ability of a molecule to bind antibody or MHC molecules. The term "immunogenic" refers to the ability of a molecule to generate immune response in a host.

In a preferred embodiment, the heterologous nucleotide sequence to be inserted is 10 derived from a negative strand RNA virus, including but not limited to, influenza virus, parainfluenza virus, respiratory syncytial virus, mammalian metapneumovirus (*e.g.*, human metapneumovirus) and avian pneumovirus. In a preferred embodiment, the heterologous sequence to be inserted includes, but is not limited to, a sequence that encodes a F or HN 15 gene of human PIV, a F gene of RSV, a HA gene of influenza virus type A, B, or C, a F gene of human MPV, a F gene of avian pneumovirus, or an immunogenic and/or antigenic fragment thereof.

In some embodiments, the heterologous nucleotide sequence to be inserted is derived 20 from a human metapneumovirus and/or an avian pneumovirus. In certain embodiments, the heterologous nucleotide sequence to be inserted is derived from (a) a human metapneumovirus and a respiratory syncytial virus; and/or (b) an avian pneumovirus and a 25 respiratory syncytial virus.

In certain preferred embodiments of the invention, the heterologous nucleotide sequence to be inserted is derived from a F gene from a human metapneumovirus and/or an avian pneumovirus. In certain embodiments, the F gene is derived from (a) a human 25 metapneumovirus and a respiratory syncytial virus; and/or (b) an avian pneumovirus and a respiratory syncytial virus.

In certain embodiments of the invention, the heterologous nucleotide sequence to be inserted is a G gene derived from a human metapneumovirus and/or an avian pneumovirus. 30 In certain embodiments, the G gene is derived from (a) a human metapneumovirus and a respiratory syncytial virus; and/or (b) an avian pneumovirus and a respiratory syncytial virus.

In certain embodiments, any combination of different F genes and/or different G genes derived from human metapneumovirus, avian pneumovirus, and respiratory syncytial virus can be inserted into the virus of the invention with the proviso that in all embodiments at least one heterologous sequence derived from either human metapneumovirus or avian pneumovirus is present in the recombinant parainfluenza virus of the invention.

In certain embodiments, the nucleotide sequence to be inserted is a nucleotide sequence encoding a F protein derived from a human metapneumovirus. In certain other embodiments, the nucleotide sequence to be inserted is a nucleotide sequence encoding a G protein derived from a human metapneumovirus. In yet other embodiments, the nucleotide sequence to be inserted is a nucleotide sequence encoding a F protein derived from an avian pneumovirus. In yet other embodiments, the nucleotide sequence to be inserted is a nucleotide sequence encoding a G protein derived from an avian pneumovirus. With the proviso that in all embodiments of the invention at least one heterologous nucleotide sequence is derived from a metapneumovirus, the heterologous nucleotide sequence to be inserted encodes a F protein or a G protein of a respiratory syncytial virus.

In certain embodiments, the nucleotide sequence to be inserted encodes a chimeric F protein or a chimeric G protein. A chimeric F protein comprises parts of F proteins from different viruses, such as a human metapneumovirus, avian pneumovirus and/or respiratory syncytial virus. A chimeric G protein comprises parts of G proteins from different viruses, such as a human metapneumovirus, avian pneumovirus and/or respiratory syncytial virus. In a specific embodiment, the F protein comprises an ectodomain of a F protein of a metapneumovirus, a transmembrane domain of a F protein of a parainfluenza virus, and luminal domain of a F protein of a parainfluenza virus. In certain embodiments, the nucleic acid to be inserted encodes a F protein, wherein the transmembrane domain of the F protein is deleted so that a soluble F protein is expressed.

In certain specific embodiments, the heterologous nucleotide sequence of the invention is any one of SEQ ID NO:1 through SEQ ID NO:5, SEQ ID NO:14, and SEQ ID NO:15 (see Table 16). In certain specific embodiments, the nucleotide sequence encodes a protein of any one of SEQ ID NO:6 through SEQ ID NO:13, SEQ ID NO:16, and SEQ ID

NO:17 (see Table 16). In certain specific embodiments, the nucleotide sequence encodes a protein of any one of SEQ ID NO. 314 to 389.

For heterologous nucleotide sequences derived from respiratory syncytial virus see,
5 e.g., PCT/US98/20230, which is hereby incorporated by reference in its entirety.

In a preferred embodiment, heterologous gene sequences that can be expressed into the chimeric viruses of the invention include but are not limited to those encoding antigenic epitopes and glycoproteins of viruses, such as influenza glycoproteins, in particular hemagglutinin H5, H7, respiratory syncytial virus epitopes, New Castle Disease virus
10 epitopes, Sendai virus and infectious Laryngotracheitis virus (ILV), that result in respiratory disease. In a most preferred embodiment, the heterologous nucleotide sequences are derived from a metapneumovirus, such as human metapneumovirus and/or avian pneumovirus. In yet another embodiment of the invention, heterologous gene sequences that can be engineered into the chimeric viruses of the invention include, but are not limited to, those
15 encoding viral epitopes and glycoproteins of viruses, such as hepatitis B virus surface antigen, hepatitis A or C virus surface glycoproteins of Epstein Barr virus, glycoproteins of human papilloma virus, simian virus 5 or mumps virus, West Nile virus, Dengue virus, glycoproteins of herpesviruses, VPI of poliovirus, and sequences derived from a human immunodeficiency virus (HIV), preferably type 1 or type 2. In yet another embodiment,
20 heterologous gene sequences that can be engineered into chimeric viruses of the invention include, but are not limited to, those encoding Marek's Disease virus (MDV) epitopes, epitopes of infectious Bursal Disease virus (IBDV), epitopes of Chicken Anemia virus, infectious laryngotracheitis virus (ILV), Avian Influenza virus (AIV), rabies, feline leukemia virus, canine distemper virus, vesicular stomatitis virus, and swinepox virus (see Fields *et al.*
25 (ed.), 1991, FUNDAMENTAL VIROLOGY, Second Edition, Raven Press, New York, incorporated by reference herein in its entirety).

Other heterologous sequences of the present invention include those encoding antigens that are characteristic of autoimmune diseases. These antigens will typically be derived from the cell surface, cytoplasm, nucleus, mitochondria and the like of mammalian
30 tissues, including antigens characteristic of diabetes mellitus, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, pernicious anemia, Addison's disease,

scleroderma, autoimmune atrophic gastritis, juvenile diabetes, and discoid lupus erythematosus.

Antigens that are allergens generally include proteins or glycoproteins, including 5 antigens derived from pollens, dust, molds, spores, dander, insects and foods. In addition, antigens that are characteristic of tumor antigens typically will be derived from the cell surface, cytoplasm, nucleus, organelles and the like of cells of tumor tissue. Examples include antigens characteristic of tumor proteins, including proteins encoded by mutated oncogenes; viral proteins associated with tumors; and glycoproteins. Tumors include, but are 10 not limited to, those derived from the types of cancer: lip, nasopharynx, pharynx and oral cavity, esophagus, stomach, colon, rectum, liver, gall bladder, pancreas, larynx, lung and bronchus, melanoma of skin, breast, cervix, uterine, ovary, bladder, kidney, uterus, brain and other parts of the nervous system, thyroid, prostate, testes, Hodgkin's disease, non-Hodgkin's lymphoma, multiple myeloma and leukemia.

15 In one specific embodiment of the invention, the heterologous sequences are derived from the genome of human immunodeficiency virus (HIV), preferably human immunodeficiency virus-1 or human immunodeficiency virus-2. In another embodiment of the invention, the heterologous coding sequences may be inserted within a PIV gene coding sequence such that a chimeric gene product, that contains the heterologous peptide sequence 20 within the PIV viral protein, is expressed. In such an embodiment of the invention, the heterologous sequences may also be derived from the genome of a human immunodeficiency virus, preferably of human immunodeficiency virus-1 or human immunodeficiency virus-2.

In instances whereby the heterologous sequences are HIV-derived, such sequences may include, but are not limited to sequences derived from the env gene (*i.e.*, sequences 25 encoding all or part of gp160, gp120, and/or gp41), the pol gene (*i.e.*, sequences encoding all or part of reverse transcriptase, endonuclease, protease, and/or integrase), the gag gene (*i.e.*, sequences encoding all or part of p7, p6, p55, p17/18, p24/25) tat, rev, nef, vif, vpu, vpr, and/or vpx.

In another embodiment, heterologous gene sequences that can be engineered into the 30 chimeric viruses include those that encode proteins with immunopotentiating activities. Examples of immunopotentiating proteins include, but are not limited to, cytokines,

interferon type 1, gamma interferon, colony stimulating factors, and interleukin -1, -2, -4, -5, -6, -12.

In addition, other heterologous gene sequences that may be engineered into the
5 chimeric viruses include those encoding antigens derived from bacteria such as bacterial surface glycoproteins, antigens derived from fungi, and antigens derived from a variety of other pathogens and parasites. Examples of heterologous gene sequences derived from bacterial pathogens include, but are not limited to, those encoding antigens derived from species of the following genera: *Salmonella*, *Shigella*, *Chlamydia*, *Helicobacter*, *Yersinia*,
10 *Bordatella*, *Pseudomonas*, *Neisseria*, *Vibrio*, *Haemophilus*, *Mycoplasma*, *Streptomyces*, *Treponema*, *Coxiella*, *Ehrlichia*, *Brucella*, *Streptobacillus*, *Fusospirocheta*, *Spirillum*, *Ureaplasma*, *Spirochaeta*, *Mycoplasma*, *Actinomycetes*, *Borrelia*, *Bacteroides*, *Trichomorpha*, *Branhamella*, *Pasteurella*, *Clostridium*, *Corynebacterium*, *Listeria*, *Bacillus*, *Erysipelothrix*, *Rhodococcus*, *Escherichia*, *Klebsiella*, *Pseudomonas*, *Enterobacter*, *Serratia*,
15 *Staphylococcus*, *Streptococcus*, *Legionella*, *Mycobacterium*, *Proteus*, *Campylobacter*, *Enterococcus*, *Acinetobacter*, *Morganella*, *Moraxella*, *Citrobacter*, *Rickettsia*, *Rochlimeae*, as well as bacterial species such as: *P. aeruginosa*; *E. coli*, *P. cepacia*, *S. epidermidis*, *E. faecalis*, *S. pneumoniae*, *S. aureus*, *N. meningitidis*, *S. pyogenes*, *Pasteurella multocida*, *Treponema pallidum*, and *P. mirabilis*.

20 Examples of heterologous gene sequences derived from pathogenic fungi, include, but are not limited to, those encoding antigens derived from fungi such as *Cryptococcus neoformans*; *Blastomyces dermatitidis*; *Aiellomyces dermatitidis*; *Histoplasma capsulatum*; *Coccidioides immitis*; *Candida species*, including *C. albicans*, *C. tropicalis*, *C. parapsilosis*, *C. guilliermondii* and *C. krusei*, *Aspergillus species*, including *A. fumigatus*, *A. flavus* and *A. niger*, *Rhizopus species*; *Rhizomucor species*; *Cunninghamella species*; *Apophysomyces species*, including *A. saksenaea*, *A. mucor* and *A. absidia*; *Sporothrix schenckii*, *Paracoccidioides brasiliensis*; *Pseudallescheria boydii*, *Torulopsis glabrata*; *Trichophyton species*, *Microsporum species* and *Dermatophytes species*, as well as any other yeast or fungus now known or later identified to be pathogenic.

30 Finally, examples of heterologous gene sequences derived from parasites include, but are not limited to, those encoding antigens derived from members of the Apicomplexa

phylum such as, for example, *Babesia*, *Toxoplasma*, *Plasmodium*, *Eimeria*, *Isospora*, *Atoxoplasma*, *Cystoisospora*, *Hammondia*, *Besniotia*, *Sarcocystis*, *Frenkelia*, *Haemoproteus*, *Leucocytozoon*, *Theileria*, *Perkinsus* and *Gregarina* spp.; *Pneumocystis carinii*; members of 5 the Microspora phylum such as, for example, *Nosema*, *Enterocytozoon*, *Encephalitozoon*, *Septata*, *Mrazekia*, *Amblyospora*, *Ameson*, *Glugea*, *Pleistophora* and *Microsporidium* spp.; and members of the Ascetospora phylum such as, for example, *Haplosporidium* spp., as well as species including *Plasmodium falciparum*, *P. vivax*, *P. ovale*, *P. malaria*; *Toxoplasma gondii*; *Leishmania mexicana*, *L. tropica*, *L. major*, *L. aethiopica*, *L. donovani*, *Trypanosoma cruzi*, *T. brucei*, *Schistosoma mansoni*, *S. haematobium*, *S. japonicum*; *Trichinella spiralis*; *Wuchereria bancrofti*; *Brugia malayli*; *Entamoeba histolytica*; *Enterobius vermicularis*; *Taenia solium*, *T. saginata*, *Trichomonas vaginalis*, *T. hominis*, *T. tenax*; *Giardia lamblia*; *Cryptosporidium parvum*; *Pneumocytis carinii*, *Babesia bovis*, *B. divergens*, *B. microti*, *Isospora belli*, *L. hominis*; *Dientamoeba fragilis*; *Onchocerca volvulus*; *Ascaris lumbricoides*; *Necator americanus*; *Ancylostoma duodenale*; *Strongyloides stercoralis*; *Capillaria philippinensis*; *Angiostrongylus cantonensis*; *Hymenolepis nana*; *Diphyllobothrium latum*; *Echinococcus granulosus*, *E. multilocularis*; *Paragonimus westermani*, *P. caliensis*; *Chlonorchis sinensis*; *Opisthorchis felineas*, *G. Viverini*, *Fasciola hepatica*, *Sarcoptes scabiei*, *Pediculus humanus*; *Phthirus pubis*; and *Dermatobia hominis*.
20 as well as any other parasite now known or later identified to be pathogenic.

5.1.2. METAPNEUMOVIRAL SEQUENCES TO BE INSERTED

proteins of a mammalian MPV. The invention further relates to nucleic acid sequences encoding fusion proteins, wherein the fusion protein contains a protein of a 25 mammalian MPV or a fragment thereof and one or more peptides or proteins that are not derived from mammalian MPV. In a specific embodiment, a fusion protein of the invention contains a protein of a mammalian MPV or a fragment thereof and a peptide tag, such as, but not limited to a polyhistidine tag. The invention further relates to fusion proteins, wherein the fusion protein contains a protein of a mammalian MPV or a fragment thereof and one or 30 more peptides or proteins that are not derived from mammalian MPV. The invention also relates to derivatives of nucleic acids encoding a protein of a mammlian MPV. The

invention also relates to derivatives of proteins of a mammalian MPV. A derivative can be, but is not limited to, mutant forms of the protein, such as, but not limited to, additions, deletions, truncations, substitutions, and inversions. A derivative can further be a chimeric 5 form of the protein of the mammalian MPV, wherein at least one domain of the protein is derived from a different protein. A derivative can also be a form of a protein of a mammalian MPV that is covalently or non-covalently linked to another molecule, such as, e.g., a drug.

The viral isolate termed NL/1/00 (also 00-1) is a mammalian MPV of variant A1 and 10 its genomic sequence is shown in SEQ ID NO:95. The viral isolate termed NL/17/00 is a mammalian MPV of variant A2 and its genomic sequence is shown in SEQ ID NO:96. The viral isolate termed NL/1/99 (also 99-1) is a mammalian MPV of variant B1 and its genomic sequence is shown in SEQ ID NO:94. The viral isolate termed NL/1/94 is a mammalian 15 MPV of variant B2 and its genomic sequence is shown in SEQ ID NO:97. A list of sequences disclosed in the present application and the corresponding SEQ ID Nos is set forth in Table 16.

The protein of a mammalian MPV can be a N protein, a P protein, a M protein, a F protein, a M2-1 protein or a M2-2 protein or a fragment thereof. A fragment of a protein of a mammalian MPV can be at least 25 amino acids, at least 50 amino acids, at least 75 20 amino acids, at least 100 amino acids, at least 125 amino acids, at least 150 amino acids, at least 175 amino acids, at least 200 amino acids, at least 225 amino acids, at least 250 amino acids, at least 275 amino acids, at least 300 amino acids, at least 325 amino acids, at least 350 amino acids, at least 375 amino acids, at least 400 amino acids, at least 425 amino acids, at 25 least 450 amino acids, at least 475 amino acids, at least 500 amino acids, at least 750 amino acids, at least 1000 amino acids, at least 1250 amino acids, at least 1500 amino acids, at least 1750 amino acids, at least 2000 amino acids or at least 2250 amino acids in length. A fragment of a protein of a mammalian MPV can be at most 25 amino acids, at most 50 amino acids, at most 75 amino acids, at most 100 amino acids, at most 125 amino acids, at most 150 amino acids, at most 175 amino acids, at most 200 amino acids, at most 225 amino 30 acids, at most 250 amino acids, at most 275 amino acids, at most 300 amino acids, at most 325 amino acids, at most 350 amino acids, at most 375 amino acids, at most 400 amino

acids, at most 425 amino acids, at most 450 amino acids, at most 475 amino acids, at most 500 amino acids, at most 750 amino acids, at most 1000 amino acids, at most 1250 amino acids, at most 1500 amino acids, at most 1750 amino acids, at most 2000 amino acids or at 5 most 2250 amino acids in length.

In certain embodiments of the invention, the protein of a mammalian MPV is a N protein, wherein the N protein is phylogenetically closer related to a N protein of a mammalian MPV, such as the N protein encoded by, e.g., the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97, (see also Table 16 for a 10 description of the SEQ ID Nos) than it is related to the N protein of APV type C. In certain embodiments of the invention, the protein of a mammalian MPV is a P protein, wherein the P protein is phylogenetically closer related to a P protein of a mammalian MPV, such as the P protein encoded by, e.g., the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97, than it is related to the N protein of APV type C. In certain 15 embodiments of the invention, the protein of a mammalian MPV is a M protein, wherein the M protein is closer related to a M protein of a mammalian MPV, such as the M protein encoded by, e.g., the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97, than it is related to the M protein of APV type C. In certain embodiments of the invention, the protein of a mammalian MPV is a F protein, wherein the F protein is 20 phylogenetically closer related to a F protein of a mammalian MPV, such as the F protein encoded by, e.g., the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97, than it is related to the F protein of APV type C. In certain embodiments of the invention, the protein of a mammalian MPV is a M2-1 protein, wherein the M2-1 protein is phylogenetically closer related to a M2-1 protein of a mammalian MPV, such as the M2-1 25 protein encoded by, e.g., the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97, than it is related to the M2-1 protein of APV type C. In certain embodiments of the invention, the protein of a mammalian MPV is a M2-2 protein, wherein the M2-2 protein is phylogenetically closer related to a M2-2 protein of a mammalian MPV, such as the M2-2 protein encoded by, e.g., the viral genome of SEQ ID NO:94, SEQ ID 30 NO:95, SEQ ID NO:96, or SEQ ID NO:97, than it is related to the M2-2 protein of APV type C. In certain embodiments of the invention, the protein of a mammalian MPV is a G protein,

wherein the G protein is phylogenetically closer related to a G protein of a mammalian MPV, such as the G protein encoded by, e.g., the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97, than it is related to any protein of APV type C. In certain 5 embodiments of the invention, the protein of a mammalian MPV is a SH protein, wherein the SH protein is phylogenetically closer related to a SH protein of a mammalian MPV, such as the SH protein encoded by, e.g., the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97, than it is related to any protein of APV type C. In certain 10 embodiments of the invention, the protein of a mammalian MPV is a L protein, wherein the L protein is phylogenetically closer related to a L protein of a mammalian MPV, such as the SH protein encoded by, e.g., the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97, than it is related to any protein of APV type C.

In certain embodiments of the invention, the protein of a mammalian MPV is a N protein, wherein the N protein is at least 60%, at least 65%, at least 70%, at least 75%, at 15 least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or at least 99.5% identical to the amino acid sequence of a N protein encoded by the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97 (the amino acid sequences of the respective N proteins are disclosed in SEQ ID NO:366-369; see also Table 16). In certain embodiments of the invention, the protein of a mammalian MPV is a N 20 protein, wherein the P protein is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or at least 99.5% identical to the amino acid sequence of a P protein encoded by the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97 (the amino acid sequences of the respective P proteins are disclosed in SEQ ID NO:78-85; see also Table 16). In certain 25 embodiments of the invention, the protein of a mammalian MPV is a M protein, wherein the M protein is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or at least 99.5% identical to the amino acid sequence of a M protein encoded by the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97 (the amino acid sequences of the respective M 30 proteins are disclosed in SEQ ID NO:358-361; see also Table 16). In certain embodiments of the invention, the protein of a mammalian MPV is a F protein, wherein the F protein is at

least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or at least 99.5% identical to the amino acid sequence of a F protein encoded by the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97 (the amino acid sequences of the respective F proteins are disclosed in SEQ ID NO:18-25; see also Table 16). In certain embodiments of the invention, the protein of a mammalian MPV is a M2-1 protein, wherein the M2-1 protein is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or at least 99.5% identical to the amino acid sequence of a M2-1 protein encoded by the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97 (the amino acid sequences of the respective M2-1 proteins are disclosed in SEQ ID NO:42-49; see also Table 16). In certain embodiments of the invention, the protein of a mammalian MPV is a M2-2 protein, wherein the M2-2 protein is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or at least 99.5% identical to the amino acid sequence of a M2-2 protein encoded by the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97 (the amino acid sequences of the respective M2-2 proteins are disclosed in SEQ ID NO:50-57; see also Table 16). In certain embodiments of the invention, the protein of a mammalian MPV is a G protein, wherein the G protein is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or at least 99.5% identical to the amino acid sequence of a G protein encoded by the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97 (the amino acid sequences of the respective G proteins are disclosed in SEQ ID NO:26-33; see also Table 16). In certain embodiments of the invention, the protein of a mammalian MPV is a SH protein, wherein the SH protein is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or at least 99.5% identical to the amino acid sequence of a SH protein encoded by the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97 (the amino acid sequences of the respective SH proteins are disclosed in SEQ ID NO:86-93; see also Table 16). In certain embodiments of the invention, the protein of a mammalian MPV is a L protein, wherein the L protein is at least 60%, at least 65%, at least 70%, at least 75%, at

least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or at least 99.5% identical to the amino acid sequence of a L protein encoded by the viral genome of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97 (the amino acid sequences of the respective L proteins are disclosed in SEQ ID NO:34-41; see also Table 16).

5 A fragment of a protein of mammalian MPV is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or at least 99.5% identical to the homologous protein encoded by the virus of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97 over the portion of the protein 10 that is homologous to the fragment. In a specific, illustrative embodiment, the invention provides a fragment of the F protein of a mammalian MPV that contains the ectodomain of the F protein and homologs thereof. The homolog of the fragment of the F protein that contains the ectodomain is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or at least 99.5% 15 identical to the corresponding fragment containing the ectodomain of the F protein encoded by a virus of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97 (the amino acid sequences of the respective F proteins are disclosed in SEQ ID NO:18-25; see also Table 16).

In certain embodiments, the invention provides a protein of a mammalian MPV of 20 subgroup A and fragments thereof. The invention provides a N protein of a mammalian MPV of subgroup A, wherein the N protein is phylogenetically closer related to the N protein encoded by a virus of SEQ ID NO:95 or SEQ ID NO:96 than it is related to the N protein encoded by a virus encoded by SEQ ID NO:94 or SEQ ID NO:97. The invention provides a G protein of a mammalian MPV of subgroup A, wherein the G protein is phylogenetically 25 closer related to the G protein encoded by a virus of SEQ ID NO:95 or SEQ ID NO:96 than it is related to the G protein encoded by a virus encoded by SEQ ID NO:94 or SEQ ID NO:97. The invention provides a P protein of a mammalian MPV of subgroup A, wherein the P protein is phylogenetically closer related to the P protein encoded by a virus of SEQ ID NO:95 or SEQ ID NO:96 than it is related to the P protein encoded by a virus encoded by 30 SEQ ID NO:94 or SEQ ID NO:97. The invention provides a M protein of a mammalian MPV of subgroup A, wherein the M protein is phylogenetically closer related to the M

protein encoded by a virus of SEQ ID NO:95 or SEQ ID NO:96 than it is related to the M protein encoded by a virus encoded by SEQ ID NO:94 or SEQ ID NO:97. The invention provides a N protein of a mammalian MPV of subgroup A, wherein the F protein is

5 phylogenetically closer related to the F protein encoded by a virus of SEQ ID NO:95 or SEQ ID NO:96 than it is related to the F protein encoded by a virus encoded by SEQ ID NO:94 or SEQ ID NO:97. The invention provides a M2-1 protein of a mammalian MPV of subgroup A, wherein the M2-1 protein is phylogenetically closer related to the M2-1 protein encoded by a virus of SEQ ID NO:95 or SEQ ID NO:96 than it is related to the M2-1 protein encoded

10 by a virus encoded by SEQ ID NO:94 or SEQ ID NO:97. The invention provides a M2-2 protein of a mammalian MPV of subgroup A, wherein the M2-2 protein is phylogenetically closer related to the M2-2 protein encoded by a virus of SEQ ID NO:95 or SEQ ID NO:96 than it is related to the M2-2 protein encoded by a virus encoded by SEQ ID NO:94 or SEQ ID NO:97. The invention provides a SH protein of a mammalian MPV of subgroup A,

15 wherein the SH protein is phylogenetically closer related to the SH protein encoded by a virus of SEQ ID NO:95 or SEQ ID NO:96 than it is related to the SH protein encoded by a virus encoded by SEQ ID NO:94 or SEQ ID NO:97. The invention provides a L protein of a mammalian MPV of subgroup A, wherein the L protein is phylogenetically closer related to the L protein encoded by a virus of SEQ ID NO:95 or SEQ ID NO:96 than it is related to the

20 L protein encoded by a virus encoded by SEQ ID NO:94 or SEQ ID NO:97.

In other embodiments, the invention provides a protein of a mammalian MPV of subgroup B or fragments thereof. The invention provides a N protein of a mammalian MPV of subgroup B, wherein the N protein is phylogenetically closer related to the N protein encoded by a virus of SEQ ID NO:94 or SEQ ID NO:97 than it is related to the N protein

25 encoded by a virus encoded by SEQ ID NO:95 or SEQ ID NO:96. The invention provides a G protein of a mammalian MPV of subgroup A, wherein the G protein is phylogenetically closer related to the G protein encoded by a virus of SEQ ID NO:94 or SEQ ID NO:97 than it is related to the G protein encoded by a virus encoded by SEQ ID NO:95 or SEQ ID NO:96. The invention provides a P protein of a mammalian MPV of subgroup A, wherein the P

30 protein is phylogenetically closer related to the P protein encoded by a virus of SEQ ID NO:94 or SEQ ID NO:97 than it is related to the P protein encoded by a virus encoded by

SEQ ID NO:95 or SEQ ID NO:96. The invention provides a M protein of a mammalian MPV of subgroup A, wherein the M protein is phylogenetically closer related to the M protein encoded by a virus of SEQ ID NO:94 or SEQ ID NO:97 than it is related to the M protein encoded by a virus encoded by SEQ ID NO:95 or SEQ ID NO:96. The invention provides a N protein of a mammalian MPV of subgroup A, wherein the F protein is phylogenetically closer related to the F protein encoded by a virus of SEQ ID NO:94 or SEQ ID NO:97 than it is related to the F protein encoded by a virus encoded by SEQ ID NO:95 or SEQ ID NO:96. The invention provides a M2-1 protein of a mammalian MPV of subgroup A, wherein the M2-1 protein is phylogenetically closer related to the M2-1 protein encoded by a virus of SEQ ID NO:94 or SEQ ID NO:97 than it is related to the M2-1 protein encoded by a virus encoded by SEQ ID NO:95 or SEQ ID NO:96. The invention provides a M2-2 protein of a mammalian MPV of subgroup A, wherein the M2-2 protein is phylogenetically closer related to the M2-2 protein encoded by a virus of SEQ ID NO:94 or SEQ ID NO:97 than it is related to the M2-2 protein encoded by a virus encoded by SEQ ID NO:95 or SEQ ID NO:96. The invention provides a SH protein of a mammalian MPV of subgroup A, wherein the SH protein is phylogenetically closer related to the SH protein encoded by a virus of SEQ ID NO:94 or SEQ ID NO:97 than it is related to the SH protein encoded by a virus encoded by SEQ ID NO:95 or SEQ ID NO:96. The invention provides a L protein of a mammalian MPV of subgroup A, wherein the L protein is phylogenetically closer related to the L protein encoded by a virus of SEQ ID NO:94 or SEQ ID NO:97 than it is related to the L protein encoded by a virus encoded by SEQ ID NO:95 or SEQ ID NO:96.

The invention provides a G protein of a mammalian MPV variant B1, wherein the G protein of a mammalian MPV variant B1 is phylogenetically closer related to the G protein of the prototype of variant B1, isolate NL/1/99, than it is related to the G protein of the prototype of variant A1, isolate NL/1/00, the G protein of the prototype of A2, isolate NL/17/00, or the G protein of the prototype of B2, isolate NL/1/94. The invention provides a G protein of a mammalian MPV variant B1, wherein the amino acid sequence of the G protein is at least 66%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, or at least 99% or at least 99.5% identical to the G protein of a mammalian MPV variant B1 as represented by the prototype NL/1/99 (SEQ ID NO:28). In a

specific embodiment, the G protein of a mammalian MPV has the amino acid sequence of SEQ ID NO:119-153. The invention provides a N protein of a mammalian MPV variant B1, wherein the N protein of a mammalian MPV variant B1 is phylogenetically closer related to the N protein of the prototype of variant B1, isolate NL/1/99, than it is related to the N protein of the prototype of variant A1, isolate NL/1/00, the N protein of the prototype of A2, isolate NL/17/00, or the N protein of the prototype of B2, isolate NL/1/94. The invention provides a N protein of a mammalian MPV variant B1, wherein the amino acid sequence of the N protein is at least 98.5% or at least 99% or at least 99.5% identical to the N protein of a mammalian MPV variant B1 as represented by the prototype NL/1/99 (SEQ ID NO:72).

The invention provides a P protein of a mammalian MPV variant B1, wherein the P protein of a mammalian MPV variant B1 is phylogenetically closer related to the P protein of the prototype of variant B1, isolate NL/1/99, than it is related to the P protein of the prototype of variant A1, isolate NL/1/00, the P protein of the prototype of A2, isolate NL/17/00, or the P protein of the prototype of B2, isolate NL/1/94. The invention provides a P protein of a mammalian MPV variant B1, wherein the amino acid sequence of the P protein is at least 96%, at least 98%, or at least 99% or at least 99.5% identical to the P protein of a mammalian MPV variant B1 as represented by the prototype NL/1/99 (SEQ ID NO:80). The invention provides a M protein of a mammalian MPV variant B1, wherein the M protein of a mammalian MPV variant B1 is phylogenetically closer related to the M protein of the prototype of variant B1, isolate NL/1/99, than it is related to the M protein of the prototype of variant A1, isolate NL/1/00, the M protein of the prototype of A2, isolate NL/17/00, or the M protein of the prototype of B2, isolate NL/1/94. The invention provides a M protein of a mammalian MPV variant B1, wherein the amino acid sequence of the M protein is identical to the M protein of a mammalian MPV variant B1 as represented by the prototype NL/1/99 (SEQ ID NO:64). The invention provides a F protein of a mammalian MPV variant B1, wherein the F protein of a mammalian MPV variant B1 is phylogenetically closer related to the F protein of variant B1, isolate NL/1/99, than it is related to the F protein of variant A1, isolate NL/1/00, the F protein of prototype A2, isolate NL/17/00, or the F protein of the prototype of B2, isolate NL/1/94. The invention provides a F protein of mammalian MPV variant B1, wherein the amino acid sequence of the F protein is identical at least 99%

identical, to the F protein of a mammalian MPV variant B1 as represented by the prototype NL/1/99 (SEQ ID NO:20). In a specific embodiment, the F protein of a mammalian MPV has the amino acid sequence of SEQ ID NO: 248-327. The invention provides a M2-1
5 protein of a mammalian MPV variant B1, wherein the M2-1 protein of a mammalian MPV variant B1 is phylogenetically closer related to the M2-1 protein of the prototype of variant B1, isolate NL/1/99, than it is related to the M2-1 protein of the prototype of variant A1, isolate NL/1/00, the M2-1 protein of the prototype of A2, isolate NL/17/00, or the M2-1 protein of the prototype of B2, isolate NL/1/94. The invention provides a M2-1 protein of a
10 mammalian MPV variant B1, wherein the amino acid sequence of the M2-1 protein is at least 98% or at least 99% or at least 99.5% identical the M2-1 protein of a mammalian MPV variant B1 as represented by the prototype NL/1/99 (SEQ ID NO:44). The invention provides a M2-2 protein of a mammalian MPV variant B1, wherein the M2-2 protein of a mammalian MPV variant B1 is phylogenetically closer related to the M2-2 protein of the
15 prototype of variant B1, isolate NL/1/99, than it is related to the M2-2 protein of the prototype of variant A1, isolate NL/1/00, the M2-2 protein of the prototype of A2, isolate NL/17/00, or the M2-2 protein of the prototype of B2, isolate NL/1/94. The invention provides a M2-2 protein of a mammalian MPV variant B1, wherein the amino acid sequence of the M2-2 protein is at least 99% or at least 99.5% identical the M2-2 protein of a
20 mammalian MPV variant B1 as represented by the prototype NL/1/99 (SEQ ID NO:52). The invention provides a SH protein of a mammalian MPV variant B1, wherein the SH protein of a mammalian MPV variant B1 is phylogenetically closer related to the SH protein of the prototype of variant B1, isolate NL/1/99, than it is related to the SH protein of the prototype of variant A1, isolate NL/1/00, the SH protein of the prototype of A2, isolate NL/17/00, or
25 the SH protein of the prototype of B2, isolate NL/1/94. The invention provides a SH protein of a mammalian MPV variant B1, wherein the amino acid sequence of the SH protein is at least 83%, at least 85%, at least 90%, at least 95%, at least 98%, or at least 99% or at least 99.5% identical the SH protein of a mammalian MPV variant B1 as represented by the prototype NL/1/99 (SEQ ID NO:88). The invention provides a L protein of a mammalian
30 MPV variant B1, wherein the L protein of a mammalian MPV variant B1 is phylogenetically closer related to the L protein of the prototype of variant B1, isolate NL/1/99, than it is

related to the L protein of the prototype of variant A1, isolate NL/1/00, the L protein of the prototype of A2, isolate NL/17/00, or the L protein of the prototype of B2, isolate NL/1/94. The invention provides a L protein of a mammalian MPV variant B1, wherein the amino acid sequence of the L protein is at least 99% or at least 99.5% identical the L protein a mammalian MPV variant B1 as represented by the prototype NL/1/99 (SEQ ID NO:36).

The invention provides a G protein of a mammalian MPV variant A1, wherein the G protein of a mammalian MPV variant A1 is phylogenetically closer related to the G protein of the prototype of variant A1, isolate NL/1/00, than it is related to the G protein of the prototype of variant B1, isolate NL/1/99, the G protein of the prototype of A2, isolate NL/17/00, or the G protein of the prototype of B2, isolate NL/1/94. The invention provides a G protein of a mammalian MPV variant A1, wherein the amino acid sequence of the G protein is at least 66%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, or at least 99% or at least 99.5% identical to the G protein of a mammalian MPV variant A1 as represented by the prototype NL/1/00 (SEQ ID NO:26). The invention provides a N protein of a mammalian MPV variant A1, wherein the N protein of a mammalian MPV variant A1 is phylogenetically closer related to the N protein of the prototype of variant A1, isolate NL/1/00, than it is related to the N protein of the prototype of variant B1, isolate NL/1/99, the N protein of the prototype of A2, isolate NL/17/00, or the N protein of the prototype of B2, isolate NL/1/94. The invention provides a N protein of a mammalian MPV variant A1, wherein the amino acid sequence of the N protein is at least 99.5% identical to the N protein of a mammalian MPV variant A1 as represented by the prototype NL/1/00 (SEQ ID NO:70). The invention provides a P protein of a mammalian MPV variant A1, wherein the P protein of a mammalian MPV variant A1 is phylogenetically closer related to the P protein of the prototype of variant A1, isolate NL/1/00, than it is related to the P protein of the prototype of variant B1, isolate NL/1/99, the P protein of the prototype of A2, isolate NL/17/00, or the P protein of the prototype of B2, isolate NL/1/94. The invention provides a P protein of a mammalian MPV variant A1, wherein the amino acid sequence of the P protein is at least 96%, at least 98%, or at least 99% or at least 99.5% identical to the P protein of a mammalian MPV variant A1 as represented by the prototype NL/1/00 (SEQ ID NO:78). The invention provides a M protein of a mammalian MPV

variant A1, wherein the M protein of a mammalian MPV variant A1 is phylogenetically closer related to the M protein of the prototype of variant A1, isolate NL/1/00, than it is related to the M protein of the prototype of variant B1, isolate NL/1/99, the M protein of the prototype of A2, isolate NL/17/00, or the M protein of the prototype of B2, isolate NL/1/94.

5 The invention provides a M protein of a mammalian MPV variant A1, wherein the amino acid sequence of the M protein is at least 99% or at least 99.5% identical to the M protein of a mammalian MPV variant A1 as represented by the prototype NL/1/00 (SEQ ID NO:62).

The invention provides a F protein of a mammalian MPV variant A1, wherein the F protein

10 of a mammalian MPV variant A1 is phylogenetically closer related to the F protein of the prototype of variant A1, isolate NL/1/00, than it is related to the F protein of the prototype of variant B1, isolate NL/1/99, the F protein of the prototype of A2, isolate NL/17/00, or the F protein of the prototype of B2, isolate NL/1/94. The invention provides a F protein of a mammalian MPV variant A1, wherein the amino acid sequence of the F protein is at least

15 98% or at least 99% or at least 99.5% identical to the F protein of a mammalian MPV variant A1 as represented by the prototype NL/1/00 (SEQ ID NO:18). The invention provides a M2-1 protein of a mammalian MPV variant A1, wherein the M2-1 protein of a mammalian MPV variant A1 is phylogenetically closer related to the M2-1 protein of the prototype of variant A1, isolate NL/1/00, than it is related to the M2-1 protein of the prototype of variant B1,

20 isolate NL/1/99, the M2-1 protein of the prototype of A2, isolate NL/17/00, or the M2-1 protein of the prototype of B2, isolate NL/1/94. The invention provides a M2-1 protein of a mammalian MPV variant A1, wherein the amino acid sequence of the M2-1 protein is at least 99% or at least 99.5% identical to the M2-1 protein of a mammalian MPV variant A1 as represented by the prototype NL/1/00 (SEQ ID NO:42). The invention provides a M2-2

25 protein of a mammalian MPV variant A1, wherein the M2-2 protein of a mammalian MPV variant A1 is phylogenetically closer related to the M2-2 protein of the prototype of variant A1, isolate NL/1/00, than it is related to the M2-2 protein of the prototype of variant B1, isolate NL/1/99, the M2-2 protein of the prototype of A2, isolate NL/17/00, or the M2-2 protein of the prototype of B2, isolate NL/1/94. The invention provides a M2-2 protein of a

30 mammalian MPV variant A1, wherein the amino acid sequence of the M2-2 protein is at least 96% or at least 99% or at least 99.5% identical to the M2-2 protein of a mammalian

MPV variant A1 as represented by the prototype NL/1/00 (SEQ ID NO:50). The invention provides a SH protein of a mammalian MPV variant A1, wherein the SH protein of a mammalian MPV variant A1 is phylogenetically closer related to the SH protein of the prototype of variant A1, isolate NL/1/00, than it is related to the SH protein of the prototype of variant B1, isolate NL/1/99, the SH protein of the prototype of A2, isolate NL/17/00, or the SH protein of the prototype of B2, isolate NL/1/94. The invention provides a SH protein of a mammalian MPV variant A1, wherein the amino acid sequence of the SH protein is at least 84%, at least 90%, at least 95%, at least 98%, or at least 99% or at least 99.5% identical to the SH protein of a mammalian MPV variant A1 as represented by the prototype NL/1/00 (SEQ ID NO:86). The invention provides a L protein of a mammalian MPV variant A1, wherein the L protein of a mammalian MPV variant A1 is phylogenetically closer related to the L protein of the prototype of variant A1, isolate NL/1/00, than it is related to the L protein of the prototype of variant B1, isolate NL/1/99, the L protein of the prototype of A2, isolate NL/17/00, or the L protein of the prototype of B2, isolate NL/1/94. The invention provides a L protein of a mammalian MPV variant A1, wherein the amino acid sequence of the L protein is at least 99% or at least 99.5% identical to the L protein of a virus of a mammalian MPV variant A1 as represented by the prototype NL/1/00 (SEQ ID NO:34).

The invention provides a G protein of a mammalian MPV variant A2, wherein the G protein of a mammalian MPV variant A2 is phylogenetically closer related to the G protein of the prototype of variant A2, isolate NL/17/00, than it is related to the G protein of the prototype of variant B1, isolate NL/1/99, the G protein of the prototype of A1, isolate NL/1/00, or the G protein of the prototype of B2, isolate NL/1/94. The invention provides a G protein of a mammalian MPV variant A2, wherein the amino acid sequence of the G protein is at least 66%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99% or at least 99.5% identical to the G protein of a mammalian MPV variant A2 as represented by the prototype NL/17/00 (SEQ ID NO:27).

The invention provides a N protein of a mammalian MPV variant A2, wherein the N protein of a mammalian MPV variant A2 is phylogenetically closer related to the N protein of the prototype of variant A2, isolate NL/17/00, than it is related to the N protein of the prototype of variant B1, isolate NL/1/99, the N protein of the prototype of A1, isolate NL/1/00, or the N

protein of the prototype of B2, isolate NL/1/94. The invention provides a N protein of a mammalian MPV variant A2, wherein the amino acid sequence of the N protein at least 99.5% identical to the N protein of a mammalian MPV variant A2 as represented by the 5 prototype NL/17/00 (SEQ ID NO:71). The invention provides a P protein of a mammalian MPV variant A2, wherein the P protein of a mammalian MPV variant A2 is phylogenetically closer related to the P protein of the prototype of variant A2, isolate NL/17/00, than it is related to the P protein of the prototype of variant B1, isolate NL/1/99, the P protein of the prototype of A1, isolate NL/1/00, or the P protein of the prototype of B2, isolate NL/1/94.

10 The invention provides a P protein of a mammalian MPV variant A2, wherein the amino acid sequence of the P protein is at least 96%, at least 98%, at least 99% or at least 99.5% identical to the P protein of a mammalian MPV variant A2 as represented by the prototype NL/17/00 (SEQ ID NO:79). The invention provides a M protein of a mammalian MPV variant A2, wherein the M protein of a mammalian MPV variant A2 is phylogenetically 15 closer related to the M protein of the prototype of variant A2, isolate NL/17/00, than it is related to the M protein of the prototype of variant B1, isolate NL/1/99, the M protein of the prototype of A1, isolate NL/1/00, or the M protein of the prototype of B2, isolate NL/1/94. The invention provides a M protein of a mammalian MPV variant A2, wherein the the amino acid sequence of the M protein is at least 99%, or at least 99.5% identical to the M protein of 20 a mammalian MPV variant A2 as represented by the prototype NL/17/00 (SEQ ID NO:63).

The invention provides a F protein of a mammalian MPV variant A2, wherein the F protein of a mammalian MPV variant A2 is phylogenetically closer related to the F protein of the prototype of variant A2, isolate NL/17/00, than it is related to the F protein of the prototype of variant B1, isolate NL/1/99, the F protein of the prototype of A1, isolate NL/1/00, or the F 25 protein of the prototype of B2, isolate NL/1/94. The invention provides a F protein of a mammalian MPV variant A2, wherein the amino acid sequence of the F protein is at least 98%, at least 99% or at least 99.5% identical to the F protein of a mammalian MPV variant A2 as represented by the prototype NL/17/00 (SEQ ID NO:19). The invention provides a M2-1 protein of a mammalian MPV variant A2, wherein the M2-1 protein of a mammalian 30 MPV variant A2 is phylogenetically closer related to the M2-1 protein of the prototype of variant A2, isolate NL/17/00, than it is related to the M2-1 protein of the prototype of variant

- B1, isolate NL/1/99, the M2-1 protein of the prototype of A1, isolate NL/1/00, or the M2-1 protein of the prototype of B2, isolate NL/1/94. The invention provides a M2-1 protein of a mammalian MPV variant A2, wherein the amino acid sequence of the M2-1 protein is at least 99%, or at least 99.5% identical to the M2-1 protein of a mammalian MPV variant A2 as represented by the prototype NL/17/00 (SEQ ID NO: 43). The invention provides a M2-2 protein of a mammalian MPV variant A2, wherein the M2-2 protein of a mammalian MPV variant A2 is phylogenetically closer related to the M2-2 protein of the prototype of variant A2, isolate NL/17/00, than it is related to the M2-2 protein of the prototype of variant B1,
- 10 isolate NL/1/99, the M2-2 protein of the prototype of A1, isolate NL/1/00, or the M2-2 protein of the prototype of B2, isolate NL/1/94. The invention provides a M2-2 protein of a mammalian MPV variant A2, wherein the amino acid sequence of the M2-2 protein is at least 96%, at least 98%, at least 99% or at least 99.5% identical to the M2-2 protein of a mammalian MPV variant A2 as represented by the prototype NL/17/00 (SEQ ID NO:51).
- 15 The invention provides a SH protein of a mammalian MPV variant A2, wherein the SH protein of a mammalian MPV variant A2 is phylogenetically closer related to the SH protein of the prototype of variant A2, isolate NL/17/00, than it is related to the SH protein of the prototype of variant B1, isolate NL/1/99, the SH protein of the prototype of A1, isolate NL/1/00, or the SH protein of the prototype of B2, isolate NL/1/94. The invention provides a
- 20 SH protein of a mammalian MPV variant A2, wherein the amino acid sequence of the SH protein is at least 84%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99% or at least 99.5% identical to the SH protein of a mammalian MPV variant A2 as represented by the prototype NL/17/00 (SEQ ID NO:87). The invention provides a L protein of a mammalian MPV variant A2, wherein the L protein of a mammalian MPV variant A2 is
- 25 phylogenetically closer related to the L protein of the prototype of variant A2, isolate NL/17/00, than it is related to the L protein of the prototype of variant B1, isolate NL/1/99, the L protein of the prototype of A1, isolate NL/1/00, or the L protein of the prototype of B2, isolate NL/1/94. The invention provides a L protein of a mammalian MPV variant A2, wherein the amino acid sequence of the L protein is at least 99% or at least 99.5% identical
- 30 to the L protein of a mammalian MPV variant A2 as represented by the prototype NL/17/00 (SEQ ID NO:35).

The invention provides a G protein of a mammalian MPV variant B2, wherein the G protein of a mammalian MPV variant B2 is phylogenetically closer related to the G protein of the prototype of variant B2, isolate NL/1/94, than it is related to the G protein of the 5 prototype of variant B1, isolate NL/1/99, the G protein of the prototype of A1, isolate NL/1/00, or the G protein of the prototype of A2, isolate NL/17/00. The invention provides a G protein of a mammalian MPV variant B2, wherein the amino acid sequence of the G protein is at least 66%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, or at least 99% or at least 99.5% identical to the G protein of a 10 mammalian MPV variant B2 as represented by the prototype NL/1/94 (SEQ ID NO:29). The invention provides a N protein of a mammalian MPV variant B2, wherein the N protein of a mammalian MPV variant B2 is phylogenetically closer related to the N protein of the prototype of variant B2, isolate NL/1/94, than it is related to the N protein of the prototype of variant B1, isolate NL/1/99, the N protein of the prototype of A1, isolate NL/1/00, or the N 15 protein of the prototype of A2, isolate NL/17/00. The invention provides a N protein of a mammalian MPV variant B2, wherein the amino acid sequence of the N protein is at least 99% or at least 99.5% identical to the N protein of a mammalian MPV variant B2 as represented by the prototype NL/1/94 (SEQ ID NO:73). The invention provides a P protein of a mammalian MPV variant B2, wherein the P protein of a mammalian MPV variant B2 is 20 phylogenetically closer related to the P protein of the prototype of variant B2, isolate NL/1/94, than it is related to the P protein of the prototype of variant B1, isolate NL/1/99, the P protein of the prototype of A1, isolate NL/1/00, or the P protein of the prototype of A2, isolate NL/17/00. The invention provides a P protein of a mammalian MPV variant B2, wherein the amino acid sequence of the P protein is at least 96%, at least 98%, or at least 25 99% or at least 99.5% identical to the P protein of a mammalian MPV variant B2 as represented by the prototype NL/1/94 (SEQ ID NO:81). The invention provides a M protein of a mammalian MPV variant B2, wherein the M protein of a mammalian MPV variant B2 is phylogenetically closer related to the M protein of the prototype of variant B2, isolate NL/1/94, than it is related to the M protein of the prototype of variant B1, isolate NL/1/99, the M protein of the prototype of A1, isolate NL/1/00, or the M protein of the prototype of 30 A2, isolate NL/17/00. The invention provides a M protein of a mammalian MPV variant B2,

wherein the amino acid sequence of its M protein is identical to the M protein of a mammalian MPV variant B2 as represented by the prototype NL/1/94 (SEQ ID NO:65). The invention provides a F protein of a mammalian MPV variant B2, wherein the F protein of a mammalian MPV variant B2 is phylogenetically closer related to the F protein of the prototype of variant B2, isolate NL/1/94, than it is related to the F protein of the prototype of variant B1, isolate NL/1/99, the F protein of the prototype of A1, isolate NL/1/00, or the F protein of the prototype of A2, isolate NL/17/00. The invention provides a F protein of a mammalian MPV variant B2, wherein the amino acid sequence of the F protein is at least 99% or at least 99.5% identical to the F protein of a mammalian MPV variant B2 as represented by the prototype NL/1/94 (SEQ ID NO:21). The invention provides a M2-1 protein of a mammalian MPV variant B2, wherein the M2-1 protein of a mammalian MPV variant B2 is phylogenetically closer related to the M2-1 protein of the prototype of variant B2, isolate NL/1/94, than it is related to the M2-1 protein of the prototype of variant B1, isolate NL/1/99, the M2-1 protein of the prototype of A1, isolate NL/1/00, or the M2-1 protein of the prototype of A2, isolate NL/17/00. The invention provides a M2-1 protein of a mammalian MPV variant B2, wherein the amino acid sequence of the M2-1 protein is at least 98% or at least 99% or at least 99.5% identical to the M2-1 protein of a mammalian MPV variant B2 as represented by the prototype NL/1/94 (SEQ ID NO:45). The invention provides a M2-2 protein of a mammalian MPV variant B2, wherein the M2-2 protein of a mammalian MPV variant B2 is phylogenetically closer related to the M2-2 protein of the prototype of variant B2, isolate NL/1/94, than it is related to the M2-2 protein of the prototype of variant B1, isolate NL/1/99, the M2-2 protein of the prototype of A1, isolate NL/1/00, or the M2-2 protein of the prototype of A2, isolate NL/17/00. The invention provides a M2-2 protein of a mammalian MPV variant B2, wherein the amino acid sequence is at least 99% or at least 99.5% identical to the M2-2 protein of a mammalian MPV variant B2 as represented by the prototype NL/1/94 (SEQ ID NO:53). The invention provides a SH protein of a mammalian MPV variant B2, wherein the SH protein of a mammalian MPV variant B2 is phylogenetically closer related to the SH protein of the prototype of variant B2, isolate NL/1/94, than it is related to the SH protein of the prototype of variant B1, isolate NL/1/99, the SH protein of the prototype of A1, isolate NL/1/00, or the SH protein of the

prototype of A2, isolate NL/17/00. The invention provides a SH protein of a mammalian MPV variant B2, wherein the amino acid sequence of the SH protein is at least 84%, at least 85%, at least 90%, at least 95%, at least 98%, or at least 99% or at least 99.5% identical to 5 the SH protein of a mammalian MPV variant B2 as represented by the prototype NL/1/94 (SEQ ID NO:89). The invention provides a L protein of a mammalian MPV variant B2, wherein the L protein of a mammalian MPV variant B2 is phylogenetically closer related to the L protein of the prototype of variant B2, isolate NL/1/94, than it is related to the L protein of the prototype of variant B1, isolate NL/1/99, the L protein of the prototype of A1, isolate 10 NL/1/00, or the L protein of the prototype of A2, isolate NL/17/00. The invention provides a L protein of a mammalian MPV variant B2, wherein the and/or if the amino acid sequence of the L protein is at least 99% or at least 99.5% identical to the L protein of a mammalian MPV variant B2 as represented by the prototype NL/1/94 (SEQ ID NO:37).

In certain embodiments, the percentage of sequence identity is based on an alignment 15 of the full length proteins. In other embodiments, the percentage of sequence identity is based on an alignment of contiguous amino acid sequences of the proteins, wherein the amino acid sequences can be 25 amino acids, 50 amino acids, 75 amino acids, 100 amino acids, 125 amino acids, 150 amino acids, 175 amino acids, 200 amino acids, 225 amino acids, 250 amino acids, 275 amino acids, 300 amino acids, 325 amino acids, 350 amino 20 acids, 375 amino acids, 400 amino acids, 425 amino acids, 450 amino acids, 475 amino acids, 500 amino acids, 750 amino acids, 1000 amino acids, 1250 amino acids, 1500 amino acids, 1750 amino acids, 2000 amino acids or 2250 amino acids in length.

The invention further provides nucleic acid sequences derived from a mammalian MPV. The invention also provides derivatives of nucleic acid sequences derived from a 25 mammalian MPV. In certain specific embodiments the nucleic acids are modified.

In certain embodiments, a nucleic acid of the invention encodes a G protein, a N protein, a P protein, a M protein, a F protein, a M2-1 protein, a M2-2 protein, a SH protein, or a L protein of a mammalian MPV as defined above. In certain embodiments, a nucleic acid of the invention encodes a G protein, a N protein, a P protein, a M protein, a F protein, a 30 M2-1 protein, a M2-2 protein, a SH protein, or a L protein of subgroup A of a mammalian MPV as defined above. In a specific embodiment, the G gene of a mammalian MPV has the

nucleotide sequence of SEQ ID NO:98-132. In a specific embodiment, the F gene of a mammalian MPV has the nucleotide sequence of SEQ ID NO:168-247. In certain embodiments, a nucleic acid of the invention encodes a G protein, a N protein, a P protein, a M protein, a F protein, a M2-1 protein, a M2-2 protein, a SH protein, or a L protein of subgroup B of a mammalian MPV as defined above. In certain embodiments, a nucleic acid of the invention encodes a G protein, a N protein, a P protein, a M protein, a F protein, a M2-1 protein, a M2-2 protein, a SH protein, or a L protein of variant A1 of a mammalian MPV as defined above. In certain embodiments, a nucleic acid of the invention encodes a G protein, a N protein, a P protein, a M protein, a F protein, a M2-1 protein, a M2-2 protein, a SH protein, or a L protein of variant A2 of a mammalian MPV as defined above. In certain embodiments, a nucleic acid of the invention encodes a G protein, a N protein, a P protein, a M protein, a F protein, a M2-1 protein, a M2-2 protein, a SH protein, or a L protein of variant B1 of a mammalian MPV as defined above. In certain embodiments, a nucleic acid of the invention encodes a G protein, a N protein, a P protein, a M protein, a F protein, a M2-1 protein, a M2-2 protein, a SH protein, or a L protein of variant B2 of a mammalian MPV as defined above.

In certain embodiments, the invention provides a nucleotide sequence that is at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or at least 99.5% identical to the nucleotide sequence of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97. In certain embodiments, the nucleic acid sequence of the invention, is at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or at least 99.5% identical to a fragment of the nucleotide sequence of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97, wherein the fragment is at least 25 nucleotides, at least 50 nucleotides, at least 75 nucleotides, at least 100 nucleotides, at least 150 nucleotides, at least 200 nucleotides, at least 250 nucleotides, at least 300 nucleotides, at least 400 nucleotides, at least 500 nucleotides, at least 750 nucleotides, at least 1,000 nucleotides, at least 1,250 nucleotides, at least 1,500 nucleotides, at least 1,750 nucleotides, at least 2,000 nucleotides, at least 2,000 nucleotides, at least 3,000 nucleotides, at least 4,000 nucleotides, at

- least 5,000 nucleotides, at least 7,500 nucleotides, at least 10,000 nucleotides, at least 12,500 nucleotides, or at least 15,000 nucleotides in length. In a specific embodiment, the nucleic acid sequence of the invention is at least 50%, at least 55%, at least 60%, at least 65%, at 5 least 70%, at least 75%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or at least 99.5% or 100% identical to one of the nucleotide sequences of SEQ ID NO:98-132; SEQ ID NO:168-247; SEQ ID NO:22-25; SEQ ID NO:30-33; SEQ ID NO:38-41; SEQ ID NO:46-49; SEQ ID NO:54-57; SEQ ID NO:58-61; SEQ ID NO:66-69; SEQ ID NO:74-77; SEQ ID NO:82-85; or SEQ ID NO:90-93.
- 10 In specific embodiments of the invention, a nucleic acid sequence of the invention is capable of hybridizing under low stringency, medium stringency or high stringency conditions to one of the nucleic acid sequences of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97. In specific embodiments of the invention, a nucleic acid sequence of the invention is capable of hybridizing under low stringency, medium stringency or high stringency conditions to one of the nucleic acid sequences of SEQ ID NO:98-132; SEQ ID NO:168-247; SEQ ID NO:22-25; SEQ ID NO:30-33; SEQ ID NO:38-41; SEQ ID NO:46-49; SEQ ID NO:54-57; SEQ ID NO:58-61; SEQ ID NO:66-69; SEQ ID NO:74-77; SEQ ID NO:82-85; or SEQ ID NO:90-93. In certain embodiments, a nucleic acid hybridizes over a length of at least 25 nucleotides, at least 50 nucleotides, at least 75 nucleotides, at least 150 nucleotides, at least 200 nucleotides, at least 250 nucleotides, at least 300 nucleotides, at least 400 nucleotides, at least 500 nucleotides, at least 750 nucleotides, at least 1,000 nucleotides, at least 1,250 nucleotides, at least 1,500 nucleotides, at least 1,750 nucleotides, at least 2,000 nucleotides, at least 2,00 nucleotides, at least 3,000 nucleotides, at least 4,000 nucleotides, at least 5,000 nucleotides, at least 7,500 nucleotides, 20 at least 10,000 nucleotides, at least 12,500 nucleotides, or at least 15,000 nucleotides with the nucleotide sequence of SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, or SEQ ID NO:97.
- 25 The invention further provides antibodies and antigen-binding fragments that bind specifically to a protein of a mammalian MPV. An antibody of the invention binds specifically to a G protein, a N protein, a P protein, a M protein, a F protein, a M2-1 protein, a M2-2 protein, a SH protein, or a L protein of a mammalian MPV. In specific 30 embodiments, the antibody is a human antibody or a humanized antibody. In certain

embodiments, an antibody of the invention binds specifically to a G protein, a N protein, a P protein, a M protein, a F protein, a M2-1 protein, a M2-2 protein, a SH protein, or a L protein of a virus of subgroup A of a mammalian MPV. In certain other embodiments, an antibody
5 of the invention binds specifically to a G protein, a N protein, a P protein, a M protein, a F protein, a M2-1 protein, a M2-2 protein, a SH protein, or a L protein of a virus of subgroup B of a mammalian MPV. In certain, more specific, embodiments, an antibody of the invention binds specifically to a G protein, a N protein, a P protein, a M protein, a F protein, a M2-1 protein, a M2-2 protein, a SH protein, or a L protein of a virus of variant A1 of a mammalian
10 MPV. In other embodiments, the antibody of the invention binds specifically to a G protein, a N protein, a P protein, a M protein, a F protein, a M2-1 protein, a M2-2 protein, a SH protein, or a L protein of a virus of subgroup A2 of a mammalian MPV. In certain embodiments, an antibody of the invention binds specifically to a G protein, a N protein, a P protein, a M protein, a F protein, a M2-1 protein, a M2-2 protein, a SH protein, or a L protein
15 of a virus of subgroup B1 of a mammalian MPV. In certain other embodiments, an antibody of the invention binds specifically to a G protein, a N protein, a P protein, a M protein, a F protein, a M2-1 protein, a M2-2 protein, a SH protein, or a L protein of a virus of subgroup B2 of a mammalian MPV.

20 **5.1.3. INSERTION OF THE HETEROLOGOUS GENE SEQUENCE**

Insertion of a foreign gene sequence into a viral vector of the invention can be accomplished by either a complete replacement of a viral coding region with a heterologous sequence, or by a partial replacement of the same, or by adding the heterologous nucleotide sequence to the viral genome. Complete replacement would probably best be accomplished
25 through the use of PCR-directed mutagenesis. Briefly, PCR-primer A would contain, from the 5' to 3' end: a unique restriction enzyme site, such as a class IIS restriction enzyme site (*i.e.*, a "shifter" enzyme; that recognizes a specific sequence but cleaves the DNA either upstream or downstream of that sequence); a stretch of nucleotides complementary to a region of the PIV gene; and a stretch of nucleotides complementary to the carboxy-terminus
30 coding portion of the heterologous sequence. PCR-primer B would contain from the 5' to 3' end: a unique restriction enzyme site; a stretch of nucleotides complementary to a PIV gene;

and a stretch of nucleotides corresponding to the 5' coding portion of the foreign gene. After a PCR reaction using these primers with a cloned copy of the foreign gene, the product may be excised and cloned using the unique restriction sites. Digestion with the class IIIS enzyme 5 and transcription with the purified phage polymerase would generate an RNA molecule containing the exact untranslated ends of the PIV gene with a foreign gene insertion. In an alternate embodiment, PCR-primed reactions could be used to prepare double-stranded DNA containing the bacteriophage promoter sequence, and the hybrid gene sequence so that RNA templates can be transcribed directly without cloning.

10 A heterologous nucleotide sequence can be added or inserted at various positions of the virus of the invention. In one embodiment, the heterologous nucleotide sequence is added or inserted at position 1. In another embodiment, the heterologous nucleotide sequence is added or inserted at position 2. In another embodiment, the heterologous nucleotide sequence is added or inserted at position 3. In another embodiment, the 15 heterologous nucleotide sequence is added or inserted at position 4. In another embodiment, the heterologous nucleotide sequence is added or inserted at position 5. In yet another embodiment, the heterologous nucleotide sequence is added or inserted at position 6. As used herein, the term "position" refers to the position of the heterologous nucleotide sequence on the viral genome to be transcribed, e.g., position 1 means that it is the first gene 20 to be transcribed, and position 2 means that it is the second gene to be transcribed. Inserting heterologous nucleotide sequences at the lower-numbered positions of the virus generally results in stronger expression of the heterologous nucleotide sequence compared to insertion at higher-numbered positions due to a transcriptional gradient that occurs across the genome of the virus. However, the transcriptional gradient also yields specific ratios of viral 25 mRNAs. Insertion of foreign genes will perturb these ratios and result in the synthesis of different amounts of viral proteins that may influence virus replication. Thus, both the transcriptional gradient and the replication kinetics must be considered when choosing an insertion site. For example, insertion of heterologous nucleotide sequence at position 2 of the b/h PIV3 vector results in the best replication rate and expression level of the 30 heterologous gene. Inserting heterologous nucleotide sequences at lower-numbered positions is the preferred embodiment of the invention if strong expression of the heterologous

nucleotide sequence is desired. In a preferred embodiment, the heterologous sequence is added or inserted at position 1, 2 or 3.

When inserting a heterologous nucleotide sequence into the virus of the invention, 5 the intergenic region between the end of the coding sequence of the heterologous gene and the start of the coding sequence of the downstream gene can be altered to achieve a desired effect. As used herein, the term "intergenic region" refers to nucleotide sequence between the stop signal of one gene and the start codon (*e.g.*, AUG) of the coding sequence of the next downstream open reading frame. An intergenic region may comprise a non-coding 10 region of a gene, *i.e.*, between the transcription start site and the start of the coding sequence (AUG) of the gene. This non-coding region occurs naturally in bPIV3 mRNAs and other viral genes, which is illustrated as non-limiting examples in Table 2:

Table 2: Lengths of Non-coding Regions for bPIV3 mRNAs

15	... CTT [Gene Start]	AUG ...
	N	45 nucleotides
	P	68 nucleotides
	M	21 nucleotides
20	F	201 nucleotides
	HN	62 nucleotides
	L	12 nucleotides
	b/h RSV F1	10 nucleotides
	b/h RSV F2	86 nucleotides
25	b/h RSV F1 NP-P	83 nucleotides

In various embodiments, the intergenic region between the heterologous nucleotide sequence and the downstream gene can be engineered, independently from each other, to be at least 10 nt in length, at least 20 nt in length, at least 30 nt in length, at least 50 nt in length, 30 at least 75 nt in length, at least 100 nt in length, at least 125 nt in length, at least 150 nt in length, at least 175 nt in length or at least 200 nt in length. In certain embodiments, the

intergenic region between the heterologous nucleotide sequence and the downstream gene can be engineered, independently from each other, to be at most 10 nt in length, at most 20 nt in length, at most 30 nt in length, at most 50 nt in length, at most 75 nt in length, at most 100 nt in length, at most 125 nt in length, at most 150 nt in length, at most 175 nt in length or at most 200 nt in length. In various embodiments, the non-coding region of a desired gene in a virus genome can also be engineered, independently from each other, to be at least 10 nt in length, at least 20 nt in length, at least 30 nt in length, at least 50 nt in length, at least 75 nt in length, at least 100 nt in length, at least 125 nt in length, at least 150 nt in length, at least 175 nt in length or at least 200 nt in length. In certain embodiments, the non-coding region of a desired gene in a virus genome can also be engineered, independently from each other, to be at most 10 nt in length, at most 20 nt in length, at most 30 nt in length, at most 50 nt in length, at most 75 nt in length, at most 100 nt in length, at most 125 nt in length, at most 150 nt in length, at most 175 nt in length, at most 200 nt in length.

When inserting a heterologous nucleotide sequence, the positional effect and the intergenic region manipulation can be used in combination to achieve a desirable effect. For example, the heterologous nucleotide sequence can be added or inserted at a position selected from the group consisting of position 1, 2, 3, 4, 5, and 6, and the intergenic region between the heterologous nucleotide sequence and the next downstream gene can be altered (*see* Table 3). In an exemplary embodiment, hRSV F gene is inserted at position 1 of a b/h PIV3 vector, and the intergenic region between F gene and N gene (*i.e.*, the next downstream gene of F) is altered to 177 nucleotides. Many more combinations are encompassed by the present invention and some are shown by way of example in Table 3.

25

30

Table 3. Examples of mode of insertion of heterologous nucleotide sequences

		Position 1	Position 2	Position 3	Position 4	Position 5	Position 6
		IGR ^a	10-20	10-20	10-20	10-20	10-20
5	IGR	21-40	21-40	21-40	21-40	21-40	21-40
	IGR	41-60	41-60	41-60	41-60	41-60	41-60
	IGR	61-80	61-80	61-80	61-80	61-80	61-80
	IGR	81-100	81-100	81-100	81-100	81-100	81-100
	IGR	101-120	101-120	101-120	101-120	101-120	101-120
	IGR	121-140	121-140	121-140	121-140	121-140	121-140
10	IGR	141-160	141-160	141-160	141-160	141-160	141-160
	IGR	161-180	161-180	161-180	161-180	161-180	161-180
	IGR	181-200	181-200	181-200	181-200	181-200	181-200
	IGR	201-220	201-220	201-220	201-220	201-220	201-220
	IGR	221-240	221-240	221-240	221-240	221-240	221-240
	IGR	241-260	241-260	241-260	241-260	241-260	241-260
	IGR	261-280	261-280	261-280	261-280	261-280	261-280
15	IGR	281-300	281-300	281-300	281-300	281-300	281-300

^a Intergenic Region, measured in nucleotide.

Depending on the purpose (e.g., to have strong immunogenicity) of the inserted heterologous nucleotide sequence, the position of the insertion and the length of the 20 intergenic region of the inserted heterologous nucleotide sequence can be determined by various indexes including, but not limited to, replication kinetics and protein or mRNA expression levels, measured by following non-limiting examples of assays: plaque assay, fluorescent-focus assay, infectious center assay, transformation assay, endpoint dilution assay, efficiency of plating, electron microscopy, hemagglutination, measurement of viral 25 enzyme activity, viral neutralization, hemagglutination inhibition, complement fixation, immunostaining, immunoprecipitation and immunoblotting, enzyme-linked immunosorbent assay, nucleic acid detection (e.g., Southern blot analysis, Northern blot analysis, Western blot analysis), growth curve, employment of a reporter gene (e.g., using a reporter gene, such as Green Fluorescence Protein (GFP) or enhanced Green Fluorescence Protein (eGFP), 30 integrated to the viral genome the same fashion as the interested heterologous gene to observe the protein expression), or a combination thereof. Procedures of performing these

assays are well known in the art (see, e.g., Flint et al., PRINCIPLES OF VIROLOGY, MOLECULAR BIOLOGY, PATHOGENESIS, AND CONTROL, 2000, ASM Press pp 25 - 56, the entire text is incorporated herein by reference), and non-limiting examples are given in the
5 Example sections, *infra*.

For example, expression levels can be determined by infecting cells in culture with a virus of the invention and subsequently measuring the level of protein expression by, e.g., Western blot analysis or ELISA using antibodies specific to the gene product of the heterologous sequence, or measuring the level of RNA expression by, e.g., Northern blot
10 analysis using probes specific to the heterologous sequence. Similarly, expression levels of the heterologous sequence can be determined by infecting an animal model and measuring the level of protein expressed from the heterologous sequence of the recombinant virus of the invention in the animal model. The protein level can be measured by obtaining a tissue sample from the infected animal and then subjecting the tissue sample to Western blot
15 analysis or ELISA, using antibodies specific to the gene product of the heterologous sequence. Further, if an animal model is used, the titer of antibodies produced by the animal against the gene product of the heterologous sequence can be determined by any technique known to the skilled artisan, including but not limited to, ELISA.

As the heterologous sequences can be homologous to a nucleotide sequence in the
20 genome of the virus, care should be taken that the probes and the antibodies are indeed specific to the heterologous sequence or its gene product.

In certain specific embodiments, expression levels of F-protein of RSV or hMPV from chimeric b/h PIV3 RSV or b/h PIV3 hMPV or b/h PIV3 RSV F and hMPV F can be determined by any technique known to the skilled artisan. Expression levels of the F-protein
25 can be determined by infecting cells in a culture with the chimeric virus of the invention and measuring the level of protein expression by, e.g., Western blot analysis or ELISA using antibodies specific to the F-protein and/or the G-protein of hMPV, or measuring the level of RNA expression by, e.g., Northern blot analysis using probes specific to the F-gene and/or the G-gene of human metapneumovirus. Similarly, expression levels of the heterologous
30 sequence can be determined using an animal model by infecting an animal and measuring the level of F-protein and/or G-protein in the animal model. The protein level can be measured

by obtaining a tissue sample from the infected animal and then subjecting the tissue sample to Western blot analysis or ELISA using antibodies specific to F-protein and/or G-protein of the heterologous sequence. Further, if an animal model is used, the titer of antibodies produced by the animal against F-protein and/or G-protein can be determined by any technique known to the skilled artisan, including but not limited to, ELISA.

The rate of replication of a recombinant virus of the invention can be determined by any technique known to the skilled artisan.

In certain embodiments, to facilitate the identification of the optimal position of the heterologous sequence in the viral genome and the optimal length of the intergenic region, the heterologous sequence encodes a reporter gene. Once the optimal parameters are determined, the reporter gene is replaced by a heterologous nucleotide sequence encoding an antigen of choice. Any reporter gene known to the skilled artisan can be used with the methods of the invention. For more detail, see section 5.5.

The rate of replication of the recombinant virus can be determined by any standard technique known to the skilled artisan. The rate of replication is represented by the growth rate of the virus and can be determined by plotting the viral titer over the time post infection. The viral titer can be measured by any technique known to the skilled artisan. In certain embodiments, a suspension containing the virus is incubated with cells that are susceptible to infection by the virus. Cell types that can be used with the methods of the invention include, but are not limited to, Vero cells, LLC-MK-2 cells, Hep-2 cells, LF 1043 (HEL) cells, MRC-5 cells, WI-38 cells, 293 T cells, QT 6 cells, QT 35 cells, chicken embryo fibroblast (CEF), or tMK cells. Subsequent to the incubation of the virus with the cells, the number of infected cells is determined. In certain specific embodiments, the virus comprises a reporter gene. Thus, the number of cells expressing the reporter gene is representative of the number of infected cells. In a specific embodiment, the virus comprises a heterologous nucleotide sequence encoding for eGFP, and the number of cells expressing eGFP, *i.e.*, the number of cells infected with the virus, is determined using FACS.

In certain embodiments, the replication rate of the recombinant virus of the invention is at most 20 % of the replication rate of the wild type virus from which the recombinant virus is derived under the same conditions. The same conditions refer to the same initial titer

of virus, the same strain of cells, the same incubation temperature, growth medium, number of cells and other test conditions that may affect the replication rate. For example, the replication rate of b/h PIV3 with RSV's F gene in position 1 is at most 20 % of the 5 replication rate of bPIV3.

In certain embodiments, the replication rate of the recombinant virus of the invention is at most 5 %, at most 10 %, at most 20 %, at most 30 %, at most 40 %, at most 50 %, at most 75 %, at most 80 %, at most 90 % of the replication rate of the wild type virus from which the recombinant virus is derived under the same conditions. In certain embodiments, 10 the replication rate of the recombinant virus of the invention is at least 5 %, at least 10 %, at least 20 %, at least 30 %, at least 40 %, at least 50 %, at least 75 %, at least 80 %, at least 90 % of the replication rate of the wild type virus from which the recombinant virus is derived under the same conditions. In certain embodiments, the replication rate of the recombinant virus of the invention is between 5 % and 20 %, between 10 % and 40 %, 15 between 25 % and 50 %, between 40 % and 75 %, between 50 % and 80 %, or between 75 % and 90 % of the replication rate of the wild type virus from which the recombinant virus is derived under the same conditions.

In certain embodiments, the expression level of the heterologous sequence in the recombinant virus of the invention is at most 20 % of the expression level of the F-protein of 20 the wild type virus from which the recombinant virus is derived under the same conditions. The same conditions refer to the same initial titer of virus, the same strain of cells, the same incubation temperature, growth medium, number of cells and other test conditions that may affect the replication rate. For example, the expression level of the heterologous sequence of the F-protein of MPV in position 1 of bPIV3 is at most 20 % of the expression level of the 25 bovine F-protein of bPIV3.

In certain embodiments, the expression level of the heterologous sequence in the recombinant virus of the invention is at most 5 %, at most 10 %, at most 20 %, at most 30 %, at most 40 %, at most 50 %, at most 75 %, at most 80 %, at most 90 % of the expression 30 level of the F-protein of the wild type virus from which the recombinant virus is derived under the same conditions. In certain embodiments, the expression level of the heterologous sequence in the recombinant virus of the invention is at least 5 %, at least 10 %, at least 20

%, at least 30 %, at least 40 %, at least 50 %, at least 75 %, at least 80 %, at least 90 % of the expression level of the F-protein of the wild type virus from which the recombinant virus is derived under the same conditions. In certain embodiments, the expression level of the heterologous sequence in the recombinant virus of the invention is between 5 % and 20 %, between 10 % and 40 %, between 25 % and 50 %, between 40 % and 75 %, between 50 % and 80 %, or between 75 % and 90 % of the expression level of the F-protein of the wild type virus from which the recombinant virus is derived under the same conditions.

10 **5.1.4. INSERTION OF THE HETEROLOGOUS GENE SEQUENCE INTO
THE HN GENE**

The protein responsible for the hemagglutinin and neuraminidase activities of PIV are coded for by a single gene, HN. The HN protein is a major surface glycoprotein of the virus. For a variety of viruses, such as parainfluenza, the hemagglutinin and neuraminidase proteins have been shown to contain a number of antigenic sites. Consequently, this protein is a potential target for the humoral immune response after infection. Therefore, substitution of antigenic sites of HN with a portion of a foreign protein may provide for a vigorous humoral response against this foreign peptide. If a sequence is inserted within the HN molecule, and it is expressed on the outside surface of the HN, it will be immunogenic. For example, a peptide derived from gp160 of HIV could replace an antigenic site of the HN protein, resulting in a humoral immune response to both gp160 and the HN protein. In a different approach, the foreign peptide sequence may be inserted within the antigenic site without deleting any viral sequences. Expression products of such constructs may be useful in vaccines against the foreign antigen, and may indeed circumvent a problem discussed earlier, that of propagation of the recombinant virus in the vaccinated host. An intact HN molecule with a substitution only in antigenic sites may allow for HN function and thus allow for the construction of a viable virus. Therefore, this virus can be grown without the need for additional helper functions. The virus may also be attenuated in other ways to avoid any danger of accidental escape.

30 Other hybrid constructions may be made to express proteins on the cell surface or enable them to be released from the cell. As a surface glycoprotein, HN has an amino-

terminal cleavable signal sequence necessary for transport to the cell surface, and a carboxy-terminal sequence necessary for membrane anchoring. In order to express an intact foreign protein on the cell surface, it may be necessary to use these HN signals to create a hybrid 5 protein. In this case, the fusion protein may be expressed as a separate fusion protein from an additional internal promoter. Alternatively, if only the transport signals are present and the membrane anchoring domain is absent, the protein may be secreted out of the cell.

5.1.5. CONSTRUCTION OF BICISTRONIC RNA

10 Bicistronic mRNA could be constructed to permit internal initiation of translation of viral sequences and allow for the expression of foreign protein coding sequences from the regular terminal initiation site. Alternatively, a bicistronic mRNA sequence may be constructed wherein the viral sequence is translated from the regular terminal open reading frame, while the foreign sequence is initiated from an internal site. Certain internal ribosome 15 entry site (IRES) sequences may be utilized. The IRES sequences that are chosen should be short enough to avoid interference with parainfluenza packaging limitations. Thus, it is preferable that the IRES chosen for such a bicistronic approach be no more than 500 nucleotides in length, with less than 250 nucleotides being of ideal length. In a specific embodiment, the IRES is derived from a picornavirus and does not include any additional 20 picornaviral sequences. Preferred IRES elements include, but are not limited to, the mammalian BiP IRES and the hepatitis C virus IRES.

25 Alternatively, a foreign protein may be expressed from a new internal transcriptional unit in which the transcriptional unit has an initiation site and polyadenylation site. In another embodiment, the foreign gene is inserted into a PIV gene such that the resulting expressed protein is a fusion protein.

5.2. EXPRESSION OF HETEROLOGOUS GENE PRODUCTS USING RECOMBINANT cDNA AND RNA TEMPLATES

The recombinant templates prepared as described above can be used in a variety of ways to express the heterologous gene products in appropriate host cells or to create chimeric 30 viruses that express the heterologous gene products. In one embodiment, the recombinant cDNA can be used to transfect appropriate host cells and the resulting RNA may direct the

expression of the heterologous gene product at high levels. Host cell systems which provide for high levels of expression include continuous cell lines that supply viral functions such as cell lines superinfected with PIV, cell lines engineered to complement PIV functions, etc.

5 In an alternate embodiment of the invention, the recombinant templates may be used to transfect cell lines that express a viral polymerase protein in order to achieve expression of the heterologous gene product. To this end, transformed cell lines that express a polymerase protein such as the L protein may be utilized as appropriate host cells. Host cells may be similarly engineered to provide other viral functions or additional functions such as HN, NP
10 or N.

In another embodiment, a helper virus may provide the RNA polymerase protein utilized by the cells in order to achieve expression of the heterologous gene product. In yet another embodiment, cells may be transfected with vectors encoding viral proteins such as the N or NP, P, M2-1 and L proteins.

15 Different technique may be used to detect the expression of heterologous gene products (*see, e.g.*, Flint et al., PRINCIPLES OF VIROLOGY, MOLECULAR BIOLOGY, PATHOGENESIS, AND CONTROL, 2000, ASM Press pp 25 - 56, the entire text is incorporated herein by reference). In an exemplary assay, cells infected with the virus are permeabilized with methanol or acetone and incubated with an antibody raised against the heterologous
20 gene products. A second antibody that recognizes the first antibody is then added. This second antibody is usually conjugated to an indicator so that the expression of heterologous gene products may be visualized or detected.

5.3. RESCUE OF RECOMBINANT VIRUS PARTICLES

25 In order to prepare chimeric virus, modified cDNAs, virus RNAs, or RNA coding for the PIV genome and/or foreign proteins in the plus or minus sense may be used to transfect cells that provide viral proteins and functions required for replication and rescue. Alternatively, cells may be transfected with helper virus before, during, or after transfection by the DNA or RNA molecule coding for the PIV genome and/or foreign proteins. The
30 synthetic recombinant plasmid PIV DNAs and RNAs can be replicated and rescued into infectious virus particles by any number of techniques known in the art, as described in U.S.

Patent No. 5,166,057 issued November 24, 1992; in U.S. Patent No. 5,854,037 issued December 29, 1998; in European Patent Publication EP 0702085A1, published February 20, 1996; in U.S. Patent Application Serial No. 09/152,845; in International Patent Publications
5 PCT WO97/12032 published April 3, 1997; WO96/34625 published November 7, 1996; in European Patent Publication EP-A780475; WO 99/02657 published January 21, 1999; WO 98/53078 published November 26, 1998; WO 98/02530 published January 22, 1998; WO 99/15672 published April 1, 1999; WO 98/13501 published April 2, 1998; WO 97/06270 published February 20, 1997; and EPO 780 47SA1 published June 25, 1997, each of which is
10 incorporated by reference herein in its entirety.

In one embodiment of the present invention, synthetic recombinant viral RNAs that contain the non-coding regions of the negative strand virus RNA essential for the recognition by viral polymerases and for packaging signals necessary to generate a mature virion, may be prepared. There are a number of different approaches that may be used to apply the reverse
15 genetics approach to rescue negative strand RNA viruses. First, the recombinant RNAs are synthesized from a recombinant DNA template and reconstituted *in vitro* with purified viral polymerase complex to form recombinant ribonucleoproteins (RNPs) that can be used to transfect cells. In another approach, a more efficient transfection is achieved if the viral polymerase proteins are present during transcription of the synthetic RNAs either *in vitro* or
20 *in vivo*. With this approach the synthetic RNAs may be transcribed from cDNA plasmids that are either co-transcribed *in vitro* with cDNA plasmids encoding the polymerase proteins, or transcribed *in vivo* in the presence of polymerase proteins, *i.e.*, in cells which transiently or constitutively express the polymerase proteins.

In additional approaches described herein, the production of infectious chimeric virus
25 may be replicated in host cell systems that express a PIV viral polymerase protein (*e.g.*, in virus/host cell expression systems; transformed cell lines engineered to express a polymerase protein, etc.), so that infectious chimeric viruses are rescued. In this instance, helper virus need not be utilized since this function is provided by the viral polymerase proteins expressed.

30 In accordance with the present invention, any technique known to those of skill in the art may be used to achieve replication and rescue of recombinant and chimeric viruses. One

approach involves supplying viral proteins and functions required for replication *in vitro* prior to transfecting host cells. In such an embodiment, viral proteins may be supplied in the form of wild type virus, helper virus, purified viral proteins or recombinantly expressed viral 5 proteins. The viral proteins may be supplied prior to, during or post transcription of the synthetic cDNAs or RNAs encoding the chimeric virus. The entire mixture may be used to transfect host cells. In another approach, viral proteins and functions required for replication may be supplied prior to or during transcription of the synthetic cDNAs or RNAs encoding the chimeric virus. In such an embodiment, viral proteins and functions required for 10 replication are supplied in the form of wild type virus, helper virus, viral extracts, synthetic cDNAs or RNAs that express the viral proteins are introduced into the host cell via infection or transfection. This infection/transfection takes place prior to or simultaneous to the introduction of the synthetic cDNAs or RNAs encoding the chimeric virus.

In a particularly desirable approach, cells engineered to express all viral genes of the 15 recombinant or chimeric virus of the invention may result in the production of infectious chimeric virus that contain the desired genotype; thus eliminating the need for a selection system. Theoretically, one can replace any one of the six genes or part of any one of the six genes encoding structural proteins of PIV with a foreign sequence. However, a necessary part of this equation is the ability to propagate the defective virus (defective because a normal 20 viral gene product is missing or altered). A number of possible approaches are available to circumvent this problem. In one approach, a virus having a mutant protein can be grown in cell lines that are constructed to constitutively express the wild type version of the same protein. By this way, the cell line complements the mutation in the virus. Similar techniques may be used to construct transformed cell lines that constitutively express any of the PIV 25 genes. These cell lines which are made to express the viral protein may be used to complement the defect in the recombinant virus and thereby propagate it. Alternatively, certain natural host range systems may be available to propagate recombinant virus.

In yet another embodiment, viral proteins and functions required for replication may be supplied as genetic material in the form of synthetic cDNAs or RNAs so that they are co- 30 transcribed with the synthetic cDNAs or RNAs encoding the chimeric virus. In a particularly desirable approach, plasmids that express the chimeric virus and the viral polymerase and/or

other viral functions are co-transfected into host cells. For example, plasmids encoding the genomic or antigenomic PIV RNA, either wild type or modified, may be co-transfected into host cells with plasmids encoding the PIV viral polymerase proteins NP or N, P, M2-1 or L.

5 Alternatively, rescue of chimeric b/h PIV3 virus may be accomplished by the use of Modified Vaccinia Virus Ankara (MVA) encoding T7 RNA polymerase, or a combination of MVA and plasmids encoding the polymerase proteins (N, P, and L). For example, MVA-T7 or Fowl Pox-T7 can be infected into Vero cells, LLC-MK-2 cells, Hep-2 cells, LF 1043 (HEL) cells, tMK cells, LLC-MK2, HUT 292, FRHL-2 (rhesus), FCL-1 (green monkey), WI-38 10 (human), MRC-5 (human) cells, 293 T cells, QT 6 cells, QT 35 cells and CEF cells. After infection with MVA-T7 or Fowl Pox-T7, a full length antigenomic b/h PIV3 cDNA may be transfected into the HeLa or Vero cells together with the NP, P, M2-1 and L encoding expression plasmids. Alternatively, the polymerase may be provided by plasmid transfection. The cells and cell supernatant can subsequently be harvested and subjected to a single freeze- 15 thaw cycle. The resulting cell lysate may then be used to infect a fresh HeLa or Vero cell monolayer in the presence of 1-beta-D-arabinofuranosylcytosine (ara C), a replication inhibitor of vaccinia virus, to generate a virus stock. The supernatant and cells from these plates can then be harvested, freeze-thawed once, and the presence of bPIV3 virus particles detected by immunostaining of virus plaques using PIV3-specific antiserum.

20 Another approach to propagating the recombinant virus involves co-cultivation with wild-type virus. This could be done by simply taking recombinant virus and co-infecting cells with this and another wild-type virus (preferably a vaccine strain). The wild-type virus should complement for the defective virus gene product and allow growth of both the wild-type and recombinant virus. Alternatively, a helper virus may be used to support propagation 25 of the recombinant virus.

In another approach, synthetic templates may be replicated in cells co-infected with recombinant viruses that express the PIV virus polymerase protein. In fact, this method may be used to rescue recombinant infectious virus in accordance with the invention. To this end, the PIV polymerase protein may be expressed in any expression vector/host cell system, 30 including but not limited to viral expression vectors (e.g., vaccinia virus, adenovirus, baculovirus, etc.) or cell lines that express a polymerase protein (e.g., see Krystal *et al.*, 1986,

Proc. Natl. Acad. Sci. USA 83: 2709-2713). Moreover, infection of host cells expressing all six PIV proteins may result in the production of infectious chimeric virus particles. It should be noted that it may be possible to construct a recombinant virus without altering virus 5 viability. These altered viruses would then be growth competent and would not need helper functions to replicate.

5.4. ATTENUATION OF RECOMBINANT VIRUSES

The recombinant viruses of the invention can be further genetically engineered to 10 exhibit an attenuated phenotype. In particular, the recombinant viruses of the invention exhibit an attenuated phenotype in a subject to which the virus is administered as a vaccine. Attenuation can be achieved by any method known to a skilled artisan. Without being bound by theory, the attenuated phenotype of the recombinant virus can be caused, e.g., by using a virus that naturally does not replicate well in an intended host (e.g., using a bovine PIV3 15 vector in human), by reduced replication of the viral genome, by reduced ability of the virus to infect a host cell, or by reduced ability of the viral proteins to assemble to an infectious viral particle relative to the wild type strain of the virus. The viability of certain sequences of the virus, such as the leader and the trailer sequence can be tested using a minigenome assay (see section 5.5.1).

20 The attenuated phenotypes of a recombinant virus of the invention can be tested by any method known to the artisan (see, e.g., section 5.5). A candidate virus can, for example, be tested for its ability to infect a host or for the rate of replication in a cell culture system. In certain embodiments, a mini-genome system is used to test the attenuated virus when the gene that is altered is N, P, L, M2 or a combination thereof. In certain embodiments, growth 25 curves at different temperatures are used to test the attenuated phenotype of the virus. For example, an attenuated virus is able to grow at 35°C, but not at 39°C or 40°C. In certain embodiments, different cell lines can be used to evaluate the attenuated phenotype of the virus. For example, an attenuated virus may only be able to grow in monkey cell lines but not the human cell lines, or the achievable virus titers in different cell lines are different for 30 the attenuated virus. In certain embodiments, viral replication in the respiratory tract of a small animal model, including but not limited to, hamsters, cotton rats, mice and guinea pigs,

is used to evaluate the attenuated phenotypes of the virus. In other embodiments, the immune response induced by the virus, including but not limited to, the antibody titers (e.g., assayed by plaque reduction neutralization assay or ELISA) is used to evaluate the attenuated phenotypes of the virus. In a specific embodiment, the plaque reduction neutralization assay or ELISA is carried out at a low dose. In certain embodiments, the ability of the recombinant virus to elicit pathological symptoms in an animal model can be tested. A reduced ability of the virus to elicit pathological symptoms in an animal model system is indicative of its attenuated phenotype. In a specific embodiment, the candidate viruses are tested in a monkey model for nasal infection, indicated by mucous production.

The viruses of the invention can be attenuated such that one or more of the functional characteristics of the virus are impaired. In certain embodiments, attenuation is measured in comparison to the wild type strain of the virus from which the attenuated virus is derived. In other embodiments, attenuation is determined by comparing the growth of an attenuated virus in different host systems. Thus, for a non-limiting example, a bovine PIV3 is said to be attenuated when grown in a human host if the growth of the bovine PIV3 in the human host is reduced compared to the growth of the bovine PIV3 in a bovine host.

In certain embodiments, the attenuated virus of the invention is capable of infecting a host, is capable of replicating in a host such that infectious viral particles are produced. In comparison to the wild type strain, however, the attenuated strain grows to lower titers or grows more slowly. Any technique known to the skilled artisan can be used to determine the growth curve of the attenuated virus and compare it to the growth curve of the wild type virus. For exemplary methods see Example section, *infra*. In a specific embodiment, the attenuated virus grows to a titer of less than 10^5 pfu/ml, of less than 10^4 pfu/ml, of less than 10^3 pfu/ml, or of less than 10^2 pfu/ml in Vero cells under conditions as described.

In certain embodiments, the attenuated virus of the invention (e.g., a chimeric PIV3) cannot replicate in human cells as well as the wild type virus (e.g., wild type PIV3) does. However, the attenuated virus can replicate well in a cell line that lack interferon functions, such as Vero cells.

In other embodiments, the attenuated virus of the invention is capable of infecting a host, of replicating in the host, and of causing proteins of the virus of the invention to be

inserted into the cytoplasmic membrane, but the attenuated virus does not cause the host to produce new infectious viral particles. In certain embodiments, the attenuated virus infects the host, replicates in the host, and causes viral proteins to be inserted in the cytoplasmic membrane of the host with the same efficiency as the wild type mammalian virus. In other embodiments, the ability of the attenuated virus to cause viral proteins to be inserted into the cytoplasmic membrane into the host cell is reduced compared to the wild type virus. In certain embodiments, the ability of the attenuated mammalian virus to replicate in the host is reduced compared to the wild type virus. Any technique known to the skilled artisan can be used to determine whether a virus is capable of infecting a mammalian cell, of replicating within the host, and of causing viral proteins to be inserted into the cytoplasmic membrane of the host. For illustrative methods see section 5.5.

In certain embodiments, the attenuated virus of the invention is capable of infecting a host. In contrast to a wild type PIV, however, the attenuated PIV cannot be replicated in the host. In a specific embodiment, the attenuated virus can infect a host and can cause the host to insert viral proteins in its cytoplasmic membranes, but the attenuated virus is incapable of being replicated in the host. Any method known to the skilled artisan can be used to test whether the attenuated virus has infected the host and has caused the host to insert viral proteins in its cytoplasmic membranes.

In certain embodiments, the ability of the attenuated mammalian virus to infect a host is reduced compared to the ability of the wild type virus to infect the same host. Any technique known to the skilled artisan can be used to determine whether a virus is capable of infecting a host. For illustrative methods see section 5.5.

In certain embodiments, mutations (e.g., missense mutations) are introduced into the genome of the virus to generate a virus with an attenuated phenotype. Mutations (e.g., missense mutations) can be introduced into the N-gene, the P-gene, the F-gene, the M2-gene, the M2-1-gene, the M2-2-gene, the SH-gene, the G-gene or the L-gene of the recombinant virus. Mutations can be additions, substitutions, deletions, or combinations thereof. In specific embodiments, a single amino acid deletion mutation for the N, P, L or M2 proteins are introduced, which can be screened for functionality in the mini-genome assay system and evaluated for predicted functionality in the virus. In more specific embodiments, the

missense mutation is a cold-sensitive mutation. In other embodiments, the missense mutation is a heat-sensitive mutation. In one embodiment, major phosphorylation sites of P protein of the virus is removed. In another embodiment, a mutation or mutations are 5 introduced into the L gene of the virus to generate a temperature sensitive strain. In yet another embodiment, the cleavage site of the F gene is mutated in such a way that cleavage does not occur or occurs at very low efficiency.

In other embodiments, deletions are introduced into the genome of the recombinant virus. In more specific embodiments, a deletion can be introduced into the N-gene, the P- 10 gene, the F-gene, the M2-gene, the M2-1-gene, the M2-2-gene, the SH-gene, the G-gene or the L-gene of the recombinant virus. In specific embodiments, the deletion is in the M2-gene of the recombinant virus of the present invention. In other specific embodiments, the deletion is in the SH-gene of the recombinant virus of the present invention. In yet another specific embodiment, both the M2-gene and the SH-gene are deleted.

15 In certain embodiments, the intergenic region of the recombinant virus is altered. In one embodiment, the length of the intergenic region is altered. See Section 5.1.2. for illustrative examples. In another embodiment, the intergenic regions are shuffled from 5' to 3' end of the viral genome.

20 In other embodiments, the genome position of a gene or genes of the recombinant virus is changed. In one embodiment, the F or G gene is moved to the 3' end of the genome. In another embodiment, the N gene is moved to the 5' end of the genome.

25 In certain embodiments, attenuation of the virus is achieved by replacing a gene of the wild type virus with a gene of a virus of a different species. In illustrative embodiments, the N-gene, the P-gene, the F-gene, the M2-gene, the M2-1-gene, the M2-2-gene, the SH-gene, the HN-gene or the L-gene of bPIV3 is replaced with the N-gene, the P-gene, the F-gene, the M2-gene, the M2-1-gene, the M2-2-gene, the SH-gene, the HN-gene or the L-gene, respectively, of hPIV3. In other illustrative embodiments, the N-gene, the P-gene, the F-gene, the M2-gene, the M2-1-gene, the M2-2-gene, the SH-gene, the HN-gene or the L-gene of hPIV3 is replaced with the N-gene, the P-gene, the F-gene, the M2-gene, the M2-1-gene, the M2-2-gene, the SH-gene, the HN-gene or the L-gene, respectively, of bPIV3. In a 30

preferred embodiment, attenuation of the virus is achieved by replacing one or more polymerase associated genes (*e.g.*, N, P, L or M2) with genes of a virus of a different species.

In certain embodiments, attenuation of the virus is achieved by replacing or deleting 5 one or more specific domains of a protein of the wild type virus with domains derived from the corresponding protein of a virus of a different species. In an illustrative embodiment, the ectodomain of a F protein of bPIV3 is replaced with an ectodomain of a F protein of a metapneumovirus. In a preferred embodiment, one or more specific domains of L, N, or P protein are replaced with domains derived from corresponding proteins of a virus of a 10 different species. In another illustrative embodiment, the transmembrane domain of the F protein is deleted so that a soluble F protein is expressed.

In certain embodiments of the invention, the leader and/or trailer sequence of the recombinant virus of the invention can be modified to achieve an attenuated phenotype. In certain, more specific embodiments, the leader and/or trailer sequence is reduced in length 15 relative to the wild type virus by at least 1 nucleotide, at least 2 nucleotides, at least 3 nucleotides, at least 4 nucleotides, at least 5 nucleotides or at least 6 nucleotides. In certain other, more specific embodiments, the sequence of the leader and/or trailer of the recombinant virus is mutated. In a specific embodiment, the leader and the trailer sequence are 100% complementary to each other. In other embodiments, 1 nucleotide, 2 nucleotides, 3 20 nucleotides, 4 nucleotides, 5 nucleotides, 6 nucleotides, 7 nucleotides, 8 nucleotides, 9 nucleotides, or 10 nucleotides are not complementary to each other where the remaining nucleotides of the leader and the trailer sequences are complementary to each other. In certain embodiments, the non-complementary nucleotides are identical to each other. In certain other embodiments, the non-complementary nucleotides are different from each other. 25 In other embodiments, if the non-complementary nucleotide in the trailer is purine, the corresponding nucleotide in the leader sequence is also a purine. In other embodiments, if the non-complementary nucleotide in the trailer is pyrimidine, the corresponding nucleotide in the leader sequence is also a purine.

When a live attenuated vaccine is used, its safety must also be considered. The 30 vaccine must not cause disease. Any techniques known in the art that can make a vaccine safe may be used in the present invention. In addition to attenuation techniques, other

techniques may be used. One non-limiting example is to use a soluble heterologous gene that cannot be incorporated into the virion membrane. For example, a single copy of the soluble RSV F gene, a version of the RSV gene lacking the transmembrane and cytosolic domains, 5 can be used. Since it cannot be incorporated into the virion membrane, the virus tropism is not expected to change.

Various assays can be used to test the safety of a vaccine. See section 5.5., *infra*. Particularly, sucrose gradients and neutralization assays can be used. A sucrose gradient assay can be used to determine whether a heterologous protein is inserted in a virion. If the 10 heterologous protein is inserted in the virion, the virion should be tested for its ability to cause symptoms even if the parental strain does not cause symptoms. Without bound by theory, if the heterologous protein is incorporated in the virion, the virus may have acquired new, possibly pathological, properties.

15 **5.5. MEASUREMENT OF VIRAL TITER, EXPRESSION OF ANTIGENIC SEQUENCES, IMMUNOGENICITY AND OTHER CHARACTERISTICS OF CHIMERIC VIRUSES**

A number of assays may be employed in accordance with the present invention in order to determine the rate of growth of a chimeric or recombinant virus in a cell culture system, an animal model system or in a subject. A number of assays may also be employed 20 in accordance with the present invention in order to determine the requirements of the chimeric and recombinant viruses to achieve infection, replication and packaging of virions.

The assays described herein may be used to assay viral titre over time to determine the growth characteristics of the virus. In a specific embodiment, the viral titre is determined 25 by obtaining a sample from the infected cells or the infected subject, preparing a serial dilution of the sample and infecting a monolayer of cells that are susceptible to infection with the virus at a dilution of the virus that allows for the emergence of single plaques. The plaques can then be counted and the viral titre express as plaque forming units per milliliter of sample. In a specific embodiment of the invention, the growth rate of a virus of the invention in a subject is estimated by the titer of antibodies against the virus in the subject. 30 Without being bound by theory, the antibody titer in the subject reflects not only the viral

titer in the subject but also the antigenicity. If the antigenicity of the virus is constant, the increase of the antibody titer in the subject can be used to determine the growth curve of the virus in the subject. In a preferred embodiment, the growth rate of the virus in animals or 5 humans is best tested by sampling biological fluids of a host at multiple time points post-infection and measuring viral titer.

The expression of heterologous gene sequence in a cell culture system or in a subject can be determined by any technique known to the skilled artisan. In certain embodiments, the expression of the heterologous gene is measured by quantifying the level of the transcript. 10 The level of the transcript can be measured by Northern blot analysis or by RT-PCR using probes or primers, respectively, that are specific for the transcript. The transcript can be distinguished from the genome of the virus because the virus is in the antisense orientation whereas the transcript is in the sense orientation. In certain embodiments, the expression of the heterologous gene is measured by quantifying the level of the protein product of the 15 heterologous gene. The level of the protein can be measured by Western blot analysis using antibodies that are specific to the protein.

In a specific embodiment, the heterologous gene is tagged with a peptide tag. The peptide tag can be detected using antibodies against the peptide tag. The level of peptide tag detected is representative for the level of protein expressed from the heterologous gene. 20 Alternatively, the protein expressed from the heterologous gene can be isolated by virtue of the peptide tag. The amount of the purified protein correlates with the expression level of the heterologous gene. Such peptide tags and methods for the isolation of proteins fused to such a peptide tag are well known in the art. A variety of peptide tags known in the art may be used in the modification of the heterologous gene, such as, but not limited to, the 25 immunoglobulin constant regions, polyhistidine sequence (Petty, 1996, Metal-chelate affinity chromatography, in Current Protocols in Molecular Biology, volume 1-3 (1994-1998). Ed. by Ausubel, F.M., Brent, R., Kunston, R.E., Moore, D.D., Seidman, J.G., Smith, J.A. and Struhl, K. Published by John Wiley and sons, Inc., USA, Greene Publish. Assoc. & Wiley Interscience), glutathione S-transferase (GST; Smith, 1993, Methods Mol. Cell Bio. 4:220-229), the *E. coli* maltose binding protein (Guan et al., 1987, Gene 67:21-30), various 30 cellulose binding domains (U.S. patent 5,496,934; 5,202,247; 5,137,819; Tomme et al.,

1994, Protein Eng. 7:117-123), and the FLAG epitope (Short Protocols in Molecular Biology, 1999, Ed. Ausubel et al., John Wiley & Sons, Inc., Unit 10.11) etc. Other peptide tags are recognized by specific binding partners and thus facilitate isolation by affinity 5 binding to the binding partner, which is preferably immobilized and/or on a solid support. As will be appreciated by those skilled in the art, many methods can be used to obtain the coding region of the above-mentioned peptide tags, including but not limited to, DNA cloning, DNA amplification, and synthetic methods. Some of the peptide tags and reagents for their detection and isolation are available commercially.

10 Samples from a subject can be obtained by any method known to the skilled artisan. In certain embodiments, the sample consists of nasal aspirate, throat swab, sputum or broncho-alveolar lavage.

5.5.1. MINIGENOME CONSTRUCTS

15 Minireplicon constructs can be generated to contain an antisense reporter gene. Any reporter gene known to the skilled artisan can be used with the invention. In a specific embodiment, the reporter gene is CAT. In certain embodiments, the reporter gene can be flanked by the negative-sense bPIV or hPIV leader linked to the hepatitis delta ribozyme (Hep-d Ribo) and T7 polymerase termination (T-T7) signals, and the bPIV or hPIV trailer 20 sequence preceded by the T7 RNA polymerase promoter.

In certain embodiments, the plasmid encoding the minireplicon is transfected into a host cell. The host cell expresses T7 RNA polymerase, the N gene, the P gene, the L gene, and the M2.1 gene. In certain embodiments, the host cell is transfected with plasmids encoding T7 RNA polymerase, the N gene, the P gene, the L gene, and the M2.1 gene. In 25 other embodiments, the plasmid encoding the minireplicon is transfected into a host cell and the host cell is infected with a helper virus.

The expression level of the reporter gene and/or its activity can be assayed by any method known to the skilled artisan, such as, but not limited to, the methods described in section 5.5.6.

30 In certain, more specific, embodiments, the minireplicon comprises the following elements, in the order listed: T7 RNA Polymerase or RNA polymerase I, leader sequence,

gene start, GFP, trailer sequence, Hepatitis delta ribozyme sequence or RNA polymerase I termination sequence. If T7 is used as RNA polymerase, Hepatitis delta ribozyme sequence should be used as termination sequence. If RNA polymerase I is used, RNA polymerase I termination sequence may be used as a termination signal. Dependent on the rescue system, the sequence of the minireplicon can be in the sense or antisense orientation. In certain embodiments, the leader sequence can be modified relative to the wild type leader sequence of the virus of the invention. The leader sequence can optionally be preceded by an AC. The T7 promoter sequence can be with or without a G-doublet or triplet, where the G-doublet or triplet provides for increased transcription.

In a specific embodiment, a cell is infected with a virus of the invention at T0. 24 hours later, at T24, the cell is transfected with a minireplicon construct. 48 hours after T0 and 72 hours after T0, the cells are tested for the expression of the reporter gene. If a fluorescent reporter gene product is used (*e.g.*, GFP), the expression of the reporter gene can be tested using FACS.

In another embodiment, a cell is transfected with six plasmids at T=0 hours. Cells are then harvested at T=40 hours and T=60 hours and analyzed for CAT or GFP expression.

In another specific embodiment, a cell is infected with MVA-T7 at T0. 1 hour later, at T1, the cell is transfected with a minireplicon construct. 24 hours after T0, the cell is infected with a virus of the invention. 72 hours after T0, the cells are tested for the expression of the reporter gene. If a fluorescent reporter gene product is used (*e.g.*, GFP), the expression of the reporter gene can be tested using FACS.

5.5.2. MEASUREMENT OF INCIDENCE OF INFECTION RATE

The incidence of infection can be determined by any method well-known in the art, including but not limited to, the testing of clinical samples (*e.g.*, nasal swabs) for the presence of an infection, *e.g.*, hMPV, RSV, hPIV, or bPIV/hPIV components can be detected by immunofluorescence assay (IFA) using an anti-hMPV-antigen antibody, an anti-RSV-antigen antibody, an anti-hPIV-antigen antibody, and/or an antibody that is specific to the gene product of the heterologous nucleotide sequence, respectively.

In certain embodiments, samples containing intact cells can be directly processed,

whereas isolates without intact cells should first be cultured on a permissive cell line (e.g. HEp-2 cells). In an illustrative embodiment, cultured cell suspensions are cleared by centrifugation at, e.g., 300xg for 5 minutes at room temperature, followed by a PBS, pH 7.4
5 (Ca⁺⁺ and Mg⁺⁺ free) wash under the same conditions. Cell pellets are resuspended in a small volume of PBS for analysis. Primary clinical isolates containing intact cells are mixed with PBS and centrifuged at 300xg for 5 minutes at room temperature. Mucus is removed from the interface with a sterile pipette tip and cell pellets are washed once more with PBS under the same conditions. Pellets are then resuspended in a small volume of PBS for
10 analysis. Five to ten microliters of each cell suspension are spotted per 5 mm well on acetone washed 12-well HTC supercured glass slides and allowed to air dry. Slides are fixed in cold (-20°C) acetone for 10 minutes. Reactions are blocked by adding PBS - 1% BSA to each well followed by a 10 minute incubation at room temperature. Slides are washed three times in PBS - 0.1% Tween-20 and air dried. Ten microliters of each primary antibody
15 reagent diluted to 250 ng/ml in blocking buffer is spotted per well and reactions are incubated in a humidified 37°C environment for 30 minutes. Slides are then washed extensively in three changes of PBS - 0.1% Tween-20 and air dried. Ten microliters of appropriate secondary conjugated antibody reagent diluted to 250 ng/ml in blocking buffer are spotted per respective well and reactions are incubated in a humidified 37°C environment
20 for an additional 30 minutes. Slides are then washed in three changes of PBS - 0.1% Tween-20. Five microliters of PBS-50% glycerol-10 mM Tris pH 8.0-1 mM EDTA are spotted per reaction well and slides are mounted with cover slips. Each reaction well is subsequently analyzed by fluorescence microscopy at 200X power using a B-2A filter (EX 450-490 nm). Positive reactions are scored against an autofluorescent background obtained from unstained
25 cells or cells stained with secondary reagent alone. RSV positive reactions are characterized by bright fluorescence punctuated with small inclusions in the cytoplasm of infected cells.

5.5.3. MEASUREMENT OF SERUM TITER

Antibody serum titer can be determined by any method well-known in the art, for
30 example, but not limited to, the amount of antibody or antibody fragment in serum samples can be quantitated by a sandwich ELISA. Briefly, the ELISA consists of coating microtiter

plates overnight at 4°C with an antibody that recognizes the antibody or antibody fragment in the serum. The plates are then blocked for approximately 30 minutes at room temperature with PBS-Tween-0.5% BSA. Standard curves are constructed using purified antibody or 5 antibody fragment diluted in PBS-BSA-BSA, and samples are diluted in PBS-BSA. The samples and standards are added to duplicate wells of the assay plate and are incubated for approximately 1 hour at room temperature. Next, the non-bound antibody is washed away with PBS-TWEEN and the bound antibody is treated with a labeled secondary antibody (e.g., horseradish peroxidase conjugated goat-anti-human IgG) for approximately 1 hour at room 10 temperature. Binding of the labeled antibody is detected by adding a chromogenic substrate specific for the label and measuring the rate of substrate turnover, e.g., by a spectrophotometer. The concentration of antibody or antibody fragment levels in the serum is determined by comparison of the rate of substrate turnover for the samples to the rate of substrate turnover for the standard curve.

15

5.5.4. CHALLENGE STUDIES

This assay is used to determine the ability of the recombinant viruses of the invention and of the vaccines of the invention to prevent lower respiratory tract viral infection in an animal model system, including but not limited to, cotton rats, Syrian Golden hamsters, and 20 Balb/c mice. The recombinant virus and/or the vaccine can be administered by intravenous (IV) route, by intramuscular (IM) route or by intranasal route (IN). The recombinant virus and/or the vaccine can be administered by any technique well-known to the skilled artisan. This assay is also used to correlate the serum concentration of antibodies with a reduction in lung titer of the virus to which the antibodies bind.

25

On day 0, groups of animals, including but not limited to, cotton rats (*Sigmodon hispidus*, average weight 100 g) and hamsters (e.g., Syrian Golden hamsters) are inoculated with the recombinant virus or the vaccine of interest or BSA by intramuscular injection, by intravenous injection, or by intranasal route. Prior to, concurrently with, or subsequent to administration of the recombinant virus or the vaccine of the invention, the animals are 30 infected with wild type virus wherein the wild type virus is the virus against which the vaccine was generated. In certain embodiments, the animals are infected with the wild type

virus at least 1 day, at least 2 days, at least 3 days, at least 4 days, at least 5 days, at least 6 days, at least 1 week, at least 2 weeks, at least 3 weeks or at least 4 weeks subsequent to the administration of the recombinant virus and/or the vaccine of the invention. In a preferred embodiment, the animals are infected with the wild type virus 21 days subsequent to the administration of the recombinant virus and/or the vaccine of the invention. In another preferred embodiment, the animals are infected with the wild type virus 28 days subsequent to the administration of the recombinant virus and/or the vaccine of the invention.

After the infection, the animals are sacrificed, and their nasal turbinete tissue and/or lung tissue are harvested and virus titers are determined by appropriate assays, e.g., plaque assay and TCID₅₀ assay. Bovine serum albumin (BSA) 10 mg/kg can be used as a negative control. Antibody concentrations in the serum at the time of challenge can be determined using a sandwich ELISA.

15 5.5.5. CLINICAL TRIALS

Vaccines of the invention or fragments thereof that have been tested in *in vitro* assays and animal models may be further evaluated for safety, tolerance, immunogenicity, infectivity and pharmacokinetics in groups of normal healthy human volunteers, including all age groups. In a preferred embodiment, the healthy human volunteers are infants at about 6 weeks of age or older, children and adults. The volunteers are administered intranasally, intramuscularly, intravenously or by a pulmonary delivery system in a single dose of a recombinant virus of the invention and/or a vaccine of the invention. Multiple doses of virus and/or vaccine of the invention may be required in seronegative children 6 to 60 months of age. Multiple doses of virus and/or vaccine of the invention may also be required in the first six months of life to stimulate local and systemic immunity and to overcome neutralization by maternal antibody. In a preferred embodiment, a primary dosing regimen at 2, 4, and 6 months of age and a booster dose at the beginning of the second year of life are used. A recombinant virus of the invention and/or a vaccine of the invention can be administered alone or concurrently with pediatric vaccines recommended at the corresponding ages.

30 In a preferred embodiment, double-blind randomized, placebo-controlled clinical trials are used. In a specific embodiment, a computer generated randomization schedule is

used. For example, each subject in the study will be enrolled as a single unit and assigned a unique case number. Multiple subjects within a single family will be treated as individuals for the purpose of enrollment. Parent/guardian, subjects, and investigators will remain 5 blinded to which treatment group subjects have been assigned for the duration of the study. Serologic and virologic studies will be performed by laboratory personnel blinded to treatment group assignment. However, it is expected that isolation of the vaccine virus from nasal wash fluid obtained after vaccination will identify likely vaccinees to the virology 10 laboratory staff. The serologic and virologic staff are separate and the serology group will be prevented from acquiring any knowledge of the culture results.

Each volunteer is preferably monitored for at least 12 hours prior to receiving the recombinant virus of the invention and/or a vaccine of the invention, and each volunteer will be monitored for at least fifteen minutes after receiving the dose at a clinical site. Then 15 volunteers are monitored as outpatients on days 1-14, 21, 28, 35, 42, 49, and 56 postdose. In a preferred embodiment, the volunteers are monitored for the first month after each vaccination as outpatients. All vaccine related serious adverse events will be reported for the entire duration of the trial. A serious adverse event is defined as an event that 1) results in death, 2) is immediately life threatening, 3) results in permanent or substantial disability, 4) results in or prolongs an existing in-patient hospitalization, 5) results in a congenital 20 anomaly, 6) is a cancer, or 7) is the result of an overdose of the study vaccine. Serious adverse events that are not vaccine related will be reported beginning on the day of the first vaccination (Day 0) and continue for 30 days following the last vaccination. Non-vaccine related serious adverse events will not be reported for 5 to 8 months after the 30 day reporting period following the last vaccination. A dose of vaccine/placebo will not be given 25 if a child has a vaccine-related serious adverse event following the previous dose. Any adverse event that is not considered vaccine related, but which is of concern, will be discussed by the clinical study monitor and the medical monitor before the decision to give another dose is made.

Blood samples are collected via an indwelling catheter or direct venipuncture (e.g., by 30 using 10 ml red-top Vacutainer tubes) at the following intervals: (1) prior to administering the dose of the recombinant virus of the invention and/or a vaccine of the invention; (2)

during the administration of the dose of the recombinant virus of the invention and/or a vaccine of the invention; (3) 5 minutes, 10 minutes, 15 minutes, 20 minutes, 30 minutes, 1 hour, 2 hours, 4 hours, 8 hours, 12 hours, 24 hours, and 48 hours after administering the dose 5 of the recombinant virus of the invention and/or a vaccine of the invention; and (4) 3 days, 7 days 14 days, 21 days, 28 days, 35 days, 42 days, 49 days, and 56 days after administering the dose of the recombinant virus of the invention and/or a vaccine of the invention. In a specific embodiment, a total of 5 blood draws (3-5 ml each) are obtained, each just prior to the first, third and booster doses and approximately one month following the third dose and booster 10 dose of administration of the vaccine or placebo. Samples are allowed to clot at room temperature and the serum is collected after centrifugation.

Sera are tested for strain-specific serum hemagglutination inhibition (HAI) antibody levels against the virus of the invention. Other indicators of immunogenicity such as IgG, IgA, or neutralizing antibodies are also tested. Serum antibody responses to one or more of 15 the other vaccines given concurrently may be measured. The amount of antibodies generated against the recombinant virus of the invention and/or a vaccine of the invention in the samples from the patients can be quantitated by ELISA.

The concentration of antibody levels in the serum of volunteers are corrected by subtracting the predose serum level (background level) from the serum levels at each 20 collection interval after administration of the dose of recombinant virus of the invention and/or a vaccine of the invention. For each volunteer the pharmacokinetic parameters are computed according to the model-independent approach (Gibaldi *et al.*, eds., 1982, *Pharmacokinetics*, 2nd edition, Marcel Dekker, New York) from the corrected serum antibody or antibody fragment concentrations.

25 Nasal washes obtained approximately 2, 3, 4, 5, 6, 7 or 8 days after each doses of vaccine/placebo will be cultured to detect shedding of the vaccine virus of the invention. In a preferred embodiment, nasal washes obtained 7 days after each doses of vaccine/placebo are cultured. A nasopharyngeal swab, a throat swab, or a nasal wash is also used to determine the presence of other viruses in volunteers with medically attended febrile illness (rectal 30 temperature greater than or equal to 102° F) and/or croup, bronchiolitis, or pneumonia at any time during the study. Samples are shipped on dry ice to designated site for study. Assays

for isolation and quantitation of the vaccine virus of the invention and immunostaining assays using MAb to identify the vaccine virus of the invention are used (examples of such assays are given in the Example sections, *infra*). Nasal wash specimens may be tested for
5 other viruses and immune responses including IgG, IgA, and neutralizing antibody.

5.5.6. REPORTER GENES

In certain embodiments, assays for measurement of reporter gene expression in tissue culture or in animal models can be used with the methods of the invention. The nucleotide
10 sequence of the reporter gene is cloned into the virus, such as bPIV, hPIV, or b/hPIV3, wherein (i) the position of the reporter gene is changed and (ii) the length of the intergenic regions flanking the reporter gene are varied. Different combinations are tested to determine the optimal rate of expression of the reporter gene and the optimal replication rate of the virus comprising the reporter gene.

15 In certain embodiments, minigenome constructs are generated to include a reporter gene. The construction of minigenome constructs is described in section 5.5.1.

The abundance of the reporter gene product can be determined by any technique known to the skilled artisan. Such techniques include, but are not limited to, Northern blot analysis or Western blot analysis using probes or antibodies, respectively, that are specific to
20 the reporter gene.

In certain embodiments, the reporter gene emits a fluorescent signal that can be detected in a FACS. FACS can be used to detect cells in which the reporter gene is expressed.

Techniques for practicing the specific aspect of this invention will employ, unless
25 otherwise indicated, conventional techniques of molecular biology, microbiology, and recombinant DNA manipulation and production, which are routinely practiced by one of skill in the art. See, e.g., Sambrook, 1989, Molecular Cloning, A Laboratory Manual, Second Edition; DNA Cloning, Volumes I and II (Glover, Ed. 1985); and Transcription and Translation (Hames & Higgins, Eds. 1984).

30 The biochemical activity of the reporter gene product represents the expression level of the reporter gene. The total level of reporter gene activity depends also on the replication

rate of the recombinant virus of the invention. Thus, to determine the true expression level of the reporter gene from the recombinant virus, the total expression level should be divided by the titer of the recombinant virus in the cell culture or the animal model.

- 5 Reporter genes that can be used with the methods of invention include, but are not limited to, the genes listed in the Table 4 below:

Table 4: Reporter genes and the biochemical properties of the respective reporter gene products

	Reporter Gene	Protein Activity & Measurement
10	CAT (chloramphenicol acetyltransferase)	Transfers radioactive acetyl groups to chloramphenicol or detection by thin layer chromatography and autoradiography
15	GAL (β -galactosidase)	Hydrolyzes colorless galactosides to yield colored products.
20	GUS (β -glucuronidase)	Hydrolyzes colorless glucuronides to yield colored products.
25	LUC (luciferase)	Oxidizes luciferin, emitting photons
	GFP (green fluorescent protein)	fluorescent protein without substrate
	SEAP (secreted alkaline phosphatase)	luminescence reaction with suitable substrates or with substrates that generate chromophores
	HRP (horseradish peroxidase)	in the presence of hydrogen oxide, oxidation of 3,3',5,5'-tetramethylbenzidine to form a colored complex
	AP (alkaline phosphatase)	luminescence reaction with suitable substrates or with substrates that generate chromophores

- 30 The abundance of the reporter gene can be measured by, *inter alia*, Western blot analysis or Northern blot analysis or any other technique used for the quantification of transcription of a nucleotide sequence, the abundance of its mRNA its protein (see Short

Protocols in Molecular Biology, Ausubel *et al.* (editors), John Wiley & Sons, Inc., 4th edition, 1999). In certain embodiments, the activity of the reporter gene product is measured as a readout of reporter gene expression from the recombinant virus. For the quantification of the 5 activity of the reporter gene product, biochemical characteristics of the reporter gene product can be investigated (see Table 1). The methods for measuring the biochemical activity of the reporter gene products are well-known to the skilled artisan. A more detailed description of illustrative reporter genes that can be used with the methods of the invention is set forth below.

10

LUCIFERASE

Luciferases are enzymes that emit light in the presence of oxygen and a substrate (luciferin) and which have been used for real-time, low-light imaging of gene expression in cell cultures, individual cells, whole organisms, and transgenic organisms (reviewed by Greer 15 & Szalay, 2002, Luminescence 17(1):43-74).

As used herein, the term "luciferase" as used in relation to the invention is intended to embrace all luciferases, or recombinant enzymes derived from luciferases that have luciferase activity. The luciferase genes from fireflies have been well characterized, for example, from the *Photinus* and *Luciola* species (see, e.g., International Patent Publication No. WO 20 95/25798 for *Photinus pyralis*, European Patent Application No. EP 0 524 448 for *Luciola cruciata* and *Luciola lateralis*, and Devine *et al.*, 1993, Biochim. Biophys. Acta 1173(2):121-132 for *Luciola mingrellica*. Other eucaryotic luciferase genes include, but are not limited to, the sea panzy (*Renilla reniformis*, see, e.g., Lorenz *et al.*, 1991, Proc Natl Acad Sci U S A 88(10):4438-4442), and the glow worm (*Lampyris noctiluca*, see e.g., Sula-Newby *et al.*, 25 1996, Biochem J. 313:761-767). Bacterial luciferin-luciferase systems include, but are not limited to, the bacterial lux genes of terrestrial *Photorhabdus luminescens* (see, e.g., Manukhov *et al.*, 2000, Genetika 36(3):322-30) and marine bacteria *Vibrio fischeri* and *Vibrio harveyi* (see, e.g., Miyamoto *et al.*, 1988, J Biol Chem. 263(26):13393-9, and Cohn *et al.*, 1983, Proc Natl Acad Sci USA., 80(1):120-3, respectively). The luciferases 30 encompassed by the present invention also includes the mutant luciferases described in U.S. Patent No. 6,265,177 to Squirrell *et al.*, which is hereby incorporated by reference in its entirety.

GREEN FLUORESCENT PROTEIN

Green fluorescent protein ("GFP") is a 238 amino acid protein with amino acids 65 to 67 involved in the formation of the chromophore that does not require additional substrates or cofactors to fluoresce (see, e.g., Prasher *et al.*, 1992, Gene 111:229-233; Yang *et al.*, 1996, Nature Biotechnol. 14:1252-1256; and Cody *et al.*, 1993, Biochemistry 32:1212-1218).

As used herein, the term "green fluorescent protein" or "GFP" as used in relation to the invention is intended to embrace all GFPs (including the various forms of GFPs that exhibit colors other than green), or recombinant enzymes derived from GFPs that have GFP activity. The native gene for GFP was cloned from the bioluminescent jellyfish *Aequorea victoria* (see, e.g., Morin *et al.*, 1972, J. Cell Physiol. 77:313-318). Wild type GFP has a major excitation peak at 395 nm and a minor excitation peak at 470 nm. The absorption peak at 470 nm allows the monitoring of GFP levels using standard fluorescein isothiocyanate (FITC) filter sets. Mutants of the GFP gene have been found useful to enhance expression and to modify excitation and fluorescence. For example, mutant GFPs with alanine, glycine, isoleucine, or threonine substituted for serine at position 65 result in mutant GFPs with shifts in excitation maxima and greater fluorescence than wild type protein when excited at 488 nm (see, e.g., Heim *et al.*, 1995, Nature 373:663-664); U.S. Patent No. 5,625,048; Delagrange *et al.*, 1995, Biotechnology 13:151-154; Cormack *et al.*, 1996, Gene 173:33-38; and Cramer *et al.*, 1996, Nature Biotechnol. 14:315-319). The ability to excite GFP at 488 nm permits the use of GFP with standard fluorescence activated cell sorting ("FACS") equipment. In another embodiment, GFPs are isolated from organisms other than the jellyfish, such as, but not limited to, the sea pansy, *Renilla reriformis*.

EGFP is a red-shifted variant of wild-type GFP (3-5) which has been optimized for brighter fluorescence and higher expression in mammalian cells. (Excitation maximum = 488 nm; emission maximum = 507 nm.) EGFP encodes the GFPmut1 variant which contains the double-amino-acid substitution of Phe-64 to Leu and Ser-65 to Thr. The coding sequence of the EGFP gene contains more than 190 silent base changes which correspond to human codon-usage preferences.

BETA GALACTOSIDASE

Beta galactosidase (" β -gal") is an enzyme that catalyzes the hydrolysis of b-galactosides, including lactose, and the galactoside analogs o-nitrophenyl- β -D-galactopyranoside ("ONPG") and chlorophenol red-b-D-galactopyranoside ("CPRG") (see, e.g., Nielsen *et al.*, 1983 Proc Natl Acad Sci USA 80(17):5198-5202; Eustice *et al.*, 1991, Biotechniques 11:739-742; and Henderson *et al.*, 1986, Clin. Chem. 32:1637-1641). The β -gal gene functions well as a reporter gene because the protein product is extremely stable, resistant to proteolytic degradation in cellular lysates, and easily assayed. When ONPG is used as the substrate, β -gal activity can be quantitated with a spectrophotometer or a microplate reader.

As used herein, the term "beta galactosidase" or " β -gal" as used in relation to the invention is intended to embrace all b-gals, including *lacZ* gene products, or recombinant enzymes derived from b-gals which have b-gal activity. The b-gal gene functions well as a reporter gene because the protein product is extremely stable, resistant to proteolytic degradation in cellular lysates, and easily assayed. In an embodiment where ONPG is the substrate, b-gal activity can be quantitated with a spectrophotometer or microplate reader to determine the amount of ONPG converted at 420 nm. In an embodiment when CPRG is the substrate, b-gal activity can be quantitated with a spectrophotometer or microplate reader to determine the amount of CPRG converted at 570 to 595 nm.

CHLORAMPHENICOL ACETYLTRANSFERASE

Chloramphenicol acetyl transferase ("CAT") is commonly used as a reporter gene in mammalian cell systems because mammalian cells do not have detectable levels of CAT activity. The assay for CAT involves incubating cellular extracts with radiolabeled chloramphenicol and appropriate co-factors, separating the starting materials from the product by, for example, thin layer chromatography ("TLC"), followed by scintillation counting (see, e.g., U.S. Patent No. 5,726,041, which is hereby incorporated by reference in its entirety).

As used herein, the term "chloramphenicol acetyltransferase" or "CAT" as used in relation to the invention is intended to embrace all CATs, or recombinant enzymes derived from CAT which have CAT activity. While it is preferable that a reporter system which does

not require cell processing, radioisotopes, and chromatographic separations would be more amenable to high through-put screening, CAT as a reporter gene may be preferable in situations when stability of the reporter gene is important. For example, the CAT reporter 5 protein has an *in vivo* half life of about 50 hours, which is advantageous when an accumulative versus a dynamic change type of result is desired.

SECRETED ALKALINE PHOSPHATASE

The secreted alkaline phosphatase ("SEAP") enzyme is a truncated form of alkaline 10 phosphatase, in which the cleavage of the transmembrane domain of the protein allows it to be secreted from the cells into the surrounding media.

As used herein, the term "secreted alkaline phosphatase" or "SEAP" as used in relation to the invention is intended to embrace all SEAP or recombinant enzymes derived 15 from SEAP which have alkaline phosphatase activity. SEAP activity can be detected by a variety of methods including, but not limited to, measurement of catalysis of a fluorescent substrate, immunoprecipitation, HPLC, and radiometric detection. The luminescent method is preferred due to its increased sensitivity over calorimetric detection methods. The advantages of using SEAP is that a cell lysis step is not required since the SEAP protein is secreted out of the cell, which facilitates the automation of sampling and assay procedures. 20 A cell-based assay using SEAP for use in cell-based assessment of inhibitors of the Hepatitis C virus protease is described in U.S. Patent No. 6,280,940 to Potts *et al.* which is hereby incorporated by reference in its entirety.

5.5.7. CELL CULTURE SYSTEMS, EMBRYONATED EGGS, AND ANIMAL MODELS

25

Cell culture systems known in the art can be used to propagate or test activities of the viruses of the present invention. (See e.g., Flint *et al.*, PRINCIPLES OF VIROLOGY, MOLECULAR BIOLOGY, PATHOGENESIS, AND CONTROL, 2000, ASM Press pp25-29, the entire text is incorporated herein by reference). Examples of such cell culture systems 30 include, but are not limited to, primary cell culture that are prepared from animal tissues (e.g., cell cultures derived from monkey kidney, human embryonic amnion, kidney, and foreskin, and chicken or mouse embryos); diploid cell strains that consist of a homogeneous

population of a single type and can divide up to 100 times before dying (e.g., cell culture derived from human embryos, such as the WI-38 strain derived from human embryonic lung); and continuous cell lines consist of a single cell type that can be propagated 5 indefinitely in culture (e.g., HEp-2 cells, Hela cells, Vero cells, L and 3T3 cells, and BHK-21 cells).

Viruses of the invention can also be propagated in embryonated chicken eggs. At 5 to 14 days after fertilization, a hole is drilled in the shell and virus is injected into the site appropriate for its replication.

10 Any animal models known in the art can be used in the present invention to accomplish various purposes, such as to determine the effectiveness and safeness of vaccines of the invention. Examples of such animal models include, but are not limited to, cotton rats (*Sigmodon hispidus*), hamsters, mice, monkeys, and chimpanzees. In a preferred embodiment, Syrian Golden hamsters are used.

15

5.5.8. NEUTRALIZATION ASSAY

Neutralization assays can be carried out to address the important safety issue of whether the heterologous surface glycoproteins are incorporated into the virion which may result in an altered virus tropism phenotype. As used herein, the term "tropism" refers to the 20 affinity of a virus for a particular cell type. Tropism is usually determined by the presence of cell receptors on specific cells which allow a virus to enter that and only that particular cell type. A neutralization assay is performed by using either MAbs of the heterologous surface glycoprotein (non-limiting example is the F protein of a negative strand RNA virus) or polyclonal antiserum comprising antibodies against the heterologous surface glycoprotein. 25 Different dilution of the antibodies are tested to see whether the chimeric virus of the invention can be neutralized. The heterologous surface glycoprotein should not be present on the virion surface in an amount sufficient to result in antibody binding and neutralization.

5.5.9. SUCROSE GRADIENT ASSAY

30 The question of whether the heterologous proteins are incorporated into the virion can be further investigated by use of a biochemical assay. Infected cell lysates can be fractionated in 20 - 60% sucrose gradients, various fractions are collected and analyzed for

the presence and distribution of heterologous proteins and the vector proteins by Western blot. The fractions and the virus proteins can also be assayed for peak virus titers by plaque assay. Examples of sucrose gradient assay are given in section 23, *infra*. When the 5 heterologous proteins are associated with the virion, they will co-migrate with the virion.

5.6. VACCINE FORMULATIONS USING THE CHIMERIC VIRUSES

The invention encompasses vaccine formulations comprising the engineered negative strand RNA virus of the present invention. The recombinant PIV viruses of the present 10 invention may be used as a vehicle to express foreign epitopes that induce a protective response to any of a variety of pathogens. In a specific embodiment, the invention encompasses the use of recombinant bPIV viruses or attenuated hPIV that have been modified in vaccine formulations to confer protection against hPIV infection.

The vaccine preparations of the invention encompass multivalent vaccines, including 15 bivalent and trivalent vaccine preparations. The bivalent and trivalent vaccines of the invention may be administered in the form of one PIV vector expressing each heterologous antigenic sequence or two or more PIV vectors each encoding different heterologous antigenic sequences. For example, a first chimeric PIV expressing one or more heterologous antigenic sequences can be administered in combination with a second chimeric PIV 20 expressing one or more heterologous antigenic sequences, wherein the heterologous antigenic sequences in the second chimeric PIV are different from the heterologous antigenic sequences in the first chimeric PIV. The heterologous antigenic sequences in the first and the second chimeric PIV can be derived from the same virus but encode different proteins, or derived from different viruses. In a preferred embodiment, the heterologous antigenic 25 sequences in the first chimeric PIV are derived from respiratory syncytial virus, and the heterologous antigenic sequences in the second chimeric PIV are derived from human metapneumovirus. In another preferred embodiment, the heterologous antigenic sequences in the first chimeric PIV are derived from respiratory syncytial virus, and the heterologous antigenic sequences in the second chimeric PIV are derived from avian pneumovirus.

30 In certain preferred embodiments, the vaccine formulation of the invention is used to protect against infections caused by a negative strand RNA virus, including but not limited to, influenza virus, parainfluenza virus, respiratory syncytial virus, and mammalian

metapneumovirus (e.g., human metapneumovirus). More specifically, the vaccine formulation of the invention is used to protect against infections by a human metapneumovirus and/or an avian pneumovirus. In certain embodiments, the vaccine 5 formulation of the invention is used to protect against infections by (a) a human metapneumovirus and a respiratory syncytial virus; and/or (b) an avian pneumovirus and a respiratory syncytial virus.

In a preferred embodiment, the invention provides a proteinaceous molecule or metapneumovirus-specific viral protein or functional fragment thereof encoded by a nucleic 10 acid according to the invention. Useful proteinaceous molecules are for example derived from any of the genes or genomic fragments derivable from a virus according to the invention. Particularly useful are the F, SH and/or G protein or antigenic fragments thereof for inclusion as antigen or subunit immunogen, but inactivated whole virus can also be used. Particularly useful are also those proteinaceous substances that are encoded by recombinant 15 nucleic acid fragments that are identified for phylogenetic analyses, of course preferred are those that are within the preferred bounds and metes of ORFs useful in phylogenetic analyses, in particular for eliciting MPV specific antibody or T cell responses, whether in vivo (e.g. for protective purposes or for providing diagnostic antibodies) or in vitro (e.g. by phage display technology or another technique useful for generating synthetic antibodies).

20 A pharmaceutical composition comprising a virus, a nucleic acid, a proteinaceous molecule or fragment thereof, an antigen and/or an antibody according to the invention can for example be used in a method for the treatment or prevention of a MPV infection and/or a respiratory illness comprising providing an individual with a pharmaceutical composition according to the invention. This is most useful when said individual is a human, specifically 25 when said human is below 5 years of age, since such infants and young children are most likely to be infected by a human MPV as provided herein. Generally, in the acute phase patients will suffer from upper respiratory symptoms predisposing for other respiratory and other diseases. Also lower respiratory illnesses may occur, predisposing for more and other serious conditions. The compositions of the invention can be used for the treatment of 30 immuno-compromised individuals including cancer patients, transplant recipients and the elderly.

The invention also provides methods to obtain an antiviral agent useful in the

- treatment of respiratory tract illness comprising establishing a cell culture or experimental animal comprising a virus according to the invention, treating said culture or animal with an candidate antiviral agent, and determining the effect of said agent on said virus or its
- 5 infection of said culture or animal. The invention also provides use of an antiviral agent according to the invention for the preparation of a pharmaceutical composition, in particular for the preparation of a pharmaceutical composition for the treatment of respiratory tract illness, specifically when caused by an MPV infection or related disease, and provides a pharmaceutical composition comprising an antiviral agent according to the invention, useful
- 10 in a method for the treatment or prevention of an MPV infection or respiratory illness, said method comprising providing an individual with such a pharmaceutical composition.

In certain embodiments of the invention, the vaccine of the invention comprises mammalian metapneumovirus. In certain, more specific embodiments, the mammalian metapneumovirus is a human metapneumovirus. In a preferred embodiment, the mammalian metapneumovirus to be used in a vaccine formulation has an attenuated phenotype. For methods to achieve an attenuated phenotype, see section 5.4.

The invention provides vaccine formulations for the prevention and treatment of infections with PIV, RSV, APV, and/or hMPV. In certain embodiments, the vaccine of the invention comprises recombinant and chimeric viruses of the invention. In certain 20 embodiments, the virus is attenuated.

In a specific embodiment, the vaccine comprises APV and the vaccine is used for the prevention and treatment for hMPV infections in humans. Without being bound by theory, because of the high degree of homology of the F protein of APV with the F protein of hMPV, infection with APV will result in the production of antibodies in the host that will cross-react 25 with hMPV and protect the host from infection with hMPV and related diseases.

In another specific embodiment, the vaccine comprises hMPV and the vaccine is used for the prevention and treatment for APV infection in birds, such as, but not limited to, in turkeys. Without being bound by theory, because of the high degree of homology of the F protein of APV with the F protein of hMPV, infection with hMPV will result in the 30 production of antibodies in the host that will cross-react with APV and protect the host from infection with APV and related diseases.

In certain embodiments, the vaccine formulation of the invention is used to protect

against infections by (a) a human metapneumovirus and a human parainfluenza virus; and/or (b) an avian pneumovirus and a human parainfluenza virus and related diseases.

In certain embodiments, the vaccine formulation of the invention is used to protect
5 against infections by (a) a human metapneumovirus, a respiratory syncytial virus, and a human parainfluenza virus; and/or (b) an avian pneumovirus, a respiratory syncytial virus, and a human parainfluenza virus and related diseases.

In certain embodiments, the vaccine formulation of the invention is used to protect against infections by a human metapneumovirus, a respiratory syncytial virus, and a human 10 parainfluenza virus. In certain other embodiments, the vaccine formulation of the invention is used to protect against infections by an avian pneumovirus, a respiratory syncytial virus, and a human parainfluenza virus, and related diseases.

Due to the high degree of homology among the F proteins of different viral species, for exemplary amino acid sequence comparisons see Figure 1, the vaccine formulations of 15 the invention can be used for protection from viruses different from the one from which the heterologous nucleotide sequence encoding the F protein was derived. In a specific exemplary embodiment, a vaccine formulation contains a virus comprising a heterologous nucleotide sequence derived from an avian pneumovirus type A, and the vaccine formulation is used to protect from infection by avian pneumovirus type A and avian pneumovirus type 20 B. In another specific exemplary embodiment, a vaccine formulation contains a virus comprising a heterologous nucleotide sequence derived from an avian pneumovirus subgroup C, and the vaccine formulation is used to protect from infection by avian pneumovirus subgroup C and avian pneumovirus subgroup D.

The invention encompasses vaccine formulations to be administered to humans and 25 animals that are useful to protect against PIV, hMPV, APV (including APV C and APV D), influenza, RSV, Sendai virus, mumps, laryngotracheitis virus, simianvirus 5, human papillomavirus, as well as other viruses, pathogens and related diseases. The invention further encompasses vaccine formulations to be administered to humans and animals that are useful to protect against human metapneumovirus infections, avian pneumovirus infections, 30 and related diseases.

In one embodiment, the invention encompasses vaccine formulations that are useful against domestic animal disease causing agents including rabies virus, feline leukemia virus

(FLV) and canine distemper virus. In yet another embodiment, the invention encompasses vaccine formulations that are useful to protect livestock against vesicular stomatitis virus, rabies virus, rinderpest virus, swinepox virus, and further, to protect wild animals against 5 rabies virus.

Attenuated viruses generated by the reverse genetics approach can be used in the vaccine and pharmaceutical formulations described herein. Reverse genetics techniques can also be used to engineer additional mutations to other viral genes important for vaccine production. For example, mutations in the 5' non-coding region may affect mRNA 10 translation, mutations in capsid proteins are believed to influence viral assembly, and temperature-sensitive and cold-adapted mutants are often less pathogenic than the parental virus. (see, e.g., Flint et al., PRINCIPLES OF VIROLOGY, MOLECULAR BIOLOGY, PATHOGENESIS, AND CONTROL, 2000, ASM Press pp 670 - 683, the entire text is incorporated herein by reference). The epitopes of useful vaccine strain variants can be 15 engineered into the attenuated virus. Alternatively, completely foreign epitopes, including antigens derived from other viral or non-viral pathogens can be engineered into the attenuated strain. For example, antigens of non-related viruses such as HIV (gp160, gp120, gp41), parasite antigens (e.g., malaria), bacterial or fungal antigens, or tumor antigens can be 20 engineered into the attenuated strain. Alternatively, epitopes which alter the tropism of the virus *in vivo* can be engineered into the chimeric attenuated viruses of the invention.

Virtually any heterologous gene sequence may be constructed into the chimeric viruses of the invention for use in vaccines. Preferably, moieties and peptides that act as biological response modifiers are constructed into the chimeric viruses of the invention for use in vaccines. Preferably, epitopes that induce a protective immune response to any of a 25 variety of pathogens, or antigens that bind neutralizing antibodies may be expressed by or as part of the chimeric viruses. For example, heterologous gene sequences that can be constructed into the chimeric viruses of the invention include, but are not limited to influenza and parainfluenza hemagglutinin neuraminidase and fusion glycoproteins such as the HN and F genes of human PIV3. In yet another embodiment, heterologous gene sequences that can 30 be engineered into the chimeric viruses include those that encode proteins with immunomodulating activities. Examples of immunomodulating proteins include, but are not limited to, cytokines, interferon type 1, gamma interferon, colony stimulating factors,

interleukin -1, -2, -4, -5, -6, -12, and antagonists of these agents.

In addition, heterologous gene sequences that can be constructed into the chimeric viruses of the invention for use in vaccines include but are not limited to sequences derived from a human immunodeficiency virus (HIV), preferably type 1 or type 2. In a preferred embodiment, an immunogenic HIV-derived peptide that may be the source of an antigen may be constructed into a chimeric PIV that may then be used to elicit a vertebrate immune response. Such HIV-derived peptides may include, but are not limited to, sequences derived from the env gene (*i.e.*, sequences encoding all or part of gp160, gp120, and/or gp41), the pol gene (*i.e.*, sequences encoding all or part of reverse transcriptase, endonuclease, protease, and/or integrase), the gag gene (*i.e.*, sequences encoding all or part of p7, p6, p55, p17/18, p24/25), tat, rev, nef, vif, vpu, vpr, and/or vpx.

Other heterologous sequences may be derived from hepatitis B virus surface antigen (HBsAg); hepatitis A or C virus surface antigens, the glycoproteins of Epstein Barr virus; the glycoproteins of human papillomavirus; the glycoproteins of respiratory syncytial virus, parainfluenza virus, Sendai virus, simianvirus 5 or mumps virus; the glycoproteins of influenza virus; the glycoproteins of herpesviruses; VP1 of poliovirus; antigenic determinants of non-viral pathogens such as bacteria and parasites, to name but a few. In another embodiment, all or portions of immunoglobulin genes may be expressed. For example, variable regions of anti-idiotypic immunoglobulins that mimic such epitopes may be constructed into the chimeric viruses of the invention.

Other heterologous sequences may be derived from tumor antigens, and the resulting chimeric viruses can be used to generate an immune response against the tumor cells leading to tumor regression *in vivo*. These vaccines may be used in combination with other therapeutic regimens, including but not limited to, chemotherapy, radiation therapy, surgery, bone marrow transplantation, etc. for the treatment of tumors. In accordance with the present invention, recombinant viruses may be engineered to express tumor-associated antigens (TAAs), including but not limited to, human tumor antigens recognized by T cells (Robbins and Kawakami, 1996, Curr. Opin. Immunol. 8:628-636, incorporated herein by reference in its entirety), melanocyte lineage proteins, including gp100, MART-1/MelanA, TRP-1 (gp75), tyrosinase; Tumor-specific widely shared antigens, MAGE-1, MAGE-3, BAGE, GAGE-1, GAGE-1, N-acetylglucosaminyltransferase-V, p15; Tumor-specific mutated antigens,

β -catenin, MUM-1, CDK4; Nonmelanoma antigens for breast, ovarian, cervical and pancreatic carcinoma, HER-2/neu, human papillomavirus -E6, -E7, MUC-1.

In even other embodiments, a heterologous nucleotide sequence is derived from a 5 metapneumovirus, such as human metapneumovirus and/or avian pneumovirus. In even other embodiments, the virus of the invention contains two different heterologous nucleotide sequences wherein one is derived from a metapneumovirus, such as human metapneumovirus and/or avian pneumovirus, and the other one is derived from a respiratory syncytial virus. The heterologous nucleotide sequence encodes a F protein or a G protein of 10 the respective virus. In a specific embodiment, a heterologous nucleotide sequences encodes a chimeric F protein, wherein the chimeric F protein contains the ectodomain of a F protein of a metapneumovirus and the transmembrane domain as well as the luminal domain of a F protein of a parainfluenza virus.

Either a live recombinant viral vaccine or an inactivated recombinant viral vaccine 15 can be formulated. A live vaccine may be preferred because multiplication in the host leads to a prolonged stimulus of similar kind and magnitude to that occurring in natural infections, and therefore, confers substantial, long-lasting immunity. Production of such live recombinant virus vaccine formulations may be accomplished using conventional methods involving propagation of the virus in cell culture or in the allantois of the chick embryo 20 followed by purification. Additionally, as bPIV has been demonstrated to be non-pathogenic in humans, this virus is highly suited for use as a live vaccine.

In this regard, the use of genetically engineered PIV (vectors) for vaccine purposes 25 may desire the presence of attenuation characteristics in these strains. The introduction of appropriate mutations (e.g., deletions) into the templates used for transfection may provide the novel viruses with attenuation characteristics. For example, specific missense mutations that are associated with temperature sensitivity or cold adaption can be made into deletion mutations. These mutations should be more stable than the point mutations associated with cold or temperature sensitive mutants and reversion frequencies should be extremely low.

Alternatively, chimeric viruses with "suicide" characteristics may be constructed. 30 Such viruses would go through only one or a few rounds of replication within the host. When used as a vaccine, the recombinant virus would go through limited replication cycle(s) and induce a sufficient level of immune response but it would not go further in the human

host and cause disease. Recombinant viruses lacking one or more of the PIV genes or possessing mutated PIV genes would not be able to undergo successive rounds of replication.

Defective viruses can be produced in cell lines which permanently express such a gene(s).

- 5 Viruses lacking an essential gene(s) would be replicated in these cell lines, however, when administered to the human host, they would not be able to complete a round of replication. Such preparations may transcribe and translate --in this abortive cycle -- a sufficient number of genes to induce an immune response. Alternatively, larger quantities of the strains could be administered, so that these preparations serve as inactivated (killed) virus vaccines. For 10 inactivated vaccines, it is preferred that the heterologous gene product be expressed as a viral component, so that the gene product is associated with the virion. The advantage of such preparations is that they contain native proteins and do not undergo inactivation by treatment with formalin or other agents used in the manufacturing of killed virus vaccines.
- 15 Alternatively, mutated PIV made from cDNA may be highly attenuated so that it replicates for only a few rounds.

In certain embodiments, the vaccine of the invention comprises an attenuated virus. Without being bound by theory, the attenuated virus can be effective as a vaccine even if the attenuated virus is incapable of causing a cell to generate new infectious viral particles because the viral proteins are inserted in the cytoplasmic membrane of the host thus 20 stimulating an immune response.

In another embodiment of this aspect of the invention, inactivated vaccine formulations may be prepared using conventional techniques to "kill" the chimeric viruses. Inactivated vaccines are "dead" in the sense that their infectivity has been destroyed. Ideally, the infectivity of the virus is destroyed without affecting its immunogenicity. In order to 25 prepare inactivated vaccines, the chimeric virus may be grown in cell culture or in the allantois of the chick embryo, purified by zonal ultracentrifugation, inactivated by formaldehyde or β -propiolactone, and pooled. The resulting vaccine is usually inoculated intramuscularly.

Inactivated viruses may be formulated with a suitable adjuvant in order to enhance the 30 immunological response. Such adjuvants may include but are not limited to mineral gels, e.g., aluminum hydroxide; surface active substances such as lysolecithin, pluronic polyols, polyanions; peptides; oil emulsions; and potentially useful human adjuvants such as BCG,

Corynebacterium parvum, ISCOMS, and virosomes.

- Many methods may be used to introduce the vaccine formulations described above, these include but are not limited to oral, intradermal, intramuscular, intraperitoneal, 5 intravenous, subcutaneous, percutaneous, and intranasal and inhalation routes. It may be preferable to introduce the chimeric virus vaccine formulation via the natural route of infection of the pathogen for which the vaccine is designed.

In certain embodiments, the invention relates to immunogenic compositions. The immunogenic compositions comprise a chimeric PIV. In certain embodiments, the 10 immunogenic composition comprises an attenuated chimeric PIV. In certain embodiments, the immunogenic composition further comprises a pharmaceutically acceptable carrier.

Various techniques may be used to evaluate the effectiveness and safeness of a vaccine according to the present invention. An effective vaccine is a vaccine that protects vaccinated individuals from illness due to pathogens, by invoking proper innate, cellular, and 15 humoral responses with minimal side effect. The vaccine must not cause disease. Any techniques that are able to measure the replication of the virus and the immune response of the vaccinated subject may be used to evaluate the vaccine. Non-limiting examples are given in the Example sections, *infra*.

20 **5.6.1. DOSAGE REGIMENS AND ADMINISTRATION OF THE VACCINES OR IMMUNOGENIC PREPARATIONS OF THE INVENTION**

The present invention provides vaccines and immunogenic preparations comprising chimeric PIV expressing one or more heterologous or non-native antigenic sequences. The vaccines or immunogenic preparations of the invention encompass single or multivalent 25 vaccines, including bivalent and trivalent vaccines. The vaccines or immunogenic formulations of the invention are useful in providing protections against various viral infections. Particularly, the vaccines or immunogenic formulations of the invention provide protection against respiratory tract infections in a host.

A recombinant virus and/or a vaccine or immunogenic formulation of the invention 30 can be administered alone or in combination with other vaccines. Preferably, a vaccine or immunogenic formulation of the invention is administered in combination with other vaccines or immunogenic formulations that provide protection against respiratory tract

diseases, such as but not limited to, respiratory syncytial virus vaccines, influenza vaccines, measles vaccines, mumps vaccines, rubella vaccines, pneumococcal vaccines, rickettsia vaccines, staphylococcus vaccines, whooping cough vaccines or vaccines against respiratory tract cancers. In a preferred embodiment, the virus and/or vaccine of the invention is administered concurrently with pediatric vaccines recommended at the corresponding ages. For example, at two, four or six months of age, the virus and/or vaccine of the invention can be administered concurrently with DtaP (IM), Hib (IM), Polio (IPV or OPV) and Hepatitis B (IM). At twelve or fifteen months of age, the virus and/or vaccine of the invention can be administered concurrently with Hib (IM), Polio (IPV or OPV), MMRII® (SubQ); Varivax® (SubQ), and hepatitis B (IM). The vaccines that can be used with the methods of invention are reviewed in various publications, e.g., The Jordan Report 2000, Division of Microbiology and Infectious Diseases, National Institute of Allergy and Infectious Diseases, National Institutes of Health, United States, the content of which is incorporated herein by reference in its entirety.

A vaccine or immunogenic formulation of the invention may be administered to a subject *per se* or in the form of a pharmaceutical or therapeutic composition. Pharmaceutical compositions comprising an adjuvant and an immunogenic antigen of the invention (e.g., a virus, a chimeric virus, a mutated virus) may be manufactured by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Pharmaceutical compositions may be formulated in conventional manner using one or more physiologically acceptable carriers, diluents, excipients or auxiliaries which facilitate processing of the immunogenic antigen of the invention into preparations which can be used pharmaceutically. Proper formulation is, or amongst others, dependent upon the route of administration chosen.

When a vaccine or immunogenic composition of the invention comprises adjuvants or is administered together with one or more adjuvants, the adjuvants that can be used include, but are not limited to, mineral salt adjuvants or mineral salt gel adjuvants, particulate adjuvants, microparticulate adjuvants, mucosal adjuvants, and immunostimulatory adjuvants. Examples of adjuvants include, but are not limited to, aluminum hydroxide, aluminum phosphate gel, Freund's Complete Adjuvant, Freund's Incomplete Adjuvant, squalene or squalane oil-in-water adjuvant formulations, biodegradable and biocompatible polyesters,

polymerized liposomes, triterpenoid glycosides or saponins (*e.g.*, QuilA and QS-21, also sold under the trademark STIMULON, ISCOPEP), N-acetyl-muramyl-L-threonyl-D-isoglutamine (Threonyl-MDP, sold under the trademark TERMURTIDE), LPS,
5 monophosphoryl Lipid A (3D-MLAsold under the trademark MPL).

The subject to which the vaccine or an immunogenic composition of the invention is administered is preferably a mammal, most preferably a human, but can also be a non-human animal, including but not limited to, primates, cows, horses, sheep, pigs, fowl (*e.g.*, chickens, turkeys), goats, cats, dogs, hamsters, mice and rodents.

10 Many methods may be used to introduce the vaccine or the immunogenic composition of the invention, including but not limited to, oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, percutaneous, intranasal and inhalation routes, and via scarification (scratching through the top layers of skin, *e.g.*, using a bifurcated needle).

15 For topical administration, the vaccine or immunogenic preparations of the invention may be formulated as solutions, gels, ointments, creams, suspensions, etc. as are well-known in the art.

For administration intranasally or by inhalation, the preparation for use according to the present invention can be conveniently delivered in the form of an aerosol spray

20 presentation from pressurized packs or a nebulizer, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the
25 compound and a suitable powder base such as lactose or starch.

For injection, the vaccine or immunogenic preparations may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. The solution may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the proteins
30 may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

Determination of an effective amount of the vaccine or immunogenic formulation for

administration is well within the capabilities of those skilled in the art, especially in light of the detailed disclosure provided herein.

An effective dose can be estimated initially from *in vitro* assays. For example, a dose 5 can be formulated in animal models to achieve an induction of an immunity response using techniques that are well known in the art. One having ordinary skill in the art could readily optimize administration to all animal species based on results described herein. Dosage amount and interval may be adjusted individually. For example, when used as an immunogenic composition, a suitable dose is an amount of the composition that when 10 administered as described above, is capable of eliciting an antibody response. When used as a vaccine, the vaccine or immunogenic formulations of the invention may be administered in about 1 to 3 doses for a 1-36 week period. Preferably, 1 or 2 doses are administered, at intervals of about 2 weeks to about 4 months, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual animals. A 15 suitable dose is an amount of the vaccine formulation that, when administered as described above, is capable of raising an immunity response in an immunized animal sufficient to protect the animal from an infection for at least 4 to 12 months. In general, the amount of the antigen present in a dose ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 μ g. Suitable 20 dose range will vary with the route of injection and the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In a specific embodiment, the viruses and/or vaccines of the invention are administered at a starting single dose of at least 10^3 TCID₅₀, at least 10^4 TCID₅₀, at least 10^5 TCID₅₀, at least 10^6 TCID₅₀. In another specific embodiment, the virus and/or vaccines of the 25 invention are administered at multiple doses. In a preferred embodiment, a primary dosing regimen at 2, 4, and 6 months of age and a booster dose at the beginning of the second year of life are used. More preferably, each dose of at least 10^5 TCID₅₀, or at least 10^6 TCID₅₀ is given in a multiple dosing regimen. The replication rate of a virus can be used as an index to adjust the dosage of a vaccine in a clinical trial. For example, assays to test the replication 30 rate of a virus (*e.g.*, a growth curve, *see* Section 5.5. for available assays) can be used to compare the replication rate of the viruses and/or vaccines of the invention to that of the bPIV3, which was demonstrated in previous studies (*see* Clements *et al.*, J. Clin. Microbiol.

29:1175-82 (1991); Karron *et al.*, J. Infect. Dis. 171:1107-14 (1995); Karron *et al.*, Ped. Inf. Dis. J. 5:650-654 (1996). These studies showed that a bovine PIV3 vaccine is generally safe and well tolerated by healthy human volunteers, including adults, children 6-60 months of age, and infants 2-6 months of age. In these studies, subjects have received at least a single dose of bPIV3 vaccine from 10^3 TCID₅₀ to 10^6 TCID₅₀. Twelve children received two doses of 10^5 TCID₅₀ PIV3 vaccine instead of one dose without untoward effects.). A comparable replication rate as to bPIV3 suggests that a comparable dosage may be used in a clinical trial. A lower replication rate compared to that of bPIV3 suggests that a higher dosage can be used.

10

5.6.1.1. CHALLENGE STUDIES

This assay is used to determine the ability of the recombinant viruses of the invention and of the vaccines of the invention to prevent lower respiratory tract viral infection in an animal model system, such as, but not limited to, cotton rats or hamsters. The recombinant virus and/or the vaccine can be administered by intravenous (IV) route, by intramuscular (IM) route or by intranasal route (IN). The recombinant virus and/or the vaccine can be administered by any technique well-known to the skilled artisan. This assay is also used to correlate the serum concentration of antibodies with a reduction in lung titer of the virus to which the antibodies bind.

20

On day 0, groups of animals, such as, but not limited to, cotton rats (*Sigmodon hispidus*, average weight 100 g) cynomolgous macaques (average weight 2.0 kg) are administered the recombinant or chimeric virus or the vaccine of interest or BSA by intramuscular injection, by intravenous injection, or by intranasal route. Prior to, concurrently with, or subsequent to administration of the recombinant virus or the vaccine of the invention, the animals are infected with wild type virus wherein the wild type virus is the virus against which the vaccine was generated. In certain embodiments, the animals are infected with the wild type virus at least 1 day, at least 2 days, at least 3 days, at least 4 days, at least 5 days, at least 6 days, 1 week or 1 or more months subsequent to the administration of the recombinant virus and/or the vaccine of the invention.

30

After the infection, cotton rats are sacrificed, and their lung tissue is harvested and pulmonary virus titers are determined by plaque titration. Bovine serum albumin (BSA) 10 mg/kg is used as a negative control. Antibody concentrations in the serum at the time of

challenge are determined using a sandwich ELISA. Similarly, in macaques, virus titers in nasal and lung lavages can be measured.

5

5.6.1.2. TARGET POPULATIONS

In certain embodiments of the invention, the target population for the therapeutic and diagnostic methods of the invention is defined by age. In certain embodiments, the target population for the therapeutic and/or diagnostic methods of the invention is characterized by a disease or disorder in addition to a respiratory tract infection.

10

In a specific embodiment, the target population encompasses young children, below 2 years of age. In a more specific embodiment, the children below the age of 2 years do not suffer from illnesses other than respiratory tract infection.

15

In other embodiments, the target population encompasses patients above 5 years of age. In a more specific embodiment, the patients above the age of 5 years suffer from an additional disease or disorder including cystic fibrosis, leukaemia, and non-Hodgkin lymphoma, or recently received bone marrow or kidney transplantation.

20

In a specific embodiment of the invention, the target population encompasses subjects in which the hMPV infection is associated with immunosuppression of the hosts. In a specific embodiment, the subject is an immunocompromised individual.

In certain embodiments, the target population for the methods of the invention encompasses the elderly.

In a specific embodiment, the subject to be treated with the methods of the invention was infected with hMPV in the winter months.

25

5.6.1.3. CLINICAL TRIALS

Vaccines of the invention or fragments thereof tested in *in vitro* assays and animal models may be further evaluated for safety, tolerance and pharmacokinetics in groups of normal healthy adult volunteers. The volunteers are administered intramuscularly, intravenously or by a pulmonary delivery system a single dose of a recombinant virus of the invention and/or a vaccine of the invention. Each volunteer is monitored at least 24 hours prior to receiving the single dose of the recombinant virus of the invention and/or a vaccine of the invention and each volunteer will be monitored for at least 48 hours after receiving the

dose at a clinical site. Then volunteers are monitored as outpatients on days 3, 7, 14, 21, 28, 35, 42, 49, and 56 postdose.

- Blood samples are collected via an indwelling catheter or direct venipuncture using
- 5 10 ml red-top Vacutainer tubes at the following intervals: (1) prior to administering the dose of the recombinant virus of the invention and/or a vaccine of the invention; (2) during the administration of the dose of the recombinant virus of the invention and/or a vaccine of the invention; (3) 5 minutes, 10 minutes, 15 minutes, 20 minutes, 30 minutes, 1 hour, 2 hours, 4 hours, 8 hours, 12 hours, 24 hours, and 48 hours after administering the dose of the
- 10 recombinant virus of the invention and/or a vaccine of the invention; and (4) 3 days, 7 days 14 days, 21 days, 28 days, 35 days, 42 days, 49 days, and 56 days after administering the dose of the recombinant virus of the invention and/or a vaccine of the invention. Samples are allowed to clot at room temperature and serum will be collected after centrifugation.

The amount of antibodies generated against the recombinant virus of the invention and/or a vaccine of the invention in the samples from the patients can be quantitated by

15 ELISA. T-cell immunity (cytotoxic and helper responses) in PBMC and lung and nasal lavages can also be monitored.

The concentration of antibody levels in the serum of volunteers are corrected by subtracting the predose serum level (background level) from the serum levels at each

20 collection interval after administration of the dose of recombinant virus of the invention and/or a vaccine of the invention. For each volunteer the pharmacokinetic parameters are computed according to the model-independent approach (Gibaldi *et al.*, eds., 1982, Pharmacokinetics, 2nd edition, Marcel Dekker, New York) from the corrected serum antibody or antibody fragment concentrations.

25

The following examples are illustrative, but not limiting, of the present invention. Cells and Viruses used in the examples are maintained as follows: the RSV A2 strain and the bovine parainfluenza type 3/human parainfluenza type 3 vectored RSV viruses (bPIV3/hPIV3/RSV viruses) were grown in Vero cells in Opti-MEM (Gibco/BRL) in the presence of gentamycin. The modified vaccinia virus Ankara (MVA-T7) or fowl-pox-T7 (FP-T7) which expressed the phage T7 RNA polymerase were grown in chicken embryonic kidney cells (SPAFAS). Vero, HeLa and Hep-2 cells were maintained in MEM (JRH

Biosciences) supplemented with 10% fetal bovine serum (FBS), 2 mM L-glutamine, non-essential amino acids, and antibiotics.

5 **6. EXAMPLE 1: CONSTRUCTION AND CLONING OF CHIMERIC BOVINE PARAINFLUENZA 3 / HUMAN PARAINFLUENZA 3 cDNA**

In order to substitute the F and HN genes of bPIV3 with those of hPIV3, additional restriction enzyme sites were introduced into the infectious bPIV3 cDNA. Using site-directed mutagenesis, a unique Nhe I site was introduced at nucleotide position 5041 and a Sal I site was introduced at nt 8529 of the bPIV3 cDNA. The modified full-length bPIV3
10 cDNA was treated with Nhe I and Sal I restriction enzymes and a ~14 kb DNA fragment encompassing all of the viral bPIV3 sequences except the F and HN genes, was isolated by gel purification.

To obtain the hPIV3 F and HN gene sequences, a 10 cm dish of confluent Vero cells was infected with a strain of hPIV3 (hPIV3/Tex/12084/1983). After 3 days of incubation at
15 37°C, the cells were harvested and total RNA was isolated using RNA STAT-LS 50 (Tel-Test Inc.). Viral cDNA was generated by reverse transcription using a hPIV3 specific oligo annealing at position 4828 of the hPIV3 genome. The hPIV3 F and HN genes were amplified by PCR (polymerase chain reaction) using Taq polymerase. The PCR product was cloned into the pT/A TOPO cloning vector (Invitrogen) and from two clones (#11 and #14)
20 the hPIV3 F and HN genes were sequenced. Sequence analysis revealed that for clone #11, the F gene was correct, but the HN gene contained aberrant sequences; for clone #14, the HN gene was correct, but the F gene contained aberrant stop codons. Thus, a plasmid, containing functional hPIV3 F and HN genes, was constructed by combining the correct F gene of #11 with the correct HN gene of #14 in the following manner. Both hPIV3 plasmids (#11 and
25 #14) were digested with NheI and EcoR1. A 1.6 kb fragment harboring the correct F gene was isolated from clone #11 and a 8.5 kb fragment containing the correct HN gene and plasmid sequences, was isolated from clone #14. The two fragments were ligated to produce the intact hPIV3 F and HN genes-containing plasmid. The correct sequence was confirmed by DNA sequence analysis. Finally, a single nucleotide was added at the 3' end of the HN
30 gene in the untranslated region to satisfy the "Rule of Six." The addition of the single nucleotide was accomplished by using the QuikChange mutagenesis kit (Stratagene) and was

confirmed by DNA sequencing. The correct hPIV3 F and HN gene DNA fragment was then isolated by digestion with Nhe 1 and Sal 1 and a 3.5 kb DNA fragment was gel purified.

- The full-length b/h PIV3 chimeric cDNA was constructed by ligating the 14.5 kb
- 5 DNA fragment harboring bPIV3 sequences described above and the 3.5 kb DNA fragment containing the hPIV3 F and HN genes (see Figure 3). The full-length chimeric plasmid DNA was confirmed by extensive restriction enzyme mapping. In addition, the M/F and HN/L gene junctions of the chimeric construct were confirmed by DNA sequencing to both contain bPIV3 and hPIV3 sequences as well as a Nhe 1 and a Sal 1 restriction enzyme site,
- 10 respectively.

7. **EXAMPLE 2: CONSTRUCTION AND CLONING OF CHIMERIC BOVINE PARAINFLUENZA 3/HUMAN PARAINFLUENZA 3 VECTORED RESPIRATORY SYNCYTIAL VIRUS F OR G cDNAs**

- In order to determine the effects of RSV antigen insertions in position 1 or 2 of the
- 15 b/h PIV3 genome on virus replication, respiratory syncytial virus (RSV) F and G genes were cloned into different positions of the chimeric bovine parainfluenza 3/human parainfluenza 3 vector (b/h PIV3 vector). See Figure 4.

- In order to insert foreign genes into the bovine/human (b/h) PIV3 cDNA, AvrII restriction enzyme sites were introduced in the b/h PIV3 cDNA plasmid (Haller *et al.*, 2000; 2001, this is the same construct as in Example 6) by site-directed mutagenesis using the QuickChange kit (Stratagene). One AvrII site was introduced at nucleotide (nt) 104 in the b/h PIV3 genome altering four nucleotides using the following oligo 5'GAA ATC CTA AGA CCC TAG GCA TGT TGA GTC3' and its complement. This restriction enzyme site was used to insert the RSV genes in the first (most 3') position of the viral genome. Another 25 AvrII site was introduced in the N-P intergenic region at nt 1774 changing two nucleotides using the following oligo 5'CCACAACTCAATCAACCTAGGATTATGGAAAGACAATG 3' and its complement. This restriction site was used to insert the RSV genes in the second position between the N and P genes of b/h PIV3 (Figure 4). Full-length b/h PIV3 cDNAs harboring the AvrII sites at nts 104 and 1774 were tested for functionality by recovering 30 viruses by reverse genetics.

Construction of RSV G cassette (N-P gene stop/start): A DNA fragment was

generated that contained the bPIV3 N-P intergenic region as well as the 3' end sequences of the RSV G gene, using the b/h PIV3 cDNA as PCR template. This fragment was generated by PCR using the following oligos: 5'CCCAACACACCACGCCAGTAGTCACAA

5 AGAGATGACCACTATCAC3' and 5'CCCAAGCTCCTAGGTGAATCTTG
GTTGATTGAGTTGTGG3'. This fragment was then used to carry out overlapping PCR to add the bPIV3 N-P intergenic region to the RSV G gene. For the second PCR reaction, a plasmid containing the RSV G and F gene was used as a DNA template, the oligo 5'CAGCGGATCCTAGGGAGAAAAGTGTGCAAGAAAAATGTCC3' and an oligo 10 generated from the short PCR fragment above were used as primers. The resulting PCR fragment containing the RSV G gene linked to the bPIV3 N-P intergenic region and flanking AvrII restriction enzyme sites, was cloned into pGEM3. The RSV G gene was sequenced to confirm the presence of an intact open reading frame and the predicted amino acid sequences. The DNA fragments harboring the RSV G gene were inserted into the first or second position 15 using the AvrII restriction enzyme sites into a subclone harboring only the first 5200 nucleotides of the bPIV3 (1-5 bPIV3) genome that was linearized with AvrII. As used herein and other Examples, 1-5 bPIV3 refers to the nucleotide 1 to 5196 (or 5200) of bovine PIV3 genome. There is a BstB1 site at this location.

Construction of RSV F cassette (N-P gene start/stop): The RSV F gene fragment was 20 isolated by PCR from a full-length bPIV3/RSV F+G cDNA plasmid using oligos that added AvrII sites at the 5' and 3' end of the RSV F gene, and introduced into the 1-5 bPIV3 plasmid harboring the AvrII site at nt 1774, which was linearized with AvrII. The bPIV3 N-P intergenic region was isolated by PCR using 1-5 bPIV3/RSV G2 as a template. The oligo 5'GACCGTCGACCACAAAGAGATGACCACTATCACC 3' and an oligo annealing in 25 the bPIV3 F gene were used to generate a PCR fragment containing the bPIV3 N-P intergenic region, AvrII site, and bPIV3 sequences up to nt 5200. The PCR fragment was digested with SalI and NheI, and added to the 1-5 bPIV3 plasmid harboring the RSV F gene in position 2, which was treated with SalI and NheI. To introduce the RSV F gene containing the N-P intergenic region into position 1, the 1.8 kb RSV F cassette was excised 30 using AvrII, and ligated into 1-5 bPIV3 containing the AvrII site at nt 104, which was linearized with AvrII.

Construction of the RSV F cassette with a short intergenic region (N stop/N start):

The generation of the RSV F gene with the short N-N intergenic region was accomplished by performing a PCR reaction using 1-5 bPIV3/RSV F2 as a template, the oligo 5'GCGCGTCGACCAAGTAAGAAAAACTTAGGATTAAAGAACCCTAGGACTGTA3', 5 and an oligo annealing upstream of the 5' end of the RSV F gene encompassing the AvrII restriction enzyme site. The PCR product containing the RSV F gene and the short N-N intergenic region, was digested with AvrII and introduced into 1-5 bPIV3 nt 104 which was linearized with AvrII.

After confirming proper orientation by restriction enzyme mapping, the plasmids 10 harboring the RSV genes in the first position were digested with SphI and BssHII and 4 kb (1-5 bPIV3/RSV G1) or 4.8 kb (1-5 bPIV3/RSV F1) DNA fragments were isolated. In a second cloning step, the remainder of the b/h PIV3 genome was added as a SphI-BssHII 15.1 kb DNA fragment, yielding full-length cDNAs. The bPIV3 subclones, harboring the RSV genes in the second position, were cut with SphI and NheI, and 5.8 kb (bPIV3/RSV G2) and 15 a 6.5 kb (bPIV3/RSV F2) DNA fragments were isolated. In a second cloning step, the rest of the b/h PIV3 genome was added as an NheI-SphI DNA fragment of 14 kb in size. The full-length chimeric b/h PIV3/RSV plasmids were propagated in STBL-2 cells (Gibco/BRL) that provided high yields of full-length virus cDNA plasmids.

20 **8. EXAMPLE 3: BOVINE PARAINFLUENZA 3/HUMAN
PARAINFLUENZA 3 VECTORED RESPIRATORY SYNCYTIAL
VIRUS F OR G DISPLAYED A POSITIONAL EFFECT WITH
REGARDS TO mRNA PRODUCTION AND PROTEIN EXPRESSION
AS WELL AS VIRUS REPLICATION *IN VITRO***

Three experiments were performed to confirm the effective expression of the RSV F 25 or G gene in the constructs of Example 2, and to determine positional effects of gene insertions in the PIV3 genome.

First, in order to demonstrate RSV protein expression by the chimeric viruses, a Western blot of chimeric virus-infected cell lysates was carried out and probed with RSV-specific antisera. See Figure 5A. Western blots were performed as follows: Chimeric viruses 30 were used to infect (70-80%) subconfluent Vero cells at a MOI of 0.1 or 1.0. Forty-eight hours post infection the media overlay was removed and infected monolayers were washed once with 1 ml of PBS. The cells were subsequently lysed in 400 ml of Laemmli buffer

(Bio-Rad) containing 0.05% b-Mercaptoethanol (Sigma). 15 ml of each sample was separated on 12% Tris-HCl Ready Gel (Bio-Rad) and transferred to nylon membranes using a semi-dry transfer cell (Bio-Rad). Nylon membranes were rinsed in PBS [pH 7.6] 5 containing 0.5% (v/v) Tween-20 (Sigma) (PBST) and blocked with PBST containing 5% (w/v) dry milk (PBST-M) for 20-30 minutes at room temperature. Membranes were incubated with either a mixture of RSV F monoclonal antibodies (WHO 1269, 1200, 1153, 1112, 1243, 1107) at a 1:1000 dilution in PBST-M or RSV G 10181 polyclonal antibody (Orbigen) at a 1:2000 dilution in PBST-M for 1 hour at room temperature. Following four 10 washes with PBST, the membranes were incubated with a secondary horseradish peroxidase-conjugated goat anti-mouse antibody (Dako) at a 1:2000 dilution in PBST-M for 1 hour at room temperature. Membranes were washed 4 times with PBST and developed using a chemiluminescence substrate (Amersham Pharmacia) and exposed to Biomax Light Film (Kodak) for visualization of protein bands.

15 Consistent with the reduced replication efficiency of b/h/RSV F1*N-N in Vero cells (Figure 5C, see below), the amount of RSV F₁ detected at 48 hours post infection was about 10 times less than that present in b/h PIV3/RSV F2 or wild-type RSV A2 infected cells (compare lanes 2, 3, and 4, Figure 5A). A 50 kDa band representing the F₁ fragment was detected in cells infected with all chimeric viruses as well as wild-type RSV. However, there 20 was greater accumulation of a 20 kDa F fragment in infected cell lysates of chimeric viruses compared to wild-type RSV. When b/h PIV3/RSV F1*N-N infections were repeated at a higher MOI of 1.0 (Figure 5A, lane 1), the F₁ fragment in b/h PIV3/RSV F1 infected cells accumulated to wild-type RSV levels at 48 hours post-infection. The relative amount of the 50 kDa and 20 kDa F₁ fragments in b/h PIV3/RSV F1 or b/h PIV3/RSV F2 infected cells was 25 approximately 1:5. No F₀ was detected in cells infected with chimeric viruses indicating that the F₀ precursors were efficiently processed during b/h PIV3/RSV F1 and b/h PIV3/RSV F2 infections as was also observed in wild-type RSV infections.

The relative expression of RSV G in b/h PIV3/RSV G1, b/h PIV3/RSV G2 and wild-type RSV infected cells is shown in Figure 5A. Both the immature and glycosylated forms of 30 RSV G that migrated at approximately 50 kDa and 90 kDa, respectively, were detected. b/h PIV3/RSV G1 infected cells showed levels of RSV G expression similar to that seen in wild-type RSV infected cells (lanes 1 and 3, Figure 5A). However, in b/h PIV3/RSV G2 infected

- cells, the accumulation of RSV G was about 2-3 times more than that present in wild-type RSV infected cells (lanes 2 and 3, Figure 5A). Collectively, these data showed that the chimeric b/h PIV3/RSV efficiently expressed the RSV proteins in either position 1 or 2.
- 5 However, the viruses harboring the RSV genes in position 2 expressed higher levels of RSV proteins.

Next, Northern blot analysis showed that the mRNA transcription correlated with the result of the protein expression demonstrated by the Western blot, *see* Figure 5B. Northern blot was performed as follows: total cellular RNA was prepared from virus-infected cells

10 using Trizol LS (Life Technologies). The RNA was further purified by one phenol-chloroform extraction and precipitated with ethanol. RNA pellets were resuspended in diethyl pyrocarbonate-treated water and stored at -80°C. Equal amounts of total RNA were separated on 1% agarose gels containing 1% formaldehyde and transferred to nylon membranes (Amersham Pharmacia Biotech) using a Turbo blotter apparatus (Schleicher & Schuell). The blots were hybridized with digoxigenin (DIG)-UTP-labeled riboprobes

15 synthesized by in vitro transcription using a DIG RNA labeling kit (Roche Molecular Biochemicals). Hybridization was carried out at 68°C for 12 h in Express Hyb solution (Clontech). The blots were washed at 68°C twice with 2X SSC (1X SSC contained 0.015 M NaCl with 0.015 M sodium citrate)-0.1% sodium dodecyl sulfate (SDS) followed by one

20 wash with 0.5X SSC-0.1% SDS and a final wash with 0.1X SSC-0.1% SDS. Signals from the hybridized probes were detected by using a DIG-Luminescent detection kit (Roche Molecular Biochemicals) and visualized by exposure to BioMax ML film (Kodak).

Northern analysis of b/h PIV3/RSV F1*N-N, b/h PIV3/RSV F2, b/h PIV3/RSV G1 and b/h PIV3/RSV G2 showed that the viral mRNA levels for RSV F or RSV G correlated

25 well with the RSV protein levels observed (Figure 5B). The lowest levels of RSV F mRNAs were observed for b/h PIV3/RSV F1*N-N which also displayed the least amount of RSV F protein produced. b/h PIV3/RSV G1 produced less RSV G mRNAs resulting in lower RSV G protein levels than was observed for b/h PIV3/RSV G2.

Finally, growth of different virus (with RSV F or G gene at either position 1 or

30 position 2) correlates with the results of the protein expression and the RNA transcription. The growth curve showed in Figure 5C was obtained as follows: Vero cells were grown to 90% confluence and infected at an MOI of 0.01 or 0.1 with b/h PIV3, b/h PIV3 RSV F1, b/h

PIV3 RSV G1, b/h PIV3 RSV F2, and b/h PIV3 RSV G2. The infected monolayers were incubated at 37°C. At 0, 24, 48, 72, 96 and 120 hours post-infection, cells and media were harvested together and stored at -70°C. Virus titers for each time point harvest were 5 determined by TCID₅₀ or plaque assays in Vero cells. TCID₅₀ assays were inspected visually for CPE following incubation at 37°C for 6 days, while plaque assays were immunostained with RSV polyclonal antisera for quantification after 5 days of incubation.

At an MOI of 0.01 in Vero cells, the chimeric viruses harboring the RSV G or F genes in the first position (b/h PIV3 RSV G1 and b/h PIV3 RSV F1*N-N) replicated at a 10 slower rate, yielded lower peak titers, and exhibited a greater lag phase than the viruses that contained the RSV genes in the second position. Peak titers of b/h PIV3/RSV F1*N-N and b/h PIV3/RSV G1 at 96 hours post-infection were 10^{6.7} and 10^{5.5} TCID₅₀/ml, respectively (Figure 5C). In contrast, peak titers of b/h PIV3/RSV F2 and b/h PIV3/RSV G2 were 10^{8.0} and 10^{7.4} at 72 and 96 hours post-infection, respectively (Figure 5C). The b/h PIV3 control 15 virus displayed peak titers of 10^{8.0} TCID₅₀/ml, respectively (Figure 5C). The b/h PIV3/RSV F2 yielded 1.3 log₁₀ higher titers than b/h PIV3/RSV F1*N-N. The b/h PIV3/RSV G2 replicated to 1.9 log₁₀ higher titers than b/h PIV3/RSV G1. The results indicated that the chimeric viruses harboring the RSV genes in the first position were delayed in onset for replication *in vitro* compared to chimeric viruses containing the RSV genes in the second 20 position.

To determine whether higher titers of b/h PIV3/RSV F1*N-N and b/h PIV3/RSV G1 could be achieved at all, the growth curves were repeated at a higher MOI of 0.1. At an MOI of 0.1, the peak titers of b/h PIV3/RSV F1*N-N and b/h PIV3/RSV G1 increased by 0.5 to 1.3 log₁₀ (data not shown). The lag phases of these viruses were reduced and peak titers were 25 achieved earlier during the growth cycle.

9. EXAMPLE 4: POSITIONAL EFFECT OF eGFP INSERTIONS IN THE BOVINE PARAINFLUENZA 3/HUMAN PARAINFLUENZA 3 GENOME ON VIRUS REPLICATION

The effect of gene insertions into the bovine/human PIV3 vector backbone was assessed systematically by introducing the eGFP gene sequentially between all genes of PIV3 30 and observing the effect on virus replication and eGFP expression (Figure 6). This type of assay investigates the importance of the transcriptional gradient observed for

paramyxoviruses that yields specific ratios of viral mRNAs. Insertion of foreign genes will perturb these ratios and result in the synthesis of different amounts of viral proteins which may influence virus replication. The eGFP gene was chosen for this assay since it will not be incorporated into the virion membrane, and therefore should not interfere with viral processes such as packaging, budding, entry, etc. The eGFP gene was inserted into four positions of the b/h PIV3 genome, three of which were characterized for eGFP expression and virus replication. The eGFP gene cassette was linked to the bPIV3 N-P intergenic region. b/h GFP1 harbored the eGFP gene cassette in the 3' most proximal position of the b/h PIV3 genome. b/h PIV3/GFP2 contained the eGFP gene cassette between the N and P genes of the b/h PIV3 genome. b/h PIV3/GFP3 was located between P and M, and b/h PIV3/GFP4 had the eGFP gene between M and F of b/h PIV3 (Figure 6).

Construction of the eGFP gene cassette: the template of the eGFP gene is commercially available, e.g., it can be purchased from BD Biosciences (pIRES2-EGFP) or 15 Clontech (pEGFP-N1). See Hoffmann *et al.*, Virology 267:310-317 (2000). The eGFP gene was isolated by PCR and the bPIV3 N-P intergenic region was added by employing the overlapping PCR method, using the following oligos: 5'ATTCCTAGGATGGTGAGCAAG 20 GGCG3', 5'GGACGAGCTGTACAAGTAAAAAAATAGCACCTAATCATG3', and 5'CTACCTAGGTGAATCTTGGTTG3'. The eGFP cassette was inserted into pCR2.1, sequenced, and adherence to the rule-of-six was confirmed. Then the eGFP cassette was digested with AvrII, gel purified, and inserted into positions 1, 2, 3, and 4 of b/h PIV3 as described below.

Generation of full-length cDNAs harboring the eGFP gene in positions 1 and 2: the eGFP gene cassette was inserted into the 1-5 bPIV3 plasmids which contained bPIV3 sequences from nts 1 – 5200 and an AvrII restriction enzyme site either at nt 104 (position 1) or nt 1774 (position 2). After confirming proper orientation by restriction enzyme mapping, the plasmid harboring the eGFP gene in the first position was digested with SphI and BssHII and 4 kb (1-5 eGFP1) DNA fragments were isolated. Next, the rest of the b/h PIV3 genome was added as a SphI-BssHII 15.1 kb DNA fragment, yielding full-length cDNAs. For 30 generation of full-length cDNA comprising the eGFP in position 2, the bPIV3 subclones harboring the eGFP genes in the second position were cut with SphI and NheI, and 5.8 kb (1-5 eGFP2) DNA fragments were isolated. Next, the rest of the b/h PIV3 genome was added

as an NheI-SphI DNA fragment of 14 kb in size. The full-length chimeric b/h PIV3/eGFP plasmids were propagated in STBL-2 cells (Gibco/BRL) that provided high yields of full-length virus cDNA plasmids.

- 5 Generation of full-length cDNAs harboring the eGFP gene in positions 3 and 4: in order to insert the eGFP cassette into position 3 of the b/h PIV3 genome, an AvrII restriction enzyme site was introduced at nt 3730 in the P-M intergenic region of a subclone containing nts 1 – 5200 of bPIV3, altering two nucleotides. The following oligo and its complement were used in a QuickChange PCR reaction to introduce the AvrII site:
- 10 5'GGACTAATCAATCCTAGGAAACAATGAGCATCACC3'. The eGFP cassette was digested with AvrII and ligated into the AvrII linearized 1-5 bPIV3 subclone harboring the AvrII site at nt 3730. A 5.5 kb DNA fragment from SphI to NheI was isolated from the GFP containing subclone and introduced into the b/h PIV3 cDNA digested with SphI and NheI to produce a full-length plasmid. In order to add the eGFP gene cassette into position 4 of the
- 15 b/h PIV3 genome, a subclone containing b/h PIV3 sequences from nts 1- 8500 was generated. This subclone was linearized with NheI (nt 5042), and the eGFP cassette containing compatible AvrII ends was inserted. Then the subclone harboring the eGFP cassette was digested with SphI and XhoI and a 7.1 kb DNA fragment was isolated. The b/h PIV3 plasmid was treated with SphI and XhoI and a 11 kb fragment was produced. These
- 20 two DNA fragments were ligated to generate b/h PIV3/GFP4.

The amount of eGFP produced by b/h PIV3/GFP1, 2, and 3 was assessed in two ways. First, the amount of green cells produced upon infecting Vero cells with b/h PIV3 GFP1, 2, and 3 at MOIs of 0.1 and 0.01 for 20 hours, was determined using a fluorescent microscope (Figure 7A). b/h PIV3/GFP3 produced strikingly fewer green cells than b/h PIV3/GFP1 or 2.

Secondly, western analysis was performed on infected cells and the blots were probed with a GFP MAb as well as a PIV3 PAb. The initial observation that b/h PIV3/GFP3 produced dramatically less eGFP protein, was confirmed (Figure 7B). b/h PIV3 GFP1 and GFP2 produced similar amounts of eGFP protein. The western blots methods controlled for

30 same volume loading by probing with a PIV3 antibody (Figure 7B). Interestingly, all three viruses showed similar amounts of PIV3 proteins (the HN protein is the most prominent band) produced. These results suggested that b/h PIV3/GFP3 transcribed less GFP mRNAs

in position 3 as compared to positions 1 and 2. This data confirmed the presence of a transcriptional gradient of viral mRNAs in paramyxoviruses. The level of production of the PIV3 HN protein was not affected by the eGFP gene insertions (Figure 7B).

5 In order to determine whether the GFP gene insertions had an effect on the kinetics of virus replication of b/h PIV3/GFP1, 2, and 3, multicycle growth curves in Vero cells were carried out (Figure 7C). The growth curves showed that b/h PIV3/GFP1 had a delayed onset of virus replication at 24 and 48 hours post-infection than b/h PIV3/GFP2 or GFP3. However, the final peak titers obtained were similar for all three viruses. The kinetics of 10 replication for b/h PIV3/GFP2 and GFP3 were nearly identical (Figure 7C). Interestingly, the altered ratios of viral mRNAs did not appear to effect virus replication significantly.

10. **EXAMPLE 5: CONSTRUCTION AND CLONING OF CHIMERIC BOVINE PARAINFLUENZA 3/HUMAN PARAINFLUENZA 3 VECTORED RESPIRATORY SYNCYTIAL VIRUS F WITH DIFFERENT INTERGENIC REGIONS**

15 Three different constructs were used to determine the effect of intergenic region (nucleotides between each mRNA, e.g., nucleotides between the F gene and the N gene) on protein expression and viral replication. See Figure 8. The first construct was b/h PIV3 vectored RSV F1* N-N in position 1, which had a shorter bPIV N gene stop/N gene start sequence (RSV F1* N-N in Figure 4); the second construct was b/h PIV3 vectored RSV F at 20 position 1 (RSV F2 in Figure 4); and the last one was b/h PIV3 vectored RSV at position 1 (RSV F1 in Figure 4). All three constructs were generated according to the cloning strategies described in section 7, Example 2.

The most dramatic difference between the two cassettes is the distance between the N gene start sequence and the N translation start codon in b/h PIV3/RSV F1*N-N which was 25 only 10 nts long. In contrast, this distance is 86 nts long in b/h PIV3/RSV F2. The other difference is the use of the N gene start sequence in b/h PIV3/RSV F1*N-N rather than the P gene start sequence as was done in b/h PIV3/RSV F2. In order to determine whether the distance between the transcription gene start and the translation start of a viral transcription unit has an effect on virus replication, the b/h PIV3/RSV F1 construct was generated that 30 contained the identical RSV F gene cassette as was used for b/h PIV3/RSV F2.

11. EXAMPLE 6: THE LENGTH AND/OR NATURE OF THE INTERGENIC REGION DOWNSTREAM OF THE RESPIRATORY SYNCYTIAL VIRUS GENE HAS AN EFFECT ON VIRUS REPLICATION

5 The three constructs in Example 5 were used in the following experiments to determine the effects of the intergenic region on viral protein expression and viral replication. See Figure 9.

First, RSV F protein expression for b/h PIV3/RSV F1, b/h PIV3/RSV F1*N-N, and b/h PIV3/RSV F2 was compared at 24 and 48 hrs post-infection at an MOI of 0.1 in Vero
10 cells using Western blots. Western blots were performed as follows: Chimeric viruses were used to infect (70-80%) subconfluent Vero cells at a MOI of 0.1. Twenty-four hours and forty-eight hours post infection the media overlay was removed and infected monolayers were washed once with 1 ml of PBS. The cells were subsequently lysed in 400 ml of Laemmli buffer (Bio-Rad) containing 0.05% b-Mercaptoethanol (Sigma). 15 ml of each
15 sample was separated on 12% Tris-HCl Ready Gel (Bio-Rad) and transferred to nylon membranes using a semi-dry transfer cell (Bio-Rad). Nylon membranes were rinsed in PBS (pH 7.6) containing 0.5% (v/v) Tween-20 (Sigma) (PBST) and blocked with PBST containing 5% (w/v) dry milk (PBST-M) for 20-30 minutes at room temperature.

Membranes were incubated with either a mixture of RSV F monoclonal antibodies (WHO
20 1269,1200, 1153, 1112, 1243, 1107) at a 1:1000 dilution in PBST-M in PBST-M for 1 hour at room temperature. Following 4 washes with PBST, the membranes were incubated with a secondary horseradish peroxidase-conjugated goat anti-mouse antibody (Dako) at a 1:2000 dilution in PBST-M for 1 hour at room temperature. Membranes were washed 4 times with PBST and developed using a chemiluminescence substrate (Amersham Pharmacia) and
25 exposed to Biomax Light Film (Kodak) for visualization of protein bands.

b/h PIV3/RSV F1 expressed RSV F₁ protein levels at 24 and 48 hrs post-infection close to the levels observed for b/h PIV3/RSV F2 but much higher than those of b/h PIV3/RSV F1*N-N. Therefore, the spacing between the gene start element and the translation start codon may be critical for virus replication. The N gene start sequences were
30 changed to P gene start sequences, however this change only incurred the alteration of a single nucleotide. Either of these factors may be responsible for rescuing the RSV F protein

expression phenotype.

Next, multicycle growth curves were carried out to compare the kinetics of virus replication of b/h PIV3/RSV F1, b/h PIV3/RSV F1*N-N, and b/h PIV3/RSV F2 in Vero cells at an MOI of 0.1 (see Figure 9B), which was performed as follows: Vero cells were grown to 90% confluence and infected at an MOI of 0.1 with b/h PIV3, b/h PIV3/RSV F1*N-N, b/h PIV3/RSV F1, and b/h PIV3/RSV F2. The infected monolayers were incubated at 37°C. At 0, 24, 48, 72, and 96 hours post-infection, cells and media were harvested together and stored at -70°C. Virus titers for each time point harvest were determined by plaque assays in Vero cells. The plaque assays were immunostained with RSV polyclonal antisera for quantification after 5 days of incubation.

As was shown on Figure 9B, the onset of replication of b/h PIV3/RSV F1*N-N was delayed and peak titers were lower than those of b/h PIV3/RSV F2. In contrast, b/h PIV3/RSV F1 displayed a growth curve that was nearly identical to that observed for b/h PIV3/RSV F2.

12. EXAMPLE 7: CLONING OF TRIVALENT BOVINE PARAINFLUENZA 3/HUMAN PARAINFLUENZA 3 VECTORED CONSTRUCTS

The following examples relate to the generation of trivalent vaccines that harbor the surface glycoproteins (F and HN) of hPIV3, RSV F, and hMPV F to protect children from disease caused by RSV, hMPV and hPIV3 using a single live attenuated virus vaccine. These trivalent viruses were recovered by reverse genetics.

The construction of two virus genomes, each comprising a chimeric b/h PIV3 backbone with two additional heterologous sequence insertions, wherein one heterologous nucleotide sequence is derived from a metapneumovirus F gene and another heterologous nucleotide sequence is derived from a respiratory syncytial virus F gene, were done as follows (see Figure 10): plasmids b/h PIV3/RSV F2 or b/h PIV3/hMPV F2 was digested with SphI and NheI, and a 6.5 kb fragment was isolated. The full-length cDNA for b/h PIV3 RSV F1 or b/h PIV3/hMPV F1 was digested with SphI and NheI and a 14.8 kb DNA fragment was isolated and ligated with the 6.5 kb DNA fragment derived from plasmid b/h PIV3/RSV F2 or b/h PIV3/hMPV F2 to generate full-length viral cDNAs.

Virus with the above described constructs has been amplified in Vero cells. The engineered virus as described herein can be used as a trivalent vaccine against the parainfluenza virus infection, metapneumovirus infection, and the respiratory syncytial virus
5 infection.

13. EXAMPLE 8: CLONING OF TWO RESPIRATORY SYNCYTIAL VIRUS F TO THE BOVINE PARAINFLUENZA 3/HUMAN PARAINFLUENZA 3 VECTOR

Chimeric viruses that carry two copies of the RSV F gene were designed in order to
10 determine whether more RSV protein produced by the chimeric virus will result in an improved immunogenicity. This virus was rescued by reverse genetics, biologically cloned and amplified in Vero cells to yield a virus stock with a titer of 1×10^6 pfu/ml. This virus, b/h PIV3/RSV F1F2, can be used to assess for virus growth kinetics, for RSV F protein production, and for replication and immunogenicity in hamsters.

15 The constructs were generated in the following manner (see Figure 11): the 1-5 RSV F2 plasmid was digested with SphI and NheI, and a 6.5 kb fragment was isolated. The full-length cDNA for b/h PIV3 RSV F1 was digested with SphI and NheI and a 14.8 kb DNA fragment was isolated and ligated with the 6.5 kb DNA fragment derived from 1-5 bPIV3/RSV F2 to generate full-length viral cDNAs.

20

14. EXAMPLE 9: CONSTRUCTION AND CLONING OF BOVINE PARAINFLUENZA 3/HUMAN PARAINFLUENZA 3 VECTORED HUMAN METAPNEUMOVIRUS F cDNA

The F gene of human metapneumovirus (hMPV) was inserted in positions 1 and 2 of the b/h PIV3 genome (Figure 12). The hMPV F gene cassette harbored the bPIV3 N-P
25 intergenic region. The hMPV F gene plasmid (pRF515) was used, and a single nucleotide mutation in the hMPV F gene was corrected (*i.e.*, nucleotide 3352 was corrected from C to T (wild type)), generating pRF515-M4. The bPIV3 N-P intergenic region was added at the 3' end of the hMPV F gene using overlapping PCR. For hMPV F, the overlapping PCR oligo
30 was 5'GGCTTCATACCACATAATTAGAAAAATAGCA CCTAATCATGTTCTTACAATGGTCGACC 3'. During this cloning step, oligos were used at the 5' end (5' GCAGCCTAGGCCGCAATAACAATGTCTTGGAAAGTGGTG ATC 3')

and at the 3' end of the hMPV F gene cassette (5' CTACCTAGGTGAATCTT TGGT TG 3') in the PCR reaction that contained AvrII restriction enzyme sites. The hMPV F gene cassette was adjusted to conform to the rule of six using QuickChange mutagenesis kit and the 5 following oligos (5'CCTAGGCCGCAATAGACAATGT CTTGG 3', 5'CCAAGACATT GTCTATTGCAGCCTAGG 3'). Full-length b/h PIV3/hMPV F1 (position 1) and F2 (position 2) cDNA plasmids were generated in the same fashion as described in section 9, Example 4, *supra*, for b/h PIV3/eGFP1 and eGFP2.

10 **15. EXAMPLE 10: IMMUNOPRECIPITATION AND REPLICATION ASSAYS OF BOVINE PARAINFLUENZA 3/HUMAN PARAINFLUENZA 3 VECTORED HUMAN METAPNEUMOVIRUS F**

To confirm that the F protein was expressed in the b/h PIV3 vectored human metapneumovirus F at position 2 (hMPV F2), guinea pig or human antiserum were used to immunoprecipitate the hMPV F protein (*see* Figure 13A). For immunoprecipitation of the 15 hMPV F protein expressed by b/h PIV3, Vero cells were infected with b/h PIV3 or b/h PIV3/hMPV F2 at an MOI of 0.1 or 0.05. Twenty-four hours post-infection, the cells were washed once with DME without cysteine and minus methionine (ICN) and incubated in the same media for 30 min. The media was removed and 0.5 ml DME lacking cysteine and methionine containing 100 μ Ci of [35 S]-Pro-Mix (Amersham) was added to the cells. The 20 infected cells were incubated in the presence of 35 S-isotopes for 5 hours at 37°C. Media was removed and the infected cells were lysed in 0.3 M RIPA buffer containing protease inhibitors. The cell lysate was incubated with hMPV guinea pig or human polyclonal antisera and bound to IgG-agarose (Sigma). After washing three times with 0.5 M RIPA buffer, the samples were fractionated on a 10% protein gel. The gel was dried and exposed 25 to X-ray film.

The expression of hMPV F protein by b/h PIV3/hMPV F2 was shown by immunoprecipitation using the gp and human anti-hMPV antisera (Figure 13A). Interestingly, a specific band migrating at approximately 80 kDa was observed in the lysates of b/h PIV3/hMPV F2. This size corresponded to the F precursor protein, F₀. Non-specific 30 bands of different sizes were also observed in the b/h PIV3 and mock control lanes (Figure 13). This data suggested that the b/h PIV3/hMPV F2 expressed the hMPV F protein.

However, the hMPV antibody reagents available are limited and these antisera interact only with the precursor of the hMPV F protein. It could also be possible that the cleaved F1 is unstable and thus not easily visualized using this method.

5 Growth curves were performed to determine the kinetics of virus replication of b/h PIV3/hMPV F2 and compare them to those observed for b/h PIV3 and b/h PIV3/RSV F2 in Vero cells at an MOI of 0.1 (Figure 13B). The data showed that b/h PIV3/hMPV F2 displayed a delayed onset of replication at 24 hours post-infection compared to b/h PIV3/RSV F2. However, at 48 hours post-infection and beyond, a difference in replication 10 was no longer observed.

Growth curves were also performed to determine the kinetics of viral replication of b/h PIV3/hMPV F1 and compare them to those observed for b/h PIV3/hMPV F2 and b/h PIV3 in Vero cells at an MOI of 0.01 (Figure 13C). The data showed that b/h PIV3/hMPV F1 had a delayed onset of replication and yields lower peak titers compared to b/h PIV3/hMPV 15 F2 or b/h PIV3. The plaque size of b/h hMPV F1 is also smaller compared to b/h hMPV F2.

The chimeric viruses, b/h PIV3/hMPV F1 and F2 were also assessed for their ability to infect and replicate in Syrian Golden hamsters (Table 5). The results showed that b/h PIV3/hMPV F1 and F2 replicated in the nasal turbinates and lungs of hamsters to levels observed for b/h PIV3. Even hMPV replicated to titers of 5.3 and 3.6 log₁₀ TCID₅₀/g tissue 20 in the upper and lower respiratory tracts of hamsters. These data showed that b/h PIV3/hMPV F1 and F2 could efficiently infect and replicate in the respiratory tract of hamsters, demonstrating thereby that hamsters represent a suitable small animal model to determine immunogenicity of hMPV as well as utilize this animal model to evaluate hMPV vaccine candidates.

25

30

Table 5

**Replication of b/h PIV3 Expressing
the hMPV F Protein in Positions 1 or 2 in Hamsters**

5	Virus ^a	Mean virus titer on day 4 post-infection	
		(log ₁₀ TCID ₅₀ /g tissue ± S.E.) ^b	
		Nasal turbinates	Lungs
	b/h PIV3	4.8 ± 0.2	5.6 ± 0.6
	b/h hMPV F1	5.3 ± 0.5	5.7 ± 0.4
10	b/h hMPV F2	5.7 ± 0.5	4.6 ± 0.3
	hMPV	5.3 ± 0.1	3.6 ± 0.3

^a Groups of six hamster were inoculated intranasally with 1x 10⁶ pfu of indicated virus.

^b Standard error

Note: TCID₅₀ assays were read for CPE on Day 10.

15 **16. EXAMPLE 11: CLONING OF THE SOLUBLE RESPIRATORY
SYNCYTIAL VIRUS F GENE CONSTRUCT**

A construct containing a single copy of the soluble RSV F gene, a version of the RSV F gene lacking the transmembrane and cytosolic domains, was also generated (Figure 14). This construct can be used to test for immunogenicity. Its advantage would be the inability 20 of the soluble RSV F to be incorporated into the virion membrane. Therefore this virus may be viewed as a safer chimeric virus since its virus tropism is not expected to change. The cDNA plasmid for b/h PIV3/sol RSV F can be rescued by reverse genetics.

The plasmid 1-5/RSV F2 (described previously) was used as a DNA template for PCR. The oligo RSV f.2 (5'GCTGTAACAGAATTGCAGTTGC 3') (which anneals at nt 25 5946 of RSV) and the oligo 5'CGTGGTCGACCATTGTAAGAACATGATTAGGTGCTAT TTTTATTAAATTGTGGTGGATTACCGGC3' were employed to remove the transmembrane and cytoplasmic domains of RSV F, deleting 150 nucleotides. The resulting PCR fragment was digested with HpaI and SalI and introduced into 1-5 RSV F2 treated with HpaI and SalI to yield 1-5 bPIV3/sol RSV F. This plasmid was digested with SphI and NheI 30 and the resulting fragment was introduced into a b/h PIV3 cDNA digested with SphI and NheI to generate a full-length cDNA.

17. **EXAMPLE 12: EXPRESSION OF HUMAN METAPNEUMOVIRUS F IN CELLS INFECTED WITH BOVINE PARAINFLUENZA 3/HUMAN PARAINFLUENZA 3 VECTORED HUMAN METAPNEUMOVIRUS F**

5 The b/h 104 hMPV F virus stocks were serially diluted 10 fold and used to infect subconfluent Vero cells. Infected cells were overlayed with optiMEM media containing gentamycin and incubated at 35°C for 5 days. Cells were fixed with 100% methanol and immunostained with 1:1000 dilution of anti-hMPV001 guinea pig sera followed by 1:1000 dilution of anti-guinea pig HRP conjugated antibodies. Expression of hMPV F is visualized
10 by specific color development in the presence of the AEC substrate system (DAKO corporation). *See Figure 15A.*

The b/h NP-P hMPV F virus stocks were serially diluted 10 fold and used to infect subconfluent Vero cells. Infected cells were overlayed with 1% methyl cellulose in EMEM/L-15 medium (JRH Biosciences; Lenexa, KS) supplemented with 1x L15/MEM
15 media containing penicillin/streptomycin, L-glutamine and fetal bovine serum. Infected cells were incubated at 35°C for 5 days, fixed with 100% methanol and immunostained with 1:1000 dilution of anti-hMPV001 guinea pig sera followed by 1:1000 dilution of anti-guinea pig HRP conjugated antibodies. (*See Figure 15B.*) The anti hMPV001 guinea pig serum is specific for hMPV001 proteins and do not bind to b/h PIV3 proteins.
20

18. **EXAMPLE 13: RESCUE OF CHIMERIC BOVINE PARAINFLUENZA TYPE 3 / HUMAN PARAINFLUENZA TYPE 3 VIRUS IN HE LA CELLS AND VERO CELLS**

Rescue of the chimeric b/h PIV3 virus was done using a similar procedure as for bPIV3 rescue. Rescue of b/h PIV3 chimeric virus by reverse genetics was carried out in
25 HeLa cells using LipofectACE (Gibco/BRL). The 80% confluent HeLa cells, Hep-2 cells, or Vero cells were infected with MVA at an MOI of 4. One hour post-infection, the full-length anti-genomic b/h PIV3 cDNA (4 µg) was transfected into the infected HeLa or Vero cells together with the NP (0.4 µg), P (0.4 µg), and L/pCITE (0.2 µg) expression plasmids.
30 Forty hours post-transfection, the cells and the cell supernatant were harvested (P0) and subjected to a single freeze-thaw cycle. The resulting cell lysate was then used to infect a fresh Vero cell monolayer in the presence of 1-beta-D-arabinofuranosylcytosine (ara C), a

replication inhibitor of vaccinia virus, to generate a P1 virus stock. The supernatant and cells from these plates were harvested, freeze-thawed once and the presence of bPIV3 virus particles was assayed for by immunostaining of virus plaques using PIV3-specific antiserum.

- 5 The cell lysates of the P1 harvest resulted in complete CPE of the Vero cell monolayers and immunostaining indicated the presence of an extensive virus infection.

19. **EXAMPLE 14: RESCUE OF BOVINE PARAINFLUENZA TYPE 3/HUMAN PARAINFLUENZA TYPE 3 VECTORED HUMAN METAPNEUMOVIRUS F VIRUSES**

- 10 The b/h PIV3 viruses expressing hMPV F at position one (b/h 104 hMPV F) or position two (b/h NP-P hMPV F) were obtained as follows. HEp-2 or Vero cells at 80-90% confluence in 6 well dishes were infected with Fowlpox-T7 at a multiplicity of infection (m.o.i) of 0.1 to 0.3. Following infection with Fowlpox-T7, cells were washed once with PBS and transfected with the following amounts of plasmid DNA: full length b/h 104 hMPV F or b/h NP-P hMPV F cDNA 2.0 µg, pCite N 0.4 µg, pCite P 0.4 µg, pCite L 0.2 µg. (The pCite plasmids have a T7 promoter followed by the IRES element derived from the encephalomyocarditis virus (EMCV)). Transfection was performed in the presence of Lipofectamine 2000 (Invitrogen) according to manufacturer's instruction. The transfection reaction was incubated at 33°C for 5 to 12 hours following which the media containing
- 15 lipofectamine 2000 was replaced with 2 ml of fresh OptiMEM containing gentamicin. The transfected cells were further incubated at 33°C for two days. Cells were stabilized with SPG and lysed by one freeze-thaw cycle at -80°C. The crude cell lysate was used to infect a new Vero monolayer in order to amplify rescued viruses.
- 20

25 **EXAMPLE 15: RESCUE OF BOVINE PARAINFLUENZA TYPE 3/HUMAN PARAINFLUENZA TYPE 3 VECTORED RESPIRATORY SYNCYTIAL VIRUS GENES BY REVERSE GENETICS**

- Infectious virus was recovered by reverse genetics in HeLa or HEp-2 cells using transfection methods described previously (see Example 13). Briefly, HEp-2 or Vero cells at 30 80-90% confluence in 6 well tissue culture dishes were infected with FP-T7 or MVA-T7 at a multiplicity of infection (m.o.i) of 0.1 - 0.3 or 1 – 5 respectively. Following infection with FP-T7 or MVA-T7, cells were washed once with PBS and transfected with the following

amounts of plasmid DNA (2.0 μ g full-length b/h PIV3 RSV F or G cDNA, 0.4 μ g pCITE/N, 0.4 μ g pCITE/P, 0.2 μ g pCITE/L). Transfections were performed in the presence of Lipofectamine2000 (Invitrogen) according to manufacturer's instruction. The transfection reactions were incubated at 33°C for 5 to 12 hours following which the media containing Lipofectamine 2000 was replaced with 2 ml of fresh OptiMEM containing gentamicin. The transfected cells were incubated further at 33°C for two days. Cells were stabilized with SPG and lysed with one freeze-thaw cycle at -80°C. The crude cell lysate was used to infect a new Vero cell monolayer in order to amplify rescued viruses. The chimeric viruses were purified by limiting dilutions in Vero cells and high titer virus stocks of 10⁶ – 10⁸ PFU/ml were generated. The RSV genes of the chimeric viruses were isolated by RT-PCR and the sequences were confirmed. Expression of the RSV proteins was confirmed by immunostaining of infected Vero cell monolayers with RSV goat polyclonal antiserum (Biogenesis).

15

21. **EXAMPLE 16: CONFIRMATION OF CHIMERIC BOVINE PARAINFLUENZA TYPE 3 / HUMAN PARAINFLUENZA TYPE 3 VIRUS RESCUE BY RT-PCR**

To ascertain that the rescued virus is chimeric in nature, *i.e.* the virus contains hPIV3 F and HN gene sequences in a bPIV3 backbone, the viral RNA genome was analyzed further by RT-PCR. Vero cells, infected with the P1 virus stock of three independently derived isolates of b/h PIV3 were harvested and total RNA was isolated. The viral RNA was amplified using an oligo that anneals at position 4757 of bPIV3. A viral region from nt 5255 to 6255 was amplified by PCR. The resulting 1 kb PCR fragment should contain hPIV3 sequences. This was confirmed by digestion with enzymes (SacI and Bgl II) specific for hPIV3 and that do not cut in the complementary region of bPIV3 (see Figure 2). As expected, SacI and Bgl II cut the PCR fragment into smaller fragments confirming that the isolated sequences are derived from hPIV3 (see lanes 3, 5, 7). In addition, a region in the polymerase L gene from nt 9075 to nt 10469 was amplified by PCR. This region should contain bPIV3 sequences. Again the resulting 1.4 kb PCR fragment was digested using enzyme specific for bPIV3 (PvuII and BamH1) that do not cut in the equivalent region of hPIV3 (Figure 3). The 1.4 kb fragment was indeed digested by both PvuII and BamH1

confirming that the polymerase gene is bPIV3 in origin (see lanes 3, 4, 6, 7, 9 and 10 of Figure 3). In summary, the RT-PCR analysis shows that the rescued b/h PIV3 virus is chimeric in nature. It contains hPIV3 F and HN genes in a bPIV3 genetic backbone.

5

**22. EXAMPLE 17: GENETIC STABILITY OF BOVINE
PARAINFLUENZA TYPE 3/HUMAN PARAINFLUENZA TYPE 3
VECTORED RESPIRATORY SYNCYTIAL VIRUS GENES**

In order to demonstrate that the b/h PIV3/RSV chimeric viruses are genetically stable and maintain the introduced RSV gene cassettes, infected cell lysates were serially blind 10 passaged ten times in Vero cells. Sub-confluent Vero cells in T25 flasks were infected with b/h PIV3/RSV at an MOI of 0.1 and incubated for 4 days at 33°C or until CPE was visible. At the end of the incubation period the infected cells and media were harvested, frozen and thawed two times, and the resulting cell lysate was used to infect a new T25 flask of Vero 15 cells. This cycle was repeated ten times. All cell lysates from P1 to P10 were analyzed by plaque assay and immunostaining with RSV polyclonal antisera for expression of RSV proteins and virus titers. At passage 10, the RSV gene cassettes were isolated by RT-PCR and the RSV gene sequences were verified by DNA sequence analysis (to identify possible nucleotide alterations). All of the isolates maintained the RSV gene cassettes and RSV protein expression for the 10 passages analyzed (data not shown).

20

**23. EXAMPLE 18: VIRION FRACTIONATION OF BOVINE
PARAINFLUENZA TYPE 3/HUMAN PARAINFLUENZA TYPE 3
VECTORED RESPIRATORY SYNCYTIAL VIRUS GENES ON
SUCROSE GRADIENTS**

25 The question of whether the RSV proteins were incorporated into the b/h PIV3 virion was investigated further by use of a biochemical assay. Vero cells were inoculated with each of the chimeric b/h PIV3/RSV viruses at an MOI of 0.1. When maximum CPE was visible, the infected monolayers were frozen, thawed, and spun for 10 minutes at 2000 rpm. The clarified supernatants were spun through a 20% sucrose cushion at 100,000 x g for 90 30 minutes. The pellet was then resuspended in PBS and layered gently on top of a 20-66% sucrose gradient. The gradients were spun at 100,000 x g for 20 hours to achieve equilibrium. Eighteen 2 ml fractions were harvested starting from the top of the gradient. 0.4 ml of each

fraction was removed for virus titer determination. Each fraction was resuspended in 2 volumes of 20% PBS and concentrated by spinning at 100,000 x g for 1 hour. The pellet was then resuspended in 0.05 ml Laemmli buffer (Biorad) and analyzed for RSV and PIV3 proteins by Western blot, using an RSV F MAb (NuMax L1FR-S28R), RSV (Biogenesis) and bPIV3 (VMRD) polyclonal antisera. C-terminally truncated RSV F protein expressed in baculovirus that was purified to homogeneity, was also analyzed on a sucrose gradients.

The fractions were also analyzed for peak virus titers by plaque assay. Control gradients of free RSV F (generated in baculovirus and C-terminally truncated), RSV A2, and b/h PIV3 were carried out initially. The majority of free RSV F was present in fractions 3, 4, 5, and 6 in the top portion of the gradient (Figure 16A). The biggest concentration of RSV virions was observed in fractions 10, 11 and 12 (Figure 16B). The RSV fractions were probed with RSV polyclonal antiserum as well as with RSV F MAb. The fractions that contained the greatest amounts of RSV virions also showed the strongest signal for RSV F, suggesting that the RSV F protein co-migrated and associated with RSV virions (Figure 16B). These fractions also displayed the highest virus titers (Figure 16B). The b/h PIV3 virions may be more pleiomorphic and thus the spread of the peak fractions containing b/h PIV3 virions was more broad. b/h PIV3 virions were present in fractions 9, 10, 11, 12, and 13 (Figure 16C). Again the fractions harboring the most amounts of virions, also displayed the highest virus titers by plaque assay (Figure 16C). Sucrose gradient fractions of b/h PIV3/RSV F2 were analyzed with both a PIV3 polyclonal antiserum and an RSV F MAb (Figure 16D). The fractions containing most of the virions were fractions 11, 12, 13, and 14 as was shown by western using the PIV3 antiserum. Correspondingly, these were also the fractions that displayed the highest amounts of RSV F protein. However, some free RSV F was also present in fractions 5 and 6. Fractions 11, 12, 13 and 14 displayed the peak virus titers (Figure 16D). Similarly, the fractions containing the most virions of b/h PIV3/RSV G2 (fractions 9, 10, 11, and 12) also showed the strongest signal for RSV G protein (Figure 16E). Again these were the fractions with the highest virus titers (Figure 16E). Collectively these data suggested that the majority of the RSV F and G proteins co-migrated and associated with the b/h PIV3 virions. However, some free RSV proteins were also present in the top fractions of the gradients.

24. EXAMPLE 19: THE CHIMERIC BOVINE PARAINFLUENZA TYPE 3/HUMAN PARAINFLUENZA TYPE 3 VECTORED RESPIRATORY SYNCYTIAL VIRUS (RSV) COULD NOT BE NEUTRALIZED WITH RSV ANTISERA

- 5 In order to address the important safety question of whether the RSV surface glycoproteins incorporated into the b/h PIV3 virion resulted in an altered virus tropism phenotype, neutralization assays were carried out (Tables 6 and 7). RSV F MAbs (WHO 1200 MAb) neutralized 50% of wildtype RSV A2 at a 1:2000 dilution (Table 6). In contrast, even a dilution of 1:25 did not neutralize any of the chimeric b/h PIV3/RSV. Similarly, a 10 dilution of 1:400 of the polyclonal RSV antiserum (Biogenesis) neutralized 50% of RSV A2, but even a dilution of 1:15.6 did not neutralize b/hPIV3 RSV (Table 6).

Table 6

The b/h PIV3 RSV Chimeric Viruses are not Neutralized by RSV Antibodies

15	Virus used in neutralization	Reciprocal 50% neutralizing antibody dilution		
		assay	RSV F MAb	RSV Ab
	RSV		2000	400.0
	b/h PIV3		<25	<15.6
20	b/h RSV F1*N-N		<25	<15.6
	b/h RSV F2		<25	<15.6
	b/h RSV G1		ND	<15.6
	b/h RSV G2		ND	<15.6

25 hPIV3 F MAb C191/9 neutralized 50% of b/h PIV3 as well as the b/h PIV3/RSV at a dilution of 1:500 (Table 7). An hPIV3 HN MAb 68/2 neutralized b/h PIV3 at a dilution of 1:16,000, and the b/h PIV3/RSV at a dilution of 1:32,000 (Table 7).

Table 7**The b/h PIV3 RSV Chimeric Viruses are Neutralized by hPIV3 Mabs**

Virus used in neutralization		Reciprocal 50% neutralizing antibody dilution	
5	assay	hPIV3 F MAb	hPIV3 HN MAb
	RSV	62.5	<500
	b/h PIV3	500	16000
	b/h RSV F1*N-N	500	32000
	b/h RSV F2	500	32000
10	b/h RSV G1	ND ^d	32000
	b/h RSV G2	ND	32000

^d not determined.

15 **25. EXAMPLE 20: THE CHIMERIC BOVINE PIV DEMONSTRATE ATTENUATED PHENOTYPES AND ELICIT STRONG PROTECTIVE RESPONSES WHEN ADMINISTERED *IN VIVO***

Five week old Syrian Golden hamsters were infected with 5×10^5 pfu of wildtype bPIV3, recombinant bPIV3, hPIV3, human/bovine PIV3, and placebo. The five different animal groups were kept separate in micro-isolator cages. Four days post-infection, the 20 animals were sacrificed. The nasal turbinates and lungs of the animals were homogenized and stored at -80°C. Virus present in the tissues was determined by TCID₅₀ assays in MDBK cells at 37°C. Virus infection was confirmed by hemabsorption with guinea pig red blood cells. Table 8 shows the replication titers of the different PIV3 strains in hamsters in the lungs and nasal turbinates. Note that recombinant bPIV3 and the b/h PIV3 chimeric viruses 25 are attenuated in the lungs of the hamsters:

Table 8
Replication of PIV3 Viruses in Syrian
Golden Hamsters in the Nasal Turbinates and Lungs.

Replication of bPIV3, r-bPIV3, r-bPIV3(l), hPIV3 and Bovine/Human PIV3(l) in the Upper and Lower Respiratory Tract of Hamsters		
	Mean virus titer on day 4 postinfection (\log_{10} TCID ₅₀ /g tissue = S. E.) ^b	
Virus ^a	Nasal turbinates	Lungs
bPIV3	5.3 ± 0.3	5.3 ± 0.2
r-bPIV3	5.0 ± 0.3	3.5 ± 0.2
r-bPIV3(l)	5.5 ± 0.2	5.4 ± 0.2
hPIV3	4.9 ± 0.2	5.4 ± 0.2
Bovine/human PIV3(l)	4.9 ± 0.2	4.5 ± 0.2

^a Groups of four hamsters were inoculated intranasally with 5×10^5 PFU of indicated virus.

^b Standard error.

Furthermore, serum samples collected from the hamsters prior to infection and at day 21 post-infection were analyzed in a hemagglutination inhibition assay. The serum samples were treated with receptor destroying enzyme (RDE, DENKA Seiken Co.) and non-specific agglutinins were removed by incubation with guinea pig red blood cells for 1 hour on ice.

Wildtype bPIV3 and hPIV3 were added to two-fold serially diluted hamster serum samples. Finally, guinea pig red blood cells (0.5%) were added, and hemagglutination was allowed to occur at room temperature. Table 9 shows the antibody response generated in the hamsters upon being infected with the different PIV3 strains. Note that the b/h PIV3 chimeric virus generates as strong an antibody response against hPIV3 as does wild type hPIV3, far exceeding the response generated by the recombinant or wildtype bPIV3:

Table 9
**Hemagglutination Inhibition Assay Using Serum from
 Hamsters Infected with Different PIV3 Viruses.**

5	Virus Used for Inoculation of the Hamsters	Hamster Serum Titers for	
		wt bPIV3	hPIV3
	Recombinant bPIV3	1:16	1:16
10	Wt bPIV3	1:16	1:8
	Wt hPIV3	1:4	1:128
	b/h PIV3 chimeric virus	1:8	1:128
	Placebo	<1:4	<1.4

These results demonstrate the properties of b/h PIV3 chimeric viruses of the present invention which make these recombinants suitable for use in vaccine formulations. Not only do the b/h PIV3 chimeric viruses demonstrate an attenuated phenotype when administered *in vivo*, but they also generate as strong an antibody response as the wildtype hPIV3. Thus, because the chimeric viruses of the present invention have a unique combination of having an attenuated phenotype and eliciting as strong an immune response as a wildtype hPIV, these chimeric viruses have the characteristics necessary for successful use in humans to inhibit and/or protect against infection with PIV.

26. **EXAMPLE 21: REPLICATION OF BOVINE PARAINFLUENZA
 3/HUMAN PARAINFLUENZA 3 VECTORED RESPIRATORY
 SYNCYTIAL VIRUS G OR F PROTEIN IN THE UPPER AND
 LOWER RESPIRATORY TRACT OF HAMSTERS**

25 Five week old Syrian Golden hamsters (six animals per group) were infected intranasally with 1×10^6 pfu or 1×10^4 PFU of b/h PIV3, b/h PIV3/RSV, RSV A2, or placebo medium in a 100 ml volume. The different groups were maintained separately in micro-isolator cages. Four days post-infection, the nasal turbinates and lungs of the animals 30 were harvested, homogenized and stored at -70°C. The titers of virus present in the tissues were determined by TCID₅₀ assays in Vero cells. For the challenge assays, the animals were inoculated on day 28 intranasally with 1×10^6 pfu/ml of hPIV3 or RSV A2. Four days post-

challenge, the nasal turbinates and lungs of the animals were isolated and assayed for challenge virus replication by plaque assays on Vero cells that were immunostained for quantification. Table 10 shows the replication titers of the different strains in hamsters in the 5 lungs and nasal turbinates.

Table 10

Replication of bovine/human PIV3 Expressing the RSV G or F proteins in the Upper and Lower Respiratory Tract of Hamsters.

		Mean virus titer on day 4 postinfection (\log_{10} TCID ₅₀ /g tissue = S. E.) ^b	
		Nasal turbinates	Lungs
10	Virus ^a		
	b/h PIV3	4.8 ± 0.4	4.4 ± 0.3
	RSV A2	3.4 ± 0.5	3.3 ± 0.5
	b/h RSV G1	4.2 ± 0.7	2.9 ± 0.7
	b/h RSV F1	3.9 ± 0.4	2.7 ± 0.2
	b/h RSV F1 N-P	4.6 ± 0.4	3.5 ± 0.2
	b/h RSV G2	4.2 ± 0.9	4.3 ± 0.2
15	b/h RSV F2	4.6 ± 0.6	4.4 ± 0.5

* Groups of four hamsters were inoculated intranasally with 5×10^6 PFU of indicated 20 virus.

^b Standard error.

Syrian Golden hamsters represent a suitable small animal model to evaluate replication and immunogenicity of recombinant bPIV3 and hPIV3 genetically engineered viruses. It was expected that the introduction of the RSV antigens would not alter the ability 25 of the chimeric b/h PIV3 to replicate in hamsters. The results showed that all of the chimeric viruses replicated to levels similar to those of b/h PIV3 in the nasal turbinates of hamsters (Table 10). In contrast, the chimeric viruses harboring the RSV genes in the first position displayed 1 – 1.5 \log_{10} reduced titers in the lungs of hamsters compared to b/h PIV3 (Table 10). The chimeric viruses containing the RSV genes in the second position replicated to 30 similar titers observed for b/h PIV3 in the lower respiratory tract of hamsters (Table 10).

27. EXAMPLE 22: BOVINE PARAINFLUENZA 3/HUMAN
PARAINFLUENZA 3 VECTORED RESPIRATORY SYNCYTIAL
VIRUS IMMUNIZED HAMSTERS WERE PROTECTED UPON
CHALLENGE WITH HUMAN PARAINFLUENZA 3 AND
RESPIRATORY SYNCYTIAL VIRUS A2

5 On Day 28 post-immunization, the hamsters were challenged with 1×10^6 PFU of either RSV A2 or hPIV3 to evaluate the immunogenicity induced by the b/h PIV3/RSV. Animals that received the b/h PIV3/RSV were protected completely from RSV as well as hPIV3 (Table 11). Only the animals that were administered the placebo medium displayed high titers of challenge virus in the lower and upper respiratory tracts. This assay also
10 showed that animals immunized with RSV, were not protected from challenge with hPIV3. Similarly, animals vaccinated with hPIV3 displayed high titers of the RSV challenge virus (Table 11).

15

20

25

30

Table 11
**b/h PIV3/RSV Immunized Hamsters were
Protected Upon Challenge with hPIV3 and RSV A2**

	Challenge	hPIV3		RSV A2	
		Mean Virus Titer on Day 4 Post-challenge (\log_{10} TCID ₅₀ /g tissue ± S.E.) ^{b,c}	Mean Virus Titer on Day 4 Post-challenge (\log_{10} pfu/g tissue ± S.E.) ^b	Nasal Turbinates	Lungs
5	Virus:				
10	Immunizing Virus ^a	Nasal turbinates	Lungs	Nasal Turbinates	Lungs
b/h PIV3	<1.2 ± 0.0	<1.0 ± 0.1	ND	ND	
b/h RSV G1	<1.2 ± 0.1	<1.1 ± 0.1	< 1.0 ± 0.3	< 0.7 ± 0.1	
b/h RSV F1	<1.2 ± 0.2	<1.0 ± 0.0	< 1.1 ± 0.5	< 0.6 ± 0.0	
b/h RSV F1 NP-P	<1.0 ± 0.0	<1.0 ± 0.0	< 0.8 ± 0.1	< 0.5 ± 0.0	
b/h RSV G2	<1.2 ± 0.2	<1.1 ± 0.2	< 0.8 ± 0.1	< 0.8 ± 0.3	
b/h RSV F2	<1.2 ± 0.1	<1.0 ± 0.1	< 1.3 ± 0.6	< 1.6 ± 1.0	
15	RSV A2	4.5 ± 0.6	4.8 ± 0.6	< 0.6 ± 0.2	< 0.6 ± 0.1
Placebo	4.4 ± 0.1	4.1 ± 0.1	3.6 ± 0.8	3.1 ± 0.7	

^a Virus used to immunize groups of six hamsters on day 0.

20 ^b On day 28, the hamsters were challenged with 10⁶ pfu of hPIV3 or RSV A2. Four days post-challenge, the lungs and nasal turbinates of the animals were harvested.

^c Standard error.

25 **28. EXAMPLE 23: VACCINATION OF HAMSTERS WITH BOVINE PARAINFLUENZA 3/HUMAN PARAINFLUENZA 3 VECTORED RESPIRATORY SYNCYTIAL VIRUS INDUCES SERUM HAI AND NEUTRALIZING ANTIBODIES**

Prior to the challenge, serum samples were obtained on Day 28 from the immunized animals. The hamster sera were analyzed for the presence of RSV neutralizing antibodies using a 50% plaque reduction assay, and for PIV3 HAI serum antibodies by carrying out 30 hemagglutination inhibition (HAI) assays (Table 8). 50% plaque reduction assay (neutralization assay) was carried out as follows: the hamster sera were two-fold serially

diluted, and incubated with 100 PFU of RSV A2 for one hour. Then the virus-serum mixtures were transferred to Vero cell monolayers and overlaid with methylcellulose. After 5 days of incubation at 35°C, the monolayers were immunostained using RSV polyclonal antiserum for quantification. Hemagglutination-inhibition (HAI) assays were performed by incubating serial two-fold dilutions of Day 28 hamster sera at 25°C for 30 min with hPIV3 in V-bottom 96-well plates. Subsequently, guinea pig erythrocytes were added to each well, incubation was continued for an additional 90 min, and the presence or absence of hemagglutination in each well was recorded.

10 The results showed that the viruses expressing the RSV F protein displayed RSV neutralizing antibody titers nearly as high as those observed with serum obtained from animals vaccinated with wildtype RSV (Table 12). In contrast, the viruses expressing the RSV G protein showed much lower levels of RSV neutralizing antibodies (Table 12). All of the chimeric b/h PIV3/RSV hamster sera showed levels of HAI serum antibodies that were 15 close to the levels observed for b/h PIV3 (Table 12). The results showed that the chimeric b/h PIV3 can infect and replicate efficiently in hamsters and elicit a protective immune response.

20

25

30

Table 12

**Vaccination of Hamsters with b/h PIV3/RSV
Induces Serum HAI and Neutralizing Antibodies**

Virus ^a	Neutralizing antibody response to RSV ^{b,c} (mean reciprocal log ₂ ± SE)	HAI antibody response to hPIV3 ^c (mean reciprocal log ₂ ± SE)
RSV	7.9 ± 1.00	ND
b/h RSV F1* N-N	7.8 ± 0.85	6.6 ± 0.5
b/h RSV F1	5.5 ± 0.53	5.5 ± 0.5
b/h RSV G1	3.4 ± 0.50	6.6 ± 0.7
b/h RSV F2	6.9 ± 0.65	6.7 ± 0.8
b/h RSV G2	3.4 ± 0.50	5.2 ± 0.4
b/h PIV3	ND	7.2 ± 0.5

15

^a Viruses used to immunize hamsters.

^b The neutralizing antibody titers were determined by a 50% plaque reduction assay.

^c The neutralizing antibody titers of hamster pre-serum were < 1.0 and the HAI antibody titers were < 4.0.

20

29. EXAMPLE 24: VACCINATION OF HAMSTERS WITH LOW DOSE OF BOVINE PARAINFLUENZA 3/HUMAN PARAINFLUENZA 3 VECTORED RESPIRATORY SYNCYTIAL VIRUS PROTECTED HAMSTERS FROM CHALLENGE WITH RESPIRATORY SYNCYTIAL VIRUS A2, AND INDUCES SERUM HAI AND NEUTRALIZING ANTIBODIES

25

In order to identify the best vaccine candidate, low dose virus with different constructs (*see Example 2*) were used to immunize hamsters. The results of the challenging experiments are summarized in Table 13.

30

Table 13

**b/h PIV3/RSV-Low Dose Immunized
Hamsters are Protected From Challenge with RSV A2**

	Replication		Challenge with RSV A2	
	Mean Virus Titer on Day 4 Post-vaccination (log ₁₀ TCID ₅₀ /g tissue ± S.E.) ^{b,c}		Mean Virus Titer on Day 4 Post-challenge (log ₁₀ pfu/g tissue ± S.E.) ^b	
Immunizing Virus ^a	Nasal turbinates	Lungs	Nasal Turbinates	Lungs
b/h PIV3	4.9 ± 0.5	4.8 ± 1.0	ND	ND
b/h RSV G1	3.0 ± 0.8	3.1 ± 0.5	< 0.9 ± 0.5	< 0.7 ± 0.4
b/h RSV F1* N-N	3.4 ± 0.1	3.5 ± 0.1	< 1.4 ± 0.7	< 0.5 ± 0.0
b/h RSV G2	4.1 ± 0.6	3.8 ± 0.4	< 0.8 ± 0.0	< 0.5 ± 0.1
b/h RSV F2	5.2 ± 0.6	3.9 ± 0.4	< 0.7 ± 0.1	< 0.5 ± 0.1
RSV A2	2.8 ± 0.3	2.7 ± 0.6	< 0.8 ± 0.1	< 0.5 ± 0.0
Placebo	ND ^d	ND	3.0 ± 0.8	3.2 ± 0.9

^a Virus used to immunize groups of six hamsters on day 0 with a low dose of 10⁴

PFU/ml.

^b On day 28, the hamsters were challenged with 10⁶ pfu of RSV A2. Four days post-challenge, the lungs and nasal turbinates of the animals were harvested.

^c Standard error.

^d not determined.

Next, the neutralizing antibody titers were determined by a 50% plaque reduction assay (neutralization assay). Neutralization assays were performed for b/h PIV3, b/h PIV3/RSV chimeric viruses or RSV using Vero cells. Serial two-fold dilutions of RSV polyclonal antiserum (Biogenesis; Poole, England), an RSV F MAb (WHO 1200 MAb)

obtained from MedImmune or hPIV3 F (C191/9) and HN (68/2) MAbs, were incubated with approximately 100 PFU of either b/h PIV3, b/h PIV3/RSV chimeric viruses or RSV in 0.5 ml

- OptiMEM at RT for 60 min. Following the incubation, virus-serum mixtures were transferred to Vero cell monolayers, incubated at 35°C for 1 hour, overlaid with 1% methyl cellulose in EMEM/L-15 medium (JRH Biosciences; Lenexa, KS) and incubated at 35°C .
- 5 Six days post-inoculation, the infected cell monolayers were immunostained. Neutralization titers were expressed as the reciprocal of the highest serum dilution that inhibited 50% of viral plaques. Neutralization assays were also carried out for serum obtained on Day 28 post-infection from hamsters immunized with b/h PIV3, b/h PIV3/RSV chimeric viruses, or RSV A2. The hamster sera were two-fold serially diluted, and incubated with 100 PFU of RSV
- 10 A2 for one hour. Then the virus-serum mixtures were transferred to Vero cell monolayers and overlaid with methylcellulose. After 5 days of incubation at 35°C the monolayers were immunostained using RSV polyclonal antiserum for quantification. The neutralizing antibody titers of hamster pre-serum were < 1.0 and the HAI antibody titers were < 4.0. Hemagglutination-inhibition (HAI) assays were performed by incubating serial two-fold
- 15 dilutions of Day 28 hamster sera at 25°C for 30 min with hPIV3 in V-bottom 96-well plates. Subsequently, guinea pig erythrocytes were added to each well, incubation was continued for an additional 90 min, and the presence or absence of hemagglutination in each well was recorded. Table 14 summarizes the results:

20

25

30

Table 14

**Vaccination of Hamsters with Lower Doses of
b/h PIV3/RSV Induces Serum HAI and Neutralizing Antibodies**

5

10

15

Virus ^a	Neutralizing antibody response to RSV ^{b,c} (mean reciprocal log ₂ ± SE)	HAI antibody response to hPIV3 ^c (mean reciprocal log ₂ ± SE)
RSV	6.5 ± 0.7	ND
b/h RSV F1* N-N	2.5 ± 0.7	5.7 ± 0.6
b/h RSV G1	2.0 ± 0.0	6.0 ± 0.0
b/h RSV F2	3.8 ± 1.5	6.7 ± 0.6
b/h RSV G2	3.8 ± 1.3	5.5 ± 0.6
b/h PIV3	ND	6.5 ± 0.7

^a Viruses used to immunize hamsters at a low dose of 10⁴ pfu/ml.

^b The neutralizing antibody titers were determined by a 50% plaque reduction assay.

^c The neutralizing antibody titers of hamster pre-serum were < 1.0 and the HAI antibody titers were < 4.0.

20

25

30

The restricted replication phenotype of the chimeric viruses possessing RSV genes in the first position was exacerbated when the inoculation dose was reduced to 1 x 10⁴ PFU per animal. b/h PIV3/RSV F1 and G1 replicated in the upper respiratory tracts of hamsters to titers that were reduced by 1.0 – 2.0 log₁₀ compared to those of b/h PIV3 (Table 13). In contrast, b/h PIV3/RSV with the RSV genes in position 2, replicated in the upper respiratory tract to levels observed for b/h PIV3. Replication in the lungs of hamsters was also more restricted for the b/h PIV3/RSV harboring RSV genes in the first position (Table 13). In contrast, b/h PIV3/RSV F2 still replicated to high titers of 10^{5.2} and 10^{3.9} in the nasal turbinates and lungs, respectively (Table 13). The vaccinated hamsters were challenged on Day 28 with 1 x 10⁶ pfu of RSV A2 (Table 13). Despite the low levels of replication observed in the respiratory tracts of hamsters, the animals were protected in both the lower

and upper respiratory tract from challenge with RSV (Table 13). The degree of protection was as good as was observed for animals vaccinated with wt RSV. Only the animals that received placebo medium showed high virus titers in the nasal turbinates and lungs (Table 5 13). Serum was collected from the immunized hamsters on Day 28, and analyzed for the presence of RSV neutralizing and PIV3 HAI serum antibodies (Table 14). An approximately 50% drop in RSV neutralizing antibody titers was observed in sera obtained from hamsters immunized with b/h PIV3/RSV as compared to the titers observed for wt RSV sera (Table 10 14). But the sera obtained from animals that had received b/h PIV3 harboring the RSV genes in position 2, still displayed higher RSV neutralization antibody titers than was observed for sera from b/h PIV3/RSV with the RSV genes in position 1. The PIV3 HAI serum antibody titers were also slightly reduced compared to the b/h PIV3 sera (Table 14).

15 **30. EXAMPLE 25: BOVINE PARAINFLUENZA 3/HUMAN PARAINFLUENZA 3 VECTORED HUMAN METAPNEUMOVIRUS F IMMUNIZED HAMSTERS WERE PROTECTED UPON CHALLENGE WITH HUMAN PARAINFLUENZA VIRUS 3 OR HUMAN METAPNEUMOVIRUS NL/001**

Five groups of Syrian Golden Hamsters (each group had six hamsters) were immunized with b/h PIV3, b/h hMPV F1, b/h hMPV F2, hMPV or placebo repectively. The 20 five different animal groups were kept separate in micro-isolator cages. On Day 28 post-immunization, the hamsters were challenged with 1×10^6 PFU of either hPIV3 or hMPV (NL/001 strain) to evaluate the immunogenicity induced by the b/h PIV3/hMPV F. Four days post-challenge, the animals were sacrificed. The nasal turbinates and lungs of the animals were homogenized and stored at -80°C. Virus present in the tissues was determined 25 by TCID₅₀ assays in MDBK cells at 37°C. Virus infection was confirmed by hemabsorption with guinea pig red blood cells. Table 15 shows the replication titers of the PIV3 strain and the MPV strain in hamsters in the lungs and nasal turbinates.

Table 15

**b/h PIV3/hMPV F-Immunized Hamsters were Protected Upon Challenge with hPIV3
or hMPV/NL/001**

	Challenge virus:	hPIV3		hMPV	
		Mean virus titer on day 4 post-challenge (\log_{10} TCID ₅₀ /g tissue ± S.E) ^b		Mean virus titer on day 4 post-challenge (\log_{10} PFU/g tissue ± S.E) ^b	
10	Immunizing virus ^a	Nasal Turbinates	Lungs	Nasal Turbinates	Lungs
	b/h PIV3	< 1.3 ± 0.2	< 1.1 ± 0.1		ND
	b/h hMPV F1	< 1.3 ± 0.1	< 1.1 ± 0.1	3.5 ± 0.8	< 0.5 ± 0.2
	b/h hMPV F2	< 1.2 ± 0.1	< 1.2 ± 0.1	< 0.9 ± 0.4	< 0.5 ± 0.1
	hMPV	ND		< 0.8 ± 0.3	< 0.4 ± 0.0
	Placebo	4.3 ± 0.3	4.5 ± 0.5	6.0 ± 0.3	4.5 ± 1.3

^a Virus used to immunize groups of six hamsters on day 0.

^b On day 28, the hamsters were challenged with 10⁶ pfu of hPIV3 or hMPV. Four days post-challenge, the lungs and nasal turbinates of the animals were harvested.

ND = not determined.

The results showed that animals that received the b/h PIV3/hMPV F2 (F at position two) were protected completely from hMPV as well as hPIV3 (Table 15). However, b/h PIV3/hMPV F1 (F at position one) only reduced the titers of infected hMPV in the upper respiratory tract (e.g., nasal turbinates) by 2.5 logs, while it provided complete protection in the lower respiratory tract (e.g., the lung) from both hMPV and hPIV3 infection (Table 15). The animals that were administered the placebo medium displayed high titers of challenge virus in the lower and upper respiratory tracts (Table 15).

The present invention is not to be limited in scope by the specific described embodiments that are intended as single illustrations of individual aspects of the invention, and any constructs, viruses or enzymes that are functionally equivalent are within the scope 5 of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

Various publications are cited herein, the disclosures of which are incorporated by 10 reference in their entireties.

15

20

25

30

Table 16

LEGEND FOR SEQUENCE LISTING

5

SEQ ID NO:1 Human metapneumovirus isolate 00-1 matrix protein (M) and fusion protein (F) genes

SEQ ID NO:2 Avian pneumovirus fusion protein gene, partial cds

10 SEQ ID NO:3 Avian pneumovirus isolate 1b fusion protein mRNA, complete cds

SEQ ID NO:4 Turkey rhinotracheitis virus gene for fusion protein (F1 and F2 subunits), complete cds

15 SEQ ID NO:5 Avian pneumovirus matrix protein (M) gene, partial cds and Avian pneumovirus fusion glycoprotein (F) gene, complete cds

SEQ ID NO:6 paramyxovirus F protein hRSV B

SEQ ID NO:7 paramyxovirus F protein hRSV A2

20 SEQ ID NO:8 human metapneumovirus 01-71 (partial sequence)

SEQ ID NO:9 Human metapneumovirus isolate 00-1 matrix protein (M) and fusion protein (F) genes

25 SEQ ID NO:10 Avian pneumovirus fusion protein gene, partial cds

SEQ ID NO:11 Avian pneumovirus isolate 1b fusion protein mRNA, complete cds

SEQ ID NO:12 Turkey rhinotracheitis virus gene for fusion protein (F1 and F2 subunits), complete cds

30 SEQ ID NO:13 Avian pneumovirus fusion glycoprotein (F) gene, complete cds

SEQ ID NO:14 Turkey rhinotracheitis virus (strain CVL14/1) attachment protein (G) mRNA, complete cds

SEQ ID NO:15 Turkey rhinotracheitis virus (strain 6574) attachment
protein (G), complete cds

5 SEQ ID NO:16 Turkey rhinotracheitis virus (strain CVL14/1) attachment
protein (G) mRNA, complete cds

SEQ ID NO:17 Turkey rhinotracheitis virus (strain 6574) attachment
protein (G), complete cds

10 SEQ ID NO:18 F protein sequence for HMPV isolate NL/1/00

SEQ ID NO:19 F protein sequence for HMPV isolate NL/17/00

SEQ ID NO:20 F protein sequence for HMPV isolate NL/1/99

SEQ ID NO:21 F protein sequence for HMPV isolate NL/1/94

15 SEQ ID NO:22 F-gene sequence for HMPV isolate NL/1/00

SEQ ID NO:23 F-gene sequence for HMPV isolate NL/17/00

SEQ ID NO:24 F-gene sequence for HMPV isolate NL/1/99

20 SEQ ID NO:25 F-gene sequence for HMPV isolate NL/1/94

SEQ ID NO:26 G protein sequence for HMPV isolate NL/1/00

SEQ ID NO:27 G protein sequence for HMPV isolate NL/17/00

25 SEQ ID NO:28 G protein sequence for HMPV isolate NL/1/99

SEQ ID NO:29 G protein sequence for HMPV isolate NL/1/94

SEQ ID NO:30 G-gene sequence for HMPV isolate NL/1/00

SEQ ID NO:31 G-gene sequence for HMPV isolate NL/17/00

30 SEQ ID NO:32 G-gene sequence for HMPV isolate NL/1/99

SEQ ID NO:33 G-gene sequence for HMPV isolate NL/1/94
SEQ ID NO:34 L protein sequence for HMPV isolate NL/1/00
5 SEQ ID NO:35 L protein sequence for HMPV isolate NL/17/00
SEQ ID NO:36 L protein sequence for HMPV isolate NL/1/99
SEQ ID NO:37 L protein sequence for HMPV isolate NL/1/94
10 SEQ ID NO:38 L-gene sequence for HMPV isolate NL/1/00
SEQ ID NO:39 L-gene sequence for HMPV isolate NL/17/00
SEQ ID NO:40 L-gene sequence for HMPV isolate NL/1/99
15 SEQ ID NO:41 L-gene sequence for HMPV isolate NL/1/94
SEQ ID NO:42 M2-1 protein sequence for HMPV isolate NL/1/00
SEQ ID NO:43 M2-1 protein sequence for HMPV isolate NL/17/00
SEQ ID NO:44 M2-1 protein sequence for HMPV isolate NL/1/99
20 SEQ ID NO:45 M2-1 protein sequence for HMPV isolate NL/1/94
SEQ ID NO:46 M2-1 gene sequence for HMPV isolate NL/1/00
SEQ ID NO:47 M2-1 gene sequence for HMPV isolate NL/17/00
25 SEQ ID NO:48 M2-1 gene sequence for HMPV isolate NL/1/99
SEQ ID NO:49 M2-1 gene sequence for HMPV isolate NL/1/94
SEQ ID NO:50 M2-2 protein sequence for HMPV isolate NL/1/00
30 SEQ ID NO:51 M2-2 protein sequence for HMPV isolate NL/17/00
SEQ ID NO:52 M2-2 protein sequence for HMPV isolate NL/1/99

SEQ ID NO:53 M2-2 protein sequence for HMPV isolate NL/1/94
SEQ ID NO:54 M2-2 gene sequence for HMPV isolate NL/1/00
5 SEQ ID NO:55 M2-2 gene sequence for HMPV isolate NL/17/00
SEQ ID NO:56 M2-2 gene sequence for HMPV isolate NL/1/99
SEQ ID NO:57 M2-2 gene sequence for HMPV isolate NL/1/94
10 SEQ ID NO:58 M2 gene sequence for HMPV isolate NL/1/00
SEQ ID NO:59 M2 gene sequence for HMPV isolate NL/17/00
SEQ ID NO:60 M2 gene sequence for HMPV isolate NL/1/99
15 SEQ ID NO:61 M2 gene sequence for HMPV isolate NL/1/94
SEQ ID NO:62 M protein sequence for HMPV isolate NL/1/00
SEQ ID NO:63 M protein sequence for HMPV isolate NL/17/00
20 SEQ ID NO:64 M protein sequence for HMPV isolate NL/1/99
SEQ ID NO:65 M protein sequence for HMPV isolate NL/1/94
SEQ ID NO:66 M gene sequence for HMPV isolate NL/1/00
25 SEQ ID NO:67 M gene sequence for HMPV isolate NL/17/00
SEQ ID NO:68 M gene sequence for HMPV isolate NL/1/99
SEQ ID NO:69 M gene sequence for HMPV isolate NL/1/94
30 SEQ ID NO:70 N protein sequence for HMPV isolate NL/1/00
SEQ ID NO:71 N protein sequence for HMPV isolate NL/17/00

SEQ ID NO:72 N protein sequence for HMPV isolate NL/1/99
SEQ ID NO:73 N protein sequence for HMPV isolate NL/1/94
5 SEQ ID NO:74 N gene sequence for HMPV isolate NL/1/00
SEQ ID NO:75 N gene sequence for HMPV isolate NL/17/00
SEQ ID NO:76 N gene sequence for HMPV isolate NL/1/99
10 SEQ ID NO:77 N gene sequence for HMPV isolate NL/1/94
SEQ ID NO:78 P protein sequence for HMPV isolate NL/1/00
SEQ ID NO:79 P protein sequence for HMPV isolate NL/17/00
15 SEQ ID NO:80 P protein sequence for HMPV isolate NL/1/99
SEQ ID NO:81 P protein sequence for HMPV isolate NL/1/94
SEQ ID NO:82 P gene sequence for HMPV isolate NL/1/00
SEQ ID NO:83 P gene sequence for HMPV isolate NL/17/00
20 SEQ ID NO:84 P gene sequence for HMPV isolate NL/1/99
SEQ ID NO:85 P gene sequence for HMPV isolate NL/1/94
SEQ ID NO:86 SH protein sequence for HMPV isolate NL/1/00
25 SEQ ID NO:87 SH protein sequence for HMPV isolate NL/17/00
SEQ ID NO:88 SH protein sequence for HMPV isolate NL/1/99
SEQ ID NO:89 SH protein sequence for HMPV isolate NL/1/94
30 SEQ ID NO:90 SH gene sequence for HMPV isolate NL/1/00
SEQ ID NO:91 SH gene sequence for HMPV isolate NL/17/00

SEQ ID NO:92 SH gene sequence for HMPV isolate NL/1/99

SEQ ID NO:93 SH gene sequence for HMPV isolate NL/1/94

5 SEQ ID NO:94 isolate NL/1/99 (99-1) HMPV (Human Metapneumovirus) cDNA sequence

SEQ ID NO:95 isolate NL/1/00 (00-1) HMPV cDNA sequence

10 SEQ ID NO:96 isolate NL/17/00 HMPV cDNA sequence

SEQ ID NO:97 isolate NL/1/94 HMPV cDNA sequence

SEQ ID NO:98 G-gene coding sequence for isolate NL/1/00 (A1)

SEQ ID NO:99 G-gene coding sequence for isolate BR/2/01 (A1)

15 SEQ ID NO:100 G-gene coding sequence for isolate FL/4/01 (A1)

SEQ ID NO:101 G-gene coding sequence for isolate FL/3/01 (A1)

SEQ ID NO:102 G-gene coding sequence for isolate FL/8/01 (A1)

20 SEQ ID NO:103 G-gene coding sequence for isolate FL/10/01 (A1)

SEQ ID NO:104 G-gene coding sequence for isolate NL/10/01 (A1)

SEQ ID NO:105 G-gene coding sequence for isolate NL/2/02 (A1)

25 SEQ ID NO:106 G-gene coding sequence for isolate NL/17/00 (A2)

SEQ ID NO:107 G-gene coding sequence for isolate NL/1/81 (A2)

SEQ ID NO:108 G-gene coding sequence for isolate NL/1/93 (A2)

30 SEQ ID NO:109 G-gene coding sequence for isolate NL/2/93 (A2)

SEQ ID NO:110 G-gene coding sequence for isolate NL/3/93 (A2)

SEQ ID NO:111 G-gene coding sequence for isolate NL/1/95 (A2)

SEQ ID NO:112 G-gene coding sequence for isolate NL/2/96 (A2)

5 SEQ ID NO:113 G-gene coding sequence for isolate NL/3/96 (A2)

SEQ ID NO:114 G-gene coding sequence for isolate NL/22/01 (A2)

SEQ ID NO:115 G-gene coding sequence for isolate NL/24/01 (A2)

10 SEQ ID NO:116 G-gene coding sequence for isolate NL/23/01 (A2)

SEQ ID NO:117 G-gene coding sequence for isolate NL/29/01 (A2)

SEQ ID NO:118 G-gene coding sequence for isolate NL/3/02 (A2)

15 SEQ ID NO:119 G-gene coding sequence for isolate NL/1/99 (B1)

SEQ ID NO:120 G-gene coding sequence for isolate NL/11/00 (B1)

SEQ ID NO:121 G-gene coding sequence for isolate NL/12/00 (B1)

20 SEQ ID NO:122 G-gene coding sequence for isolate NL/5/01 (B1)

SEQ ID NO:123 G-gene coding sequence for isolate NL/9/01 (B1)

SEQ ID NO:124 G-gene coding sequence for isolate NL/21/01 (B1)

25 SEQ ID NO:125 G-gene coding sequence for isolate NL/1/94 (B2)

SEQ ID NO:126 G-gene coding sequence for isolate NL/1/82 (B2)

SEQ ID NO:127 G-gene coding sequence for isolate NL/1/96 (B2)

SEQ ID NO:128 G-gene coding sequence for isolate NL/6/97 (B2)

30 SEQ ID NO:129 G-gene coding sequence for isolate NL/9/00 (B2)

	SEQ ID NO:130	G-gene coding sequence for isolate NL/3/01 (B2)
	SEQ ID NO:131	G-gene coding sequence for isolate NL/4/01 (B2)
5	SEQ ID NO:132	G-gene coding sequence for isolate UK/5/01 (B2)
	SEQ ID NO:133	G-protein sequence for isolate NL/1/00 (A1)
	SEQ ID NO:134	G-protein sequence for isolate BR/2/01 (A1)
10	SEQ ID NO:135	G-protein sequence for isolate FL/4/01 (A1)
	SEQ ID NO:136	G-protein sequence for isolate FL/3/01 (A1)
	SEQ ID NO:137	G-protein sequence for isolate FL/8/01 (A1)
	SEQ ID NO:138	G-protein sequence for isolate FL/10/01 (A1)
15	SEQ ID NO:139	G-protein sequence for isolate NL/10/01 (A1)
	SEQ ID NO:140	G-protein sequence for isolate NL/2/02 (A1)
	SEQ ID NO:141	G-protein sequence for isolate NL/17/00 (A2)
20	SEQ ID NO:142	G-protein sequence for isolate NL/1/81 (A2)
	SEQ ID NO:143	G-protein sequence for isolate NL/1/93 (A2)
	SEQ ID NO:144	G-protein sequence for isolate NL/2/93 (A2)
25	SEQ ID NO:145	G-protein sequence for isolate NL/3/93 (A2)
	SEQ ID NO:146	G-protein sequence for isolate NL/1/95 (A2)
	SEQ ID NO:147	G-protein sequence for isolate NL/2/96 (A2)
30	SEQ ID NO:148	G-protein sequence for isolate NL/3/96 (A2)
	SEQ ID NO:149	G-protein sequence for isolate NL/22/01 (A2)

SEQ ID NO:150 G-protein sequence for isolate NL/24/01 (A2)

SEQ ID NO:151 G-protein sequence for isolate NL/23/01 (A2)

5 SEQ ID NO:152 G-protein sequence for isolate NL/29/01 (A2)

SEQ ID NO:153 G-protein sequence for isolate NL/3/02 (A2)

SEQ ID NO:154 G-protein sequence for isolate NL/1/99 (B1)

10 SEQ ID NO:155 G-protein sequence for isolate NL/11/00 (B1)

SEQ ID NO:156 G-protein sequence for isolate NL/12/00 (B1)

SEQ ID NO:157 G-protein sequence for isolate NL/5/01 (B1)

15 SEQ ID NO:158 G-protein sequence for isolate NL/9/01 (B1)

SEQ ID NO:159 G-protein sequence for isolate NL/21/01 (B1)

SEQ ID NO:160 G-protein sequence for isolate NL/1/94 (B2)

20 SEQ ID NO:161 G-protein sequence for isolate NL/1/82 (B2)

SEQ ID NO:162 G-protein sequence for isolate NL/1/96 (B2)

SEQ ID NO:163 G-protein sequence for isolate NL/6/97 (B2)

25 SEQ ID NO:164 G-protein sequence for isolate NL/9/00 (B2)

SEQ ID NO:165 G-protein sequence for isolate NL/3/01 (B2)

SEQ ID NO:166 G-protein sequence for isolate NL/4/01 (B2)

SEQ ID NO:167 G-protein sequence for isolate NL/5/01 (B2)

30 SEQ ID NO:168 F-gene coding sequence for isolate NL/1/00

SEQ ID NO:169 F-gene coding sequence for isolate UK/1/00
SEQ ID NO:170 F-gene coding sequence for isolate NL/2/00
5 SEQ ID NO:171 F-gene coding sequence for isolate NL/13/00
SEQ ID NO:172 F-gene coding sequence for isolate NL/14/00
SEQ ID NO:173 F-gene coding sequence for isolate FL/3/01
10 SEQ ID NO:174 F-gene coding sequence for isolate FL/4/01
SEQ ID NO:175 F-gene coding sequence for isolate FL/8/01
SEQ ID NO:176 F-gene coding sequence for isolate UK/1/01
SEQ ID NO:177 F-gene coding sequence for isolate UK/7/01
15 SEQ ID NO:178 F-gene coding sequence for isolate FL/10/01
SEQ ID NO:179 F-gene coding sequence for isolate NL/6/01
SEQ ID NO:180 F-gene coding sequence for isolate NL/8/01
20 SEQ ID NO:181 F-gene coding sequence for isolate NL/10/01
SEQ ID NO:182 F-gene coding sequence for isolate NL/14/01
SEQ ID NO:183 F-gene coding sequence for isolate NL/20/01
25 SEQ ID NO:184 F-gene coding sequence for isolate NL/25/01
SEQ ID NO:185 F-gene coding sequence for isolate NL/26/01
SEQ ID NO:186 F-gene coding sequence for isolate NL/28/01
30 SEQ ID NO:187 F-gene coding sequence for isolate NL/30/01
SEQ ID NO:188 F-gene coding sequence for isolate BR/2/01

SEQ ID NO:189 F-gene coding sequence for isolate BR/3/01
5 SEQ ID NO:190 F-gene coding sequence for isolate NL/2/02
SEQ ID NO:191 F-gene coding sequence for isolate NL/4/02
SEQ ID NO:192 F-gene coding sequence for isolate NL/5/02
SEQ ID NO:193 F-gene coding sequence for isolate NL/6/02
10 SEQ ID NO:194 F-gene coding sequence for isolate NL/7/02
SEQ ID NO:195 F-gene coding sequence for isolate NL/9/02
SEQ ID NO:196 F-gene coding sequence for isolate FL/1/02
15 SEQ ID NO:197 F-gene coding sequence for isolate NL/1/81
SEQ ID NO:198 F-gene coding sequence for isolate NL/1/93
SEQ ID NO:199 F-gene coding sequence for isolate NL/2/93
20 SEQ ID NO:200 F-gene coding sequence for isolate NL/4/93
SEQ ID NO:201 F-gene coding sequence for isolate NL/1/95
SEQ ID NO:202 F-gene coding sequence for isolate NL/2/96
25 SEQ ID NO:203 F-gene coding sequence for isolate NL/3/96
SEQ ID NO:204 F-gene coding sequence for isolate NL/1/98
SEQ ID NO:205 F-gene coding sequence for isolate NL/17/00
SEQ ID NO:206 F-gene coding sequence for isolate NL/22/01
30 SEQ ID NO:207 F-gene coding sequence for isolate NL/29/01

	SEQ ID NO:208	F-gene coding sequence for isolate NL/23/01
	SEQ ID NO:209	F-gene coding sequence for isolate NL/17/01
5	SEQ ID NO:210	F-gene coding sequence for isolate NL/24/01
	SEQ ID NO:211	F-gene coding sequence for isolate NL/3/02
	SEQ ID NO:212	F-gene coding sequence for isolate NL/3/98
10	SEQ ID NO:213	F-gene coding sequence for isolate NL/1/99
	SEQ ID NO:214	F-gene coding sequence for isolate NL/2/99
	SEQ ID NO:215	F-gene coding sequence for isolate NL/3/99
	SEQ ID NO:216	F-gene coding sequence for isolate NL/11/00
15	SEQ ID NO:217	F-gene coding sequence for isolate NL/12/00
	SEQ ID NO:218	F-gene coding sequence for isolate NL/1/01
	SEQ ID NO:219	F-gene coding sequence for isolate NL/5/01
20	SEQ ID NO:220	F-gene coding sequence for isolate NL/9/01
	SEQ ID NO:221	F-gene coding sequence for isolate NL/19/01
	SEQ ID NO:222	F-gene coding sequence for isolate NL/21/01
25	SEQ ID NO:223	F-gene coding sequence for isolate UK/11/01
	SEQ ID NO:224	F-gene coding sequence for isolate FL/1/01
	SEQ ID NO:225	F-gene coding sequence for isolate FL/2/01
30	SEQ ID NO:226	F-gene coding sequence for isolate FL/5/01
	SEQ ID NO:227	F-gene coding sequence for isolate FL/7/01

SEQ ID NO:228 F-gene coding sequence for isolate FL/9/01
SEQ ID NO:229 F-gene coding sequence for isolate UK/10/01
5 SEQ ID NO:230 F-gene coding sequence for isolate NL/1/02
SEQ ID NO:231 F-gene coding sequence for isolate NL/1/94
SEQ ID NO:232 F-gene coding sequence for isolate NL/1/96
10 SEQ ID NO:233 F-gene coding sequence for isolate NL/6/97
SEQ ID NO:234 F-gene coding sequence for isolate NL/7/00
SEQ ID NO:235 F-gene coding sequence for isolate NL/9/00
15 SEQ ID NO:236 F-gene coding sequence for isolate NL/19/00
SEQ ID NO:237 F-gene coding sequence for isolate NL/28/00
SEQ ID NO:238 F-gene coding sequence for isolate NL/3/01
20 SEQ ID NO:239 F-gene coding sequence for isolate NL/4/01
SEQ ID NO:240 F-gene coding sequence for isolate NL/11/01
SEQ ID NO:241 F-gene coding sequence for isolate NL/15/01
25 SEQ ID NO:242 F-gene coding sequence for isolate NL/18/01
SEQ ID NO:243 F-gene coding sequence for isolate FL/6/01
SEQ ID NO:244 F-gene coding sequence for isolate UK/5/01
SEQ ID NO:245 F-gene coding sequence for isolate UK/8/01
30 SEQ ID NO:246 F-gene coding sequence for isolate NL/12/02

SEQ ID NO:247 F-gene coding sequence for isolate HK/1/02

SEQ ID NO:248 F-protein sequence for isolate NL/1/00

5 SEQ ID NO:249 F-protein sequence for isolate UK/1/00

SEQ ID NO:250 F-protein sequence for isolate NL/2/00

SEQ ID NO:251 F-protein sequence for isolate NL/13/00

10 SEQ ID NO:252 F-protein sequence for isolate NL/14/00

SEQ ID NO:253 F-protein sequence for isolate FL/3/01

SEQ ID NO:254 F-protein sequence for isolate FL/4/01

SEQ ID NO:255 F-protein sequence for isolate FL/8/01

15 SEQ ID NO:256 F-protein sequence for isolate UK/1/01

SEQ ID NO:257 F-protein sequence for isolate UK/7/01

SEQ ID NO:258 F-protein sequence for isolate FL/10/01

20 SEQ ID NO:259 F-protein sequence for isolate NL/6/01

SEQ ID NO:260 F-protein sequence for isolate NL/8/01

SEQ ID NO:261 F-protein sequence for isolate NL/10/01

25 SEQ ID NO:262 F-protein sequence for isolate NL/14/01

SEQ ID NO:263 F-protein sequence for isolate NL/20/01

SEQ ID NO:264 F-protein sequence for isolate NL/25/01

30 SEQ ID NO:265 F-protein sequence for isolate NL/26/01

SEQ ID NO:266 F-protein sequence for isolate NL/28/01

SEQ ID NO:267 F-protein sequence for isolate NL/30/01
SEQ ID NO:268 F-protein sequence for isolate BR/2/01
5 SEQ ID NO:269 F-protein sequence for isolate BR/3/01
SEQ ID NO:270 F-protein sequence for isolate NL/2/02
SEQ ID NO:271 F-protein sequence for isolate NL/4/02
10 SEQ ID NO:272 F-protein sequence for isolate NL/5/02
SEQ ID NO:273 F-protein sequence for isolate NL/6/02
SEQ ID NO:274 F-protein sequence for isolate NL/7/02
15 SEQ ID NO:275 F-protein sequence for isolate NL/9/02
SEQ ID NO:276 F-protein sequence for isolate FL/1/02
SEQ ID NO:277 F-protein sequence for isolate NL/1/81
20 SEQ ID NO:278 F-protein sequence for isolate NL/1/93
SEQ ID NO:279 F-protein sequence for isolate NL/2/93
SEQ ID NO:280 F-protein sequence for isolate NL/4/93
25 SEQ ID NO:281 F-protein sequence for isolate NL/1/95
SEQ ID NO:282 F-protein sequence for isolate NL/2/96
SEQ ID NO:283 F-protein sequence for isolate NL/3/96
SEQ ID NO:284 F-protein sequence for isolate NL/1/98
30 SEQ ID NO:285 F-protein sequence for isolate NL/17/00

SEQ ID NO:286 F-protein sequence for isolate NL/22/01
SEQ ID NO:287 F-protein sequence for isolate NL/29/01
5 SEQ ID NO:288 F-protein sequence for isolate NL/23/01
SEQ ID NO:289 F-protein sequence for isolate NL/17/01
SEQ ID NO:290 F-protein sequence for isolate NL/24/01
10 SEQ ID NO:291 F-protein sequence for isolate NL/3/02
SEQ ID NO:292 F-protein sequence for isolate NL/3/98
SEQ ID NO:293 F-protein sequence for isolate NL/1/99
SEQ ID NO:294 F-protein sequence for isolate NL/2/99
15 SEQ ID NO:295 F-protein sequence for isolate NL/3/99
SEQ ID NO:296 F-protein sequence for isolate NL/11/00
SEQ ID NO:297 F-protein sequence for isolate NL/12/00
20 SEQ ID NO:298 F-protein sequence for isolate NL/1/01
SEQ ID NO:299 F-protein sequence for isolate NL/5/01
SEQ ID NO:300 F-protein sequence for isolate NL/9/01
25 SEQ ID NO:301 F-protein sequence for isolate NL/19/01
SEQ ID NO:302 F-protein sequence for isolate NL/21/01
SEQ ID NO:303 F-protein sequence for isolate UK/11/01
30 SEQ ID NO:304 F-protein sequence for isolate FL/1/01
SEQ ID NO:305 F-protein sequence for isolate FL/2/01

SEQ ID NO:306 F-protein sequence for isolate FL/5/01
SEQ ID NO:307 F-protein sequence for isolate FL/7/01
5
SEQ ID NO:308 F-protein sequence for isolate FL/9/01
SEQ ID NO:309 F-protein sequence for isolate UK/10/01
SEQ ID NO:310 F-protein sequence for isolate NL/1/02
10
SEQ ID NO:311 F-protein sequence for isolate NL/1/94
SEQ ID NO:312 F-protein sequence for isolate NL/1/96
SEQ ID NO:313 F-protein sequence for isolate NL/6/97
15
SEQ ID NO:314 F-protein sequence for isolate NL/7/00
SEQ ID NO:315 F-protein sequence for isolate NL/9/00
SEQ ID NO:316 F-protein sequence for isolate NL/19/00
20
SEQ ID NO:317 F-protein sequence for isolate NL/28/00
SEQ ID NO:318 F-protein sequence for isolate NL/3/01
SEQ ID NO:319 F-protein sequence for isolate NL/4/01
SEQ ID NO:320 F-protein sequence for isolate NL/11/01
25
SEQ ID NO:321 F-protein sequence for isolate NL/15/01
SEQ ID NO:322 F-protein sequence for isolate NL/18/01
SEQ ID NO:323 F-protein sequence for isolate FL/6/01
30
SEQ ID NO:324 F-protein sequence for isolate UK/5/01

SEQ ID NO:325 F-protein sequence for isolate UK/8/01

SEQ ID NO:326 F-protein sequence for isolate NL/12/02

5 SEQ ID NO:327 F-protein sequence for isolate HK/1/02

10

15

20

25

30

WHAT IS CLAIMED IS:

1. A chimeric bovine parainfluenza virus type 3 comprising a heterologous
5 nucleotide sequence encoding a metapneumovirus polypeptide.
 2. A chimeric human parainfluenza virus type 3 comprising a heterologous nucleotide sequence encoding a metapneumovirus polypeptide.
 3. A chimeric bovine parainfluenza virus type 3/human parainfluenza virus type 3 comprising a heterologous nucleotide sequence encoding a metapneumovirus polypeptide.
- 10
4. The virus of claim 1, 2, or 3, wherein said virus comprises heterologous nucleotide sequences derived from the same gene of a metapneumovirus.
 5. The virus of claim 1, 2, or 3, wherein said virus comprises heterologous nucleotide sequences derived from at least two different genes of a metapneumovirus.
- 15
6. The virus of claim 1, 2, or 3, wherein one or more of the open reading frames in the genome of the virus have been replaced by an ORF which encodes one or more of (i) an avian pneumovirus (APV) F protein; (ii) an APV G protein; (iii) an APV SH protein; (iv) an APV N protein; (v) an APV P protein; (vi) an APV M2 protein; (vii) an APV M2-1 protein; (viii) an APV M2-2 protein; or (ix) an APV L protein.
- 20
7. The virus of claim 1, 2, or 3, wherein one or more of the open reading frames in the genome of virus have been replaced by an ORF which encodes one or more of (i) a mammalian metapneumovirus (MPV) F protein; (ii) a mammalian MPV G protein; (iii) a

mammalian MPV SH protein; (iv) a mammalian MPV N protein; (v) a mammalian MPV P protein; (vi) a mammalian MPV M2 protein; (vii) a mammalian MPV M2-1 protein; (viii) a mammalian MPV M2-2 protein; or (ix) a mammalian MPV L protein.

5

8. The virus of claim 6, wherein the avian pneumovirus is APV type A, APV type B, APV type C, or APV type D.

10

9. The virus of claim 7, wherein the mammalian MPV is variant A1, variant A2, variant B1, or variant B2.

15

10. The virus of claim 1, 2, or 3, wherein said heterologous nucleotide sequence is added to the complete genome of said virus.

15

11. The virus of claim 1, 2, or 3, wherein said nucleotide sequence is added at a nucleotide position of the parainfluenza virus genome of 104, 1774, and 3724.

20

12. The virus of claim 1, 2, or 3, wherein a nucleotide sequence of said parainfluenza virus has been substituted by said heterologous nucleotide sequence.

25

13. The virus of claim 1, 2, or 3, wherein the heterologous sequences are inserted
25 into the genome of said parainfluenza virus, wherein the genome has been deleted of one or
more genes.

14. The virus of claim 1, wherein said bovine parainfluenza virus is a Kansas-strain
30 bovine parainfluenza virus type 3.

15. The virus of claim 1, 2, or 3, wherein said heterologous nucleotide sequence is derived from the nucleotide sequences encoding a F protein, a G protein or a fragment thereof.

5

16. The virus of claim 15, wherein said F protein comprises an ectodomain of a F protein of a metapneumovirus, a transmembrane domain of a F protein of a parainfluenza virus, and luminal domain of a F protein of a parainfluenza virus.

10

17. The virus of claim 1, 2, or 3, wherein said nucleotide sequence is SEQ ID Nos: 1 to 5, 14, or 15.

15

18. The virus of claim 1, 2, or 3, wherein said nucleotide sequence encodes a protein of SEQ ID Nos: 6 to 13, 16, or 17.

19

19. The virus of claim 1, 2, or 3, wherein said virus further comprises a heterologous nucleotide sequence derived from a respiratory syncytial virus or a mutated form of 20 respiratory syncytial virus.

25

20. The virus of claim 19, wherein the respiratory syncytial virus is a respiratory syncytial virus type A, a respiratory syncytial virus type B, a bovine respiratory syncytial virus, or an ovine respiratory syncytial virus.

21. The virus of claim 19, wherein said sequence is derived from the nucleotide sequences encoding a F protein, a G protein or a fragment thereof of said respiratory syncytial virus.

30

22. The chimeric parainfluenza virus of claim 1, 2, or 3, wherein the genome of said virus contains mutations or modifications, in addition to said heterologous nucleotide sequences, which result in a chimeric virus having a phenotype more suitable for use in
5 vaccine formulations such as an attenuated phenotype or a phenotype with enhanced antigenicity.

23. The chimeric parainfluenza virus of claim 1, 2, or 3, wherein the intergenic region of said heterologous nucleotide sequence is altered.
10

24. The chimeric parainfluenza virus of claim 1, 2, or 3, wherein said heterologous nucleotide sequence is added at a position of the parainfluenza virus genome selected from the group consisting of position 1, 2, 3, 4, 5, and 6, and wherein the intergenic region of said
15 heterologous nucleotide sequence is altered.

25. A recombinant DNA or RNA molecule encoding the genome of the virus of
claim 1, 2, or 3.
20

26. A recombinant DNA or RNA molecule encoding the genome of the virus of
claim 18.
25

27. A vaccine formulation comprising the chimeric virus of claim 1, 2, or 3, and a pharmaceutically acceptable excipient.
30

28. A vaccine formulation comprising the chimeric virus of claim 18 and a pharmaceutically acceptable excipient.

29. The vaccine formulation of claim 27, wherein said chimeric virus comprises a genomic modification or mutation which results in an attenuated phenotype or enhanced antigenicity.

5

30. The vaccine formulation of claim 29, wherein said modification or mutation is derived from a naturally occurring mutant.

10 31. The vaccine formulation of claim 27, wherein said vaccine is used to modulate the immune response of humans, primates, horses, cows, sheep, pigs, goats, dogs, cats, avian species or rodents.

15 32. The vaccine formulation of claim 30, wherein the vaccine is used to modulate the immune response of a human infant or a child.

20 33. An immunogenic formulation comprising the chimeric virus of claim 1, 2, or 3, and a pharmaceutically acceptable excipient.

34. An immuriogenic formulation comprising the chimeric virus of claim 18 and a pharmaceutically acceptable excipient.

25 35. The immunogenic formulation of claim 33, wherein said chimeric virus comprises a genomic modification or mutation which results in an attenuated phenotype or enhanced antigenicity.

30 36. The immunogenic formulation of claim 35, wherein said modification or mutation is derived from a naturally occurring mutant.

37. The vaccine formulation of claim 33, wherein said vaccine is used to modulate the immune response of humans, primates, horses, cows, sheep, pigs, goats, dogs, cats, avian species or rodents.

5

38. The vaccine formulation of claim 36, wherein the vaccine is used to modulate the immune response of a human infant or a child.

10 39. A method for treating or preventing a respiratory tract infection in a mammal, said method comprising administering a vaccine of claim 27.

15 40. The method of claim 39, wherein the respiratory tract infection is a MPV infection.

41. The method of claim 39, wherein the respiratory tract infection is an infection with MPV, RSV, hPIV or a combination thereof.

20 42. The method of claim 39, wherein the subject is a human.

43. The method of claim 42, wherein the human subject is less than 5 years of age.

25 44. The method of claim 42, wherein the human subject is less than 2 years of age.

45. The method of claim 42, wherein the human subject suffers from a disease or a condition in addition to the respiratory tract infection.

30

46. The method of claim 45, wherein the disease or a condition is of cystic fibrosis, leukemia, non-Hodgkin lymphoma, asthma, and bone marrow transplantation and kidney transplantation.

5

47. The human subject of claim 42, wherein the human subject is an immunocompromised individual.

10 48. The human subject of claim 42, wherein the human subject is an elderly.

15

20

25

30

1/27

Human	1 MSWKVVIIFSLLITPQHGLKESYLEEESCSTITEGYLSVLRTGWTNVFTLEVDVENLTC	60
	MSWKVV++ LL TP GL+ESYLEEESCST+T GYLSVLRTGWTNVFTLEVDVENLTC	
Avian	1 MSWKVVLLVLLATPTGGLEESYLEEESCSTVTRGYLSVLRTGWTNVFTLEVDVENLTC	60
Human	61 ADGPSLIKTEDLTKSALRELRTVSADQLAREEQIENPROSRFVLGAIALGVATAAAVTA	120
	DGPSLI+TEL+LTK+AL EL+TV ADQLA+E +I +PR++RFVLGAIALGVAT AAVTA	
Avian	61 TDGPSLIRTELELTKNALEELKTPADQLAKEARIMSPRKRKFVLGAIALGVATTAAVTA	120
Human	121 GVIAIKTIRLESEVTAIKNALKKTNEAVSTLGNNGVRVLATAVRELKDFVSKNLTRAINKN	180
	GVIAIKTIRLE EV A1+ AL+ TNEAVSTLGNNGVRVLATAV +LKDF+SK LT AINKN	
Avian	121 GVIAIKTIRLEGEVAAIRGALRNTNEAVSTLGNNGVRVLATAVNDLKDFISKKLTPAINKN	180
Human	181 KCDIADLKMVASFSQFNRRFLNVVRQFSNDAGITPAISLDLMTDAELARA VSNMPTSAGQ	240
	KCDI+DLKMASF Q+NRRFLNVVRQFSNDAGITPAISLDLMTDAEL RAVSNMPTS+GQ	
Avian	181 KCDISDLKMVASFGQYNRRFLNVVRQFSNDAGITPAISLDLMTDAELVRAVSNMPTSSGQ	240
Human	241 IKLMLENRAMVRRKGFGFLIGVYGSIVYMVQLPIFGVIDTPCWIVKAAPCSGKKGNYA	300
	I LMLENRAMVRRKGFG LIGVYGSIVYMVQLPIFGVIDTPCW VKAAP CSGK G+YA	
Avian	241 INLMLLENRAMVRRKGFGILIGVYGSIVYMVQLPIFGVIDTPCWVKAAPLCSGKDGSYA	300
Human	301 CLLREDQGWCQNAGSTVYYPPNEKDCETRGDHVFCDTAAGINVAEQSKECNINISTTNYP	360
	C LREDQGWCQNAGSTVYYPPNE+DC R DHVFCDTAAGINVA++S+ECN NISTT YP	
Avian	301 CPLREDQGWCQNAGSTVYYPPNEEDCVVRSDHVFCDTAAGINVAKESEECCRNIISTTKYP	360
Human	361 CKVSTGRHPISMVALSPLGALVACYKGVSIGSNRVGIIKQLNKGSYITNQDADTVTI	420
	CKVSTGRHPISMVALSPLGALVACY GSIGSN+VGII+ L KGSYI+NQDADTVTI	
Avian	361 CKVSTGRHPISMVALSPLGALVACYDGVSIGSNKVGIIIRRLKGGSYISNQDADTVTI	420
Human	421 DNTVYQLSKVEGEQHQVIKGRPVSSFDPKFPEDQFNVALDQVFESIENSQALVDQSNRI	480
	DNTVYQLSKVEGEQH IKG+PVSS+FDP++FPEDQFN+ALDQVFES+E S+ L+DQSN+I	
Avian	421 DNTVYQLSKVEGEQHTIKGKPVSSNDFPIEFPEDQFNIALDQVFESVEKSKNLIDQSNKI	480
Human	481 LSSAEKGNTGFIIVIILIAVLGSTMILVSVFIIKKTKRPTGAPPELSGVTN	532
	L S EKGN GF+IVI LI +L + V +F ++KK K P E++GV N	
Avian	481 LDSTEKGNAFVIVIALIVLMLAAGVVGIFFVVKRKAAPKFPMEMNGVNN	532

FIG. 1A

2/27

Human	1	MSWKVVIIFSLLITPQHGLKESYLEESCSTITEGYLSVLRTGWTNVFTLEVGDVENLTC	60
	M ++ ++ L+ P ++E+Y EESCST+T GY SVLRTGWTNVF LE+G+VEN+TC		
Turkey	1	MDVRICLLLFLISNPSSCIQETYNEECSCTVTRGYKSVLRTGWTNVFNLEIGNVENITC	60
Human	61	ADGPSLIKTTELDTKSALRELRTVSADQLAREEQIENPRQSRFLGAIALGVATAAAVTA	120
	DGPSLI TEL LTK+ALREL+TVSADQ+A+E ++ +PR+ RFVLGAIALGVATAAAVTA		
Turkey	61	NDGPSLIDTELVLTKNALRELKTVSADQVAKESRLSSPRRRRFVLGAIALGVATAAAVTA	120
Human	121	GVAIAKTIRLESEVTAIKNALKKTNEAVSTLGNV~VLATAVRELKDFVSKNLTRAINKN	180
	GVA+AKTIRLE EV AIKNAL+ TNEAVSTLGNVVRVLATAV +LK+F+SK LT AIN+N		
Turkey	121	GVALAKTIRLEGEVKAIKNALRNTNEAVSTLGNVVRVLATAVNDLKEFISKKLTPAINQN	180
Human	181	KCDIADLKMAVSFSQFNRRFLNVVRQFSNDAGITPAISLDLMTDAELARAVSNMPTSAGQ	240
	KC+IAD+KMA+SF Q NRRFLNVVRQFSD+AGIT A+SLDLMTD EL RA++ MPTS+GQ		
Turkey	181	KCNIADIJKMAISFGQNNRRFLNVVRQFSDSAGITSAVSLDLMTDELVRAINRMPTSSGQ	240
Human	241	IKLMLENRAMVRRKGFGFLIGVYGSIVIYMVQLPIFGVIDTPCWIVKAAPSCSGKKGNYA	300
	I LML NRAMVRRKGFG LIGVY +V+YMVQLPIFGVI+TPCW V AAP C +KGNYA		
Turkey	241	ISLMLNNRAMVRRKGFGILIGVYDGTVVYMYVQLPIFGVIETPCWRVVAAPLCRKEKGNYA	300
Human	301	CLLRDQQWYCQNAGSTVYYPNEKDCETRGDHVFCDTAAGINVAEQSKECNINISTTNYP	360
	C+LREDQQWYC NAGST YYPN+ DCE R D+VFCDTAAGINV A + ++CN NIST+ YP		
Turkey	301	CILREDQQWYCTNAGSTAYYPNKDDCEVRDDYVFCDTAAGINVALEVEQCNYNISTSKYD	360
Human	361	CKVSTGRHPISMVALSPLGALVACYKGVSIGNSNRVGIIKQLNKGSYITNQDADTVI	420
	CKVSTGRHP+SMVAL+PLG LV+CY+ VSCSIGSN+VGIIKQL KGC++I N +ADT+TI		
Turkey	361	CKVSTGRHPVSMVALTPLGGLVSCYESVSCSIGSNKVGIIKQLKGCTHIPNNEADTITI	420
Human	421	DNTVYQLSKVGEQHVIKGRPVSSEFDPKFPEDQFVALIDQVFESIENSQALVDQSNRI	480
	DNTVYQLSKV GEQ IKG PV ++F+P+ FPEDQFVALIDQVFESI+ SQ L+D+SN +		
Turkey	421	DNTVYQLSKVVGQRTIKGAPVNNFNPILFPEDQFVALIDQVFESIDRSQDLIDKSNDL	480
Human	481	LSSAEKGNTGFIIVIIILIAVLGSTMILVSFII--IKKTKRPTGAPP else GVTNNNGFI	536
	L + K G I I+++ +LG +L ++ ++KTK P P +G ++ ++		
Turkey	481	LGADAKSKAGIAIAIVVLVILGIFFLLAVIYYCSRVRKTK-PKHDYPATTGHSSMAYV	537

FIG.1B

SUBSTITUTE SHEET (RULE 26)

3/27

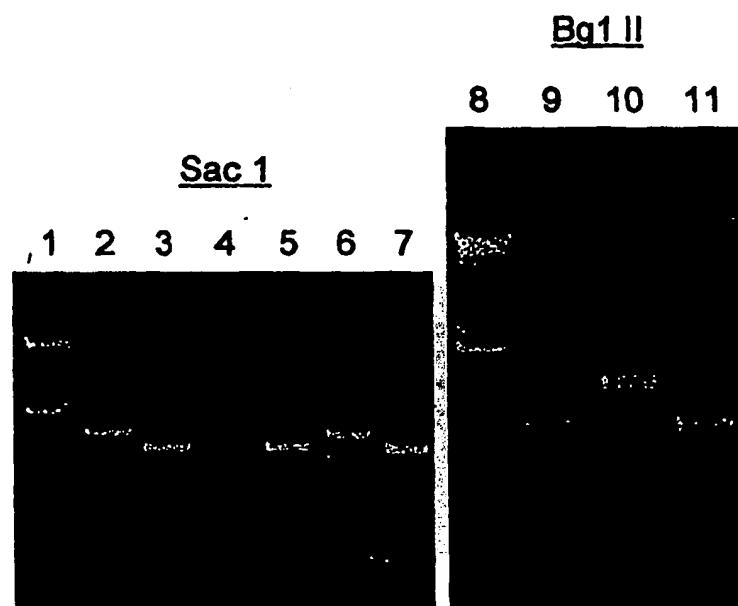


FIG.2

SUBSTITUTE SHEET (RULE 26)

4/27

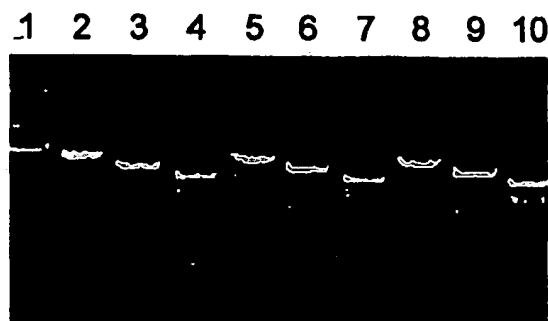
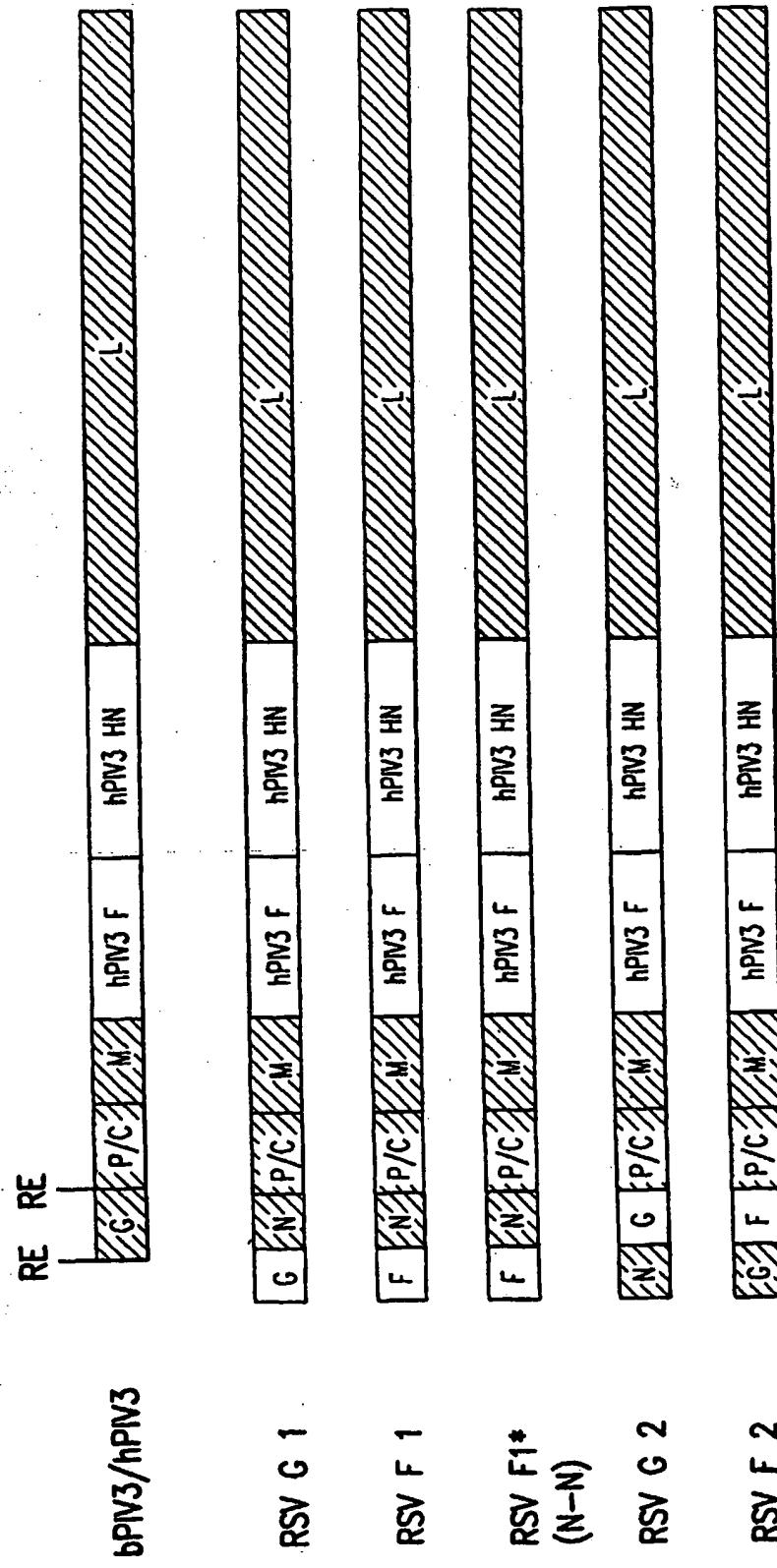


FIG.3

SUBSTITUTE SHEET (RULE 26)

5/27

Rescued bPIV3/hPIV3-Vectored RSV Constructs

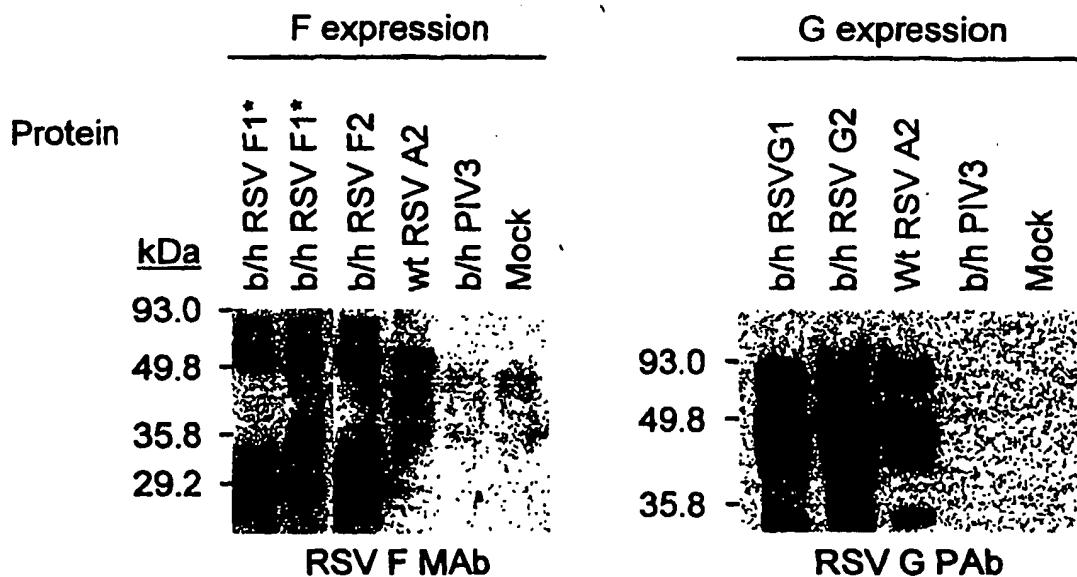


Note: all RSV genes are linked to the bPIV3 N-P intergenic region with the exception of RSV F1* which is followed by the shorter bPIV3 N gene stop/N gene start sequences.

FIG. 4

6/27

**Expression of RSV F and G
Proteins from Chimeric Bovine/Human PIV3**



7/27

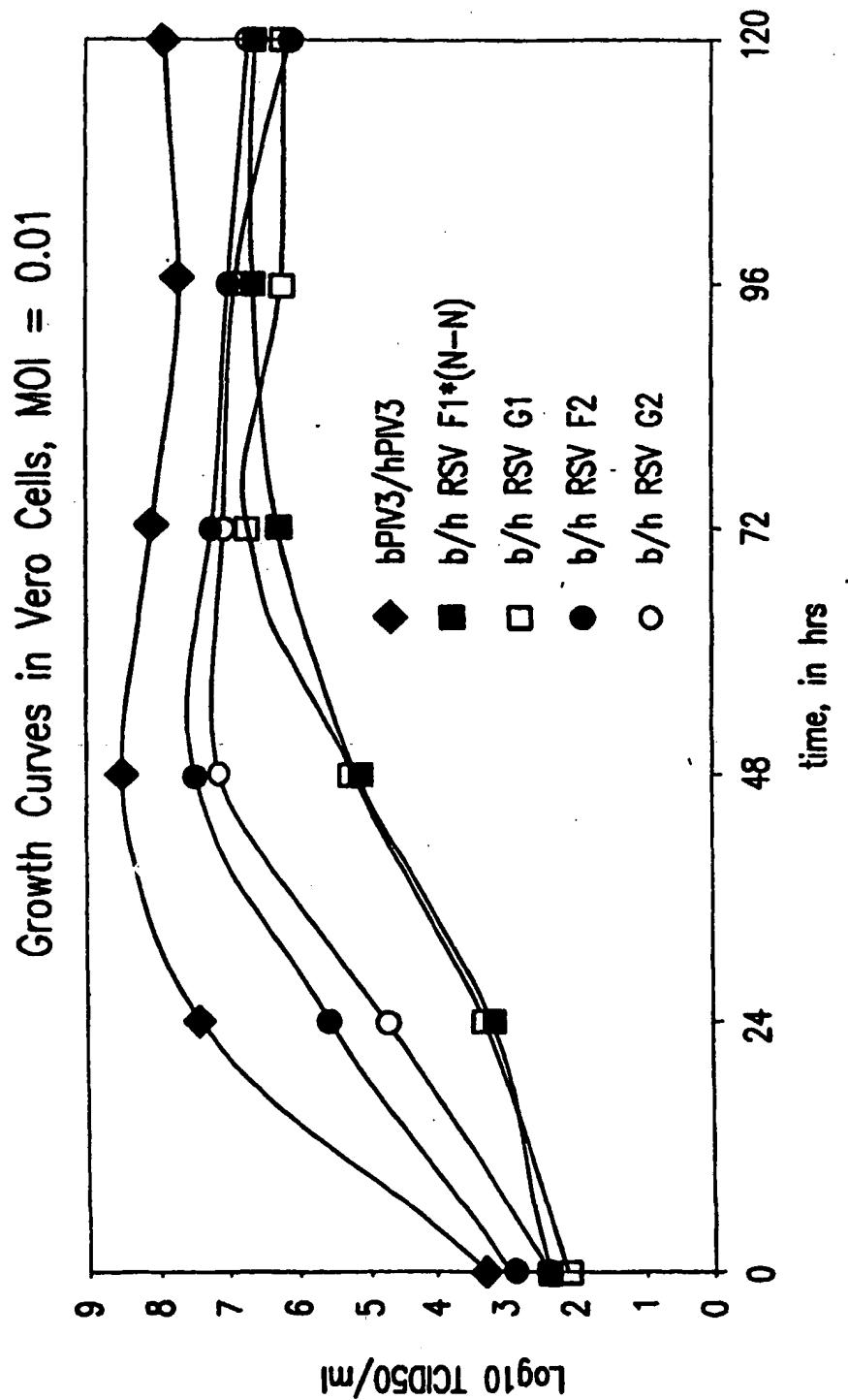


FIG. 5(C)

8/27

**Positional Effect of eGFP Insertions in the PIV3
Genome on Virus Replication**

b/h GFP1	GFP	N	P/C	M	hPIV3 F	hPIV3 HN	

Status: virus stocks prepared

Titer: 4×10^8 PFU/ml

b/h GFP2	N	GFP	P/C	M	hPIV3 F	hPIV3 HN	

Status: virus stocks prepared

Titer: 3×10^8 PFU/ml

b/h GFP3	N	P/C	GFP	M	hPIV3 F	hPIV3 HN	

Status: virus stocks prepared

Titer: 1.1×10^7 PFU/ml

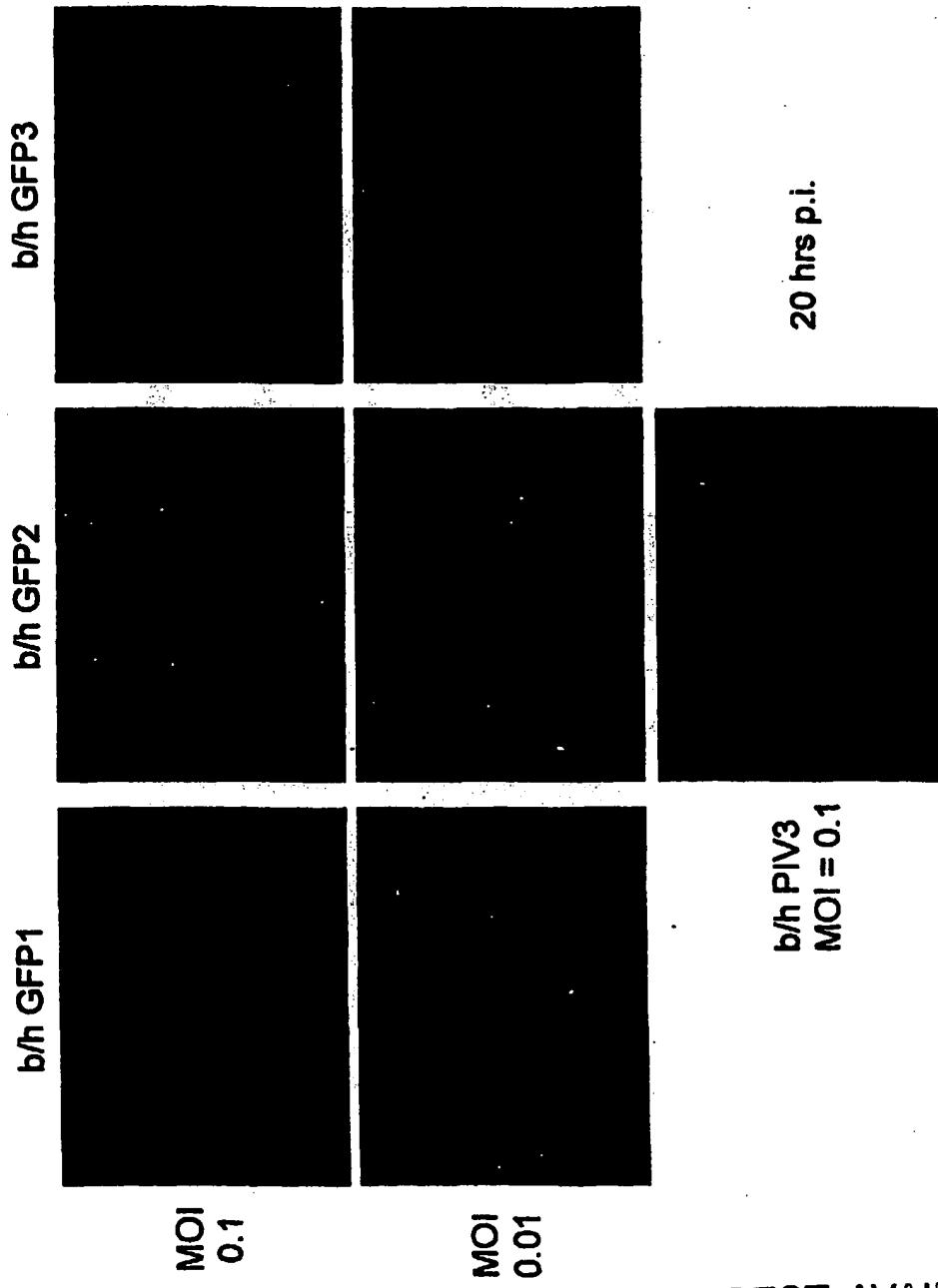
b/h GFP4	N	P/C	GFP	M	hPIV3 F	hPIV3 HN	

Status: virus rescued, biological cloning in progress.

b/h GFP5 and b/h GFP 6 construction in progress.**FIG. 6****SUBSTITUTE SHEET (RULE 26)**

9/27

GFP Expression of b/h PIV3-GFP1, 2, 3

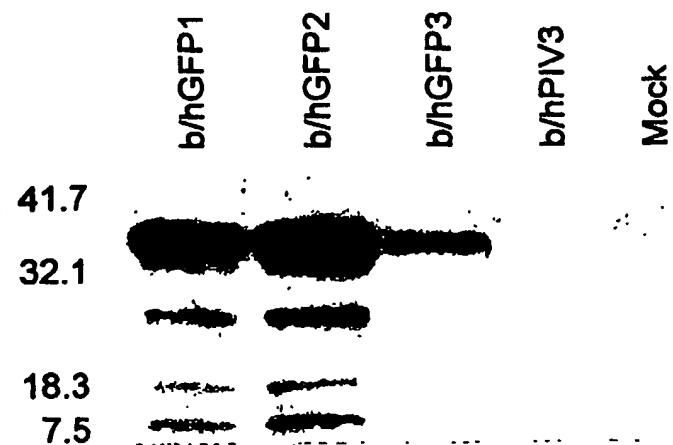


BEST AVAILABLE COPY

FIG. 7(A)

10/27

eGFP Expression in b/h PIV3 in Positions
1, 2 and 3



MOI of 0.1 in Vero cells
24 hours post-infection

FIG. 7(B)

SUBSTITUTE SHEET (RULE 26)

11/27

Growth Curves for b/h PV3/GFP1, 2, and 3
in Vero Cells, MOI = 0.1

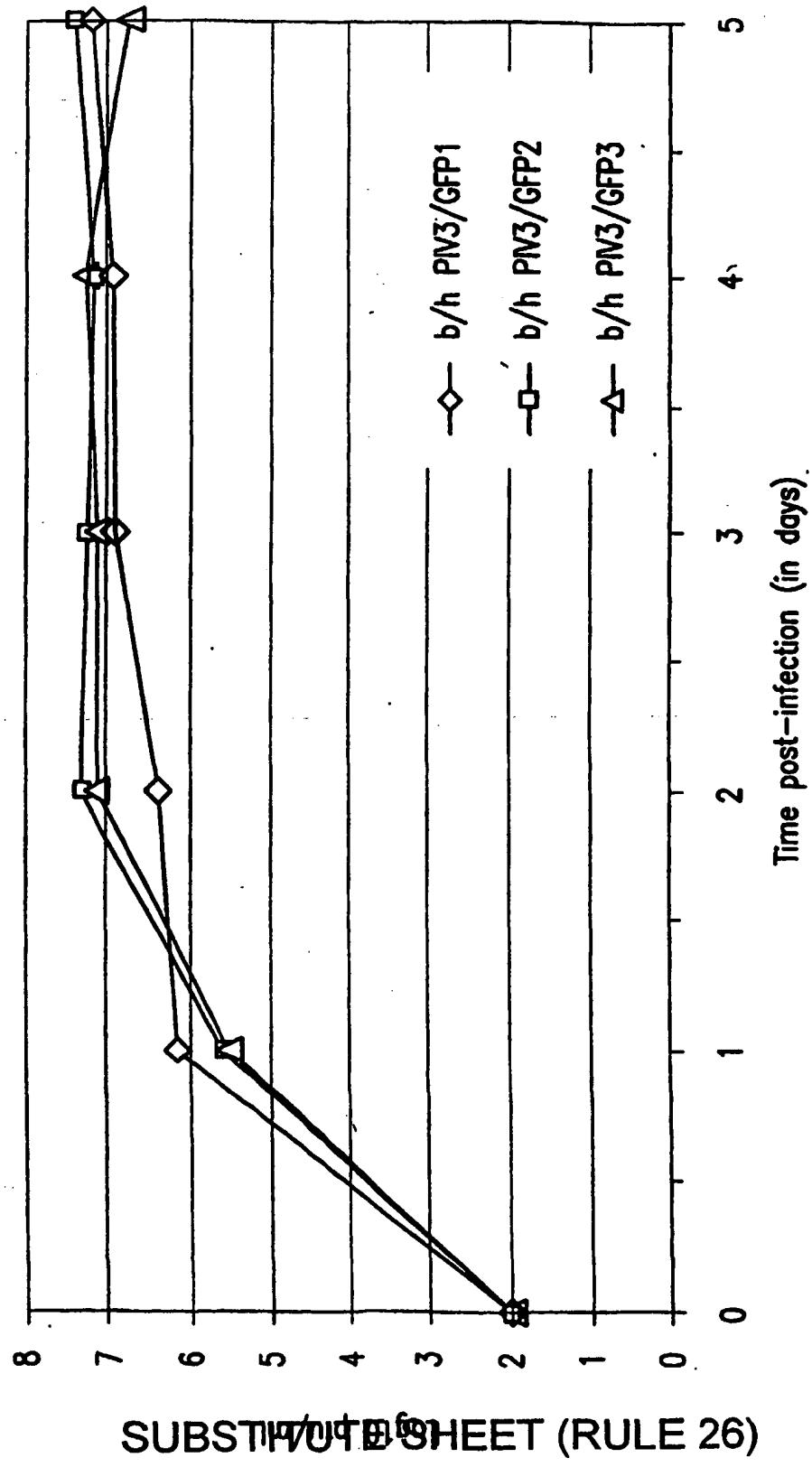
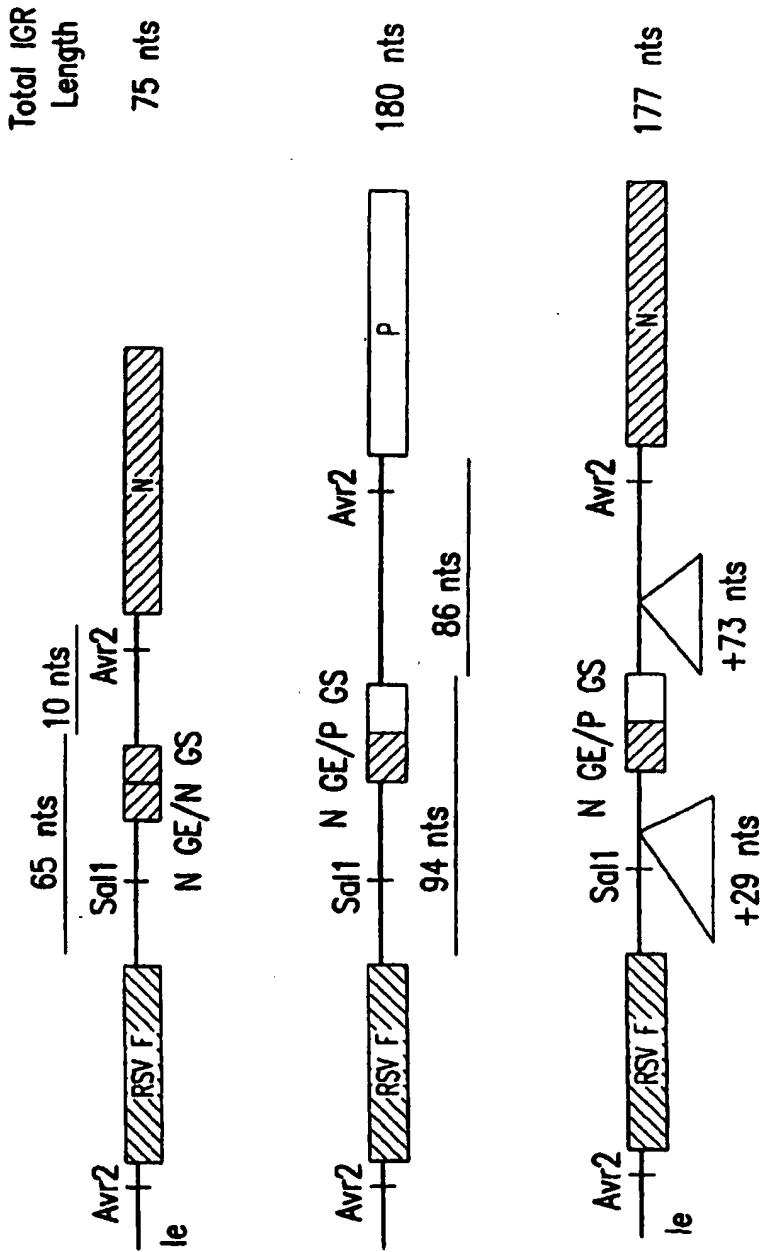


FIG. 7(C)

SUBSTITUTE SHEET (RULE 26)

12/27

Differences between b/h PIV3 RSV F1* and
b/h PIV3 RSV F2 Intergenic Regions



SUBSTITUTE SHEET (RULE 26)

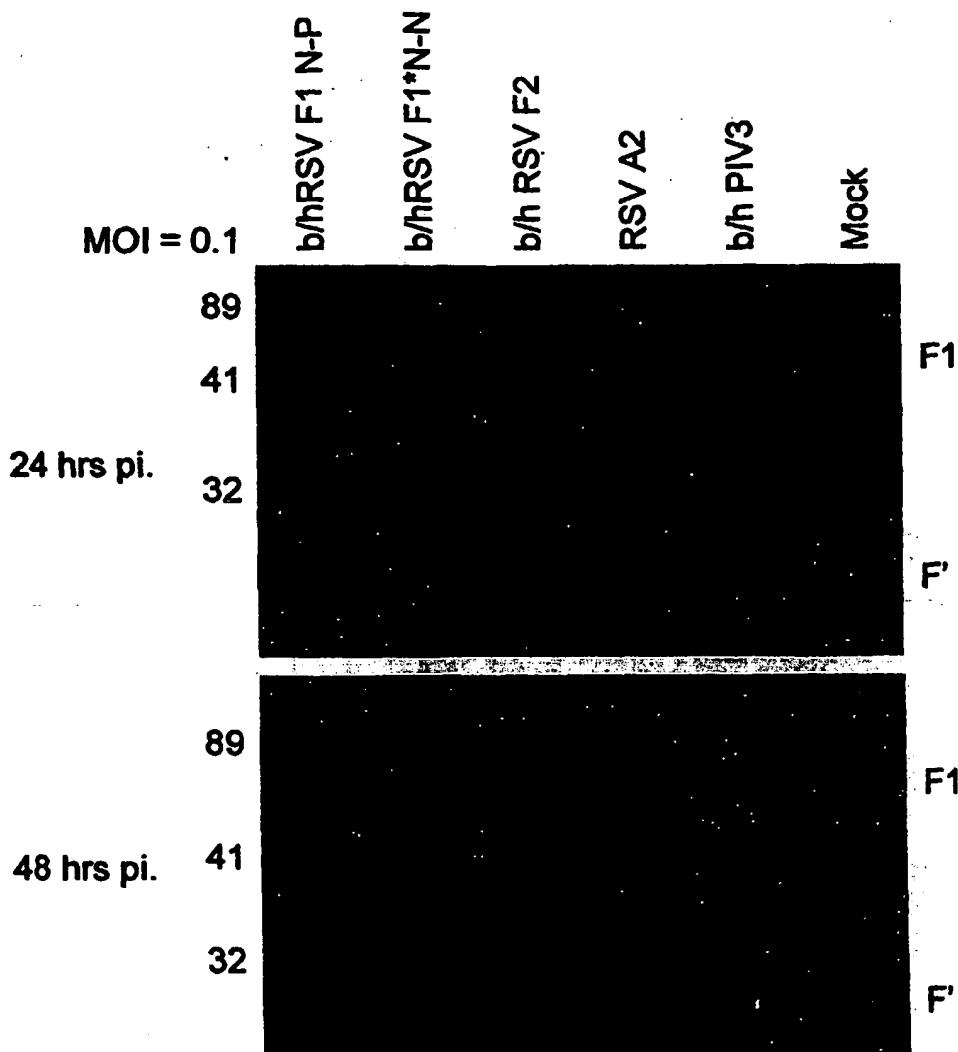
RSV F1 RSV F2

N-P N-P

+29 nts

FIG. 8

13/27

RSV F Expression in Chimeric Viruses**FIG.9(A)**

14/27

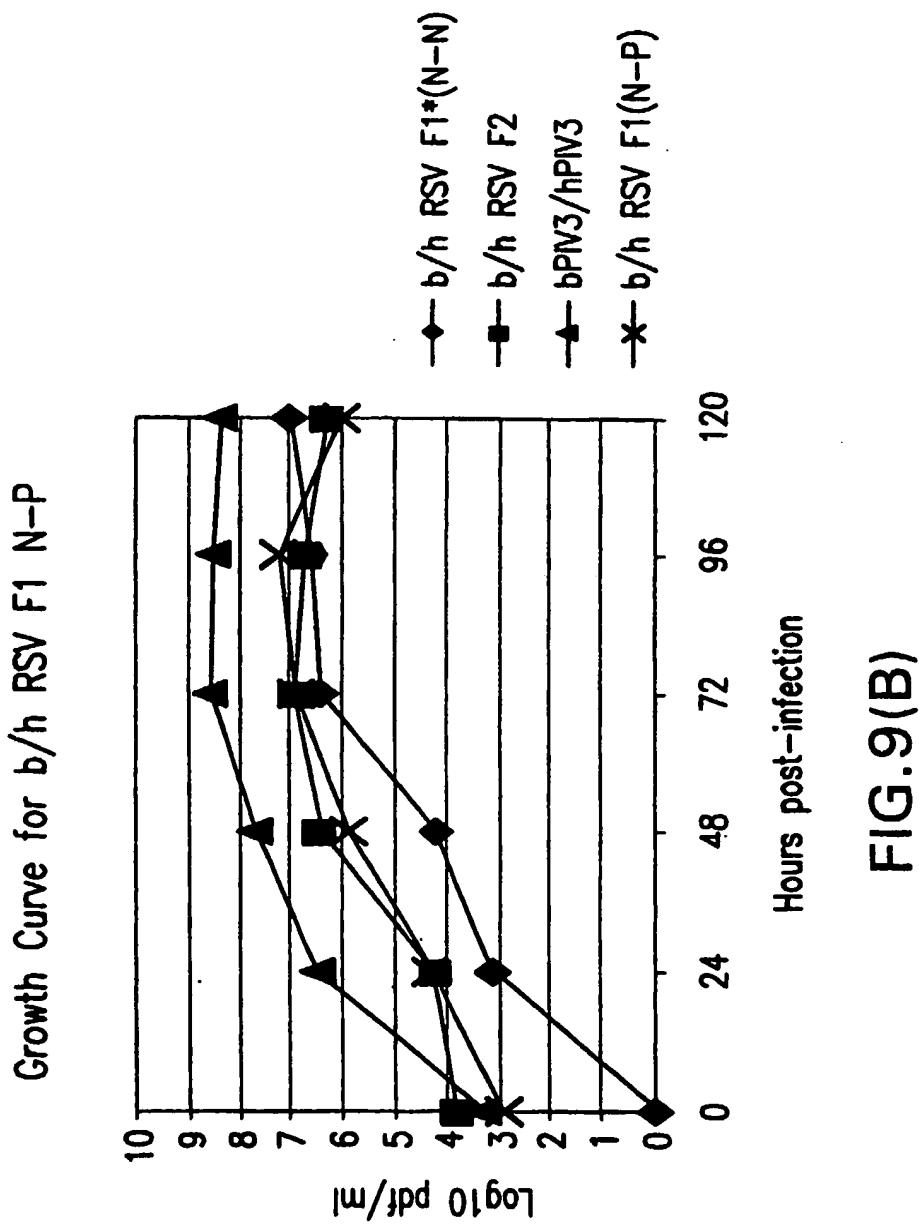
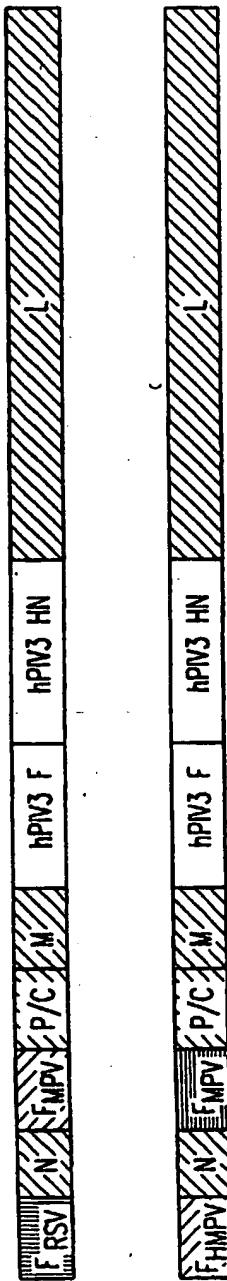


FIG. 9(B)

SUBSTITUTE SHEET (RULE 26)

15/27

Trivalent bPIV3/hPIV3 vectored Constructs

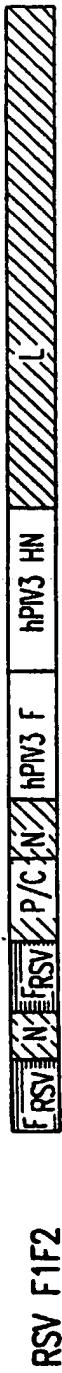


Status: Constructs were rescued, viruses are being amplified in Vero cells.

FIG.10

16/27

Cloning of Two RSV F to the b/h PIV3 Vector



Status: Virus titer = 1.0×10^6 PFU/ml

Purpose: to study whether two RSV F genes will increase immunogenicity.

FIG. 11

SUBSTITUTE SHEET (RULE 26)

17/27

bPV3/hPV3 vectored hMPV F Constructs**1. b/h PV3/hMPV F1**

F	N	P/C	M	hPV3 F	hPV3 HN	1
---	---	-----	---	--------	---------	---

Status: Virus stocks generated**Titer:** 5×10^6 PFU/ml**2. b/h PV3/hMPV F2**

F	N	P/C	M	hPV3 F	hPV3 HN	1
---	---	-----	---	--------	---------	---

Status: Virus stock generated**Titer:** 1.5×10^7 PFU/ml**FIG. 12**

18/27

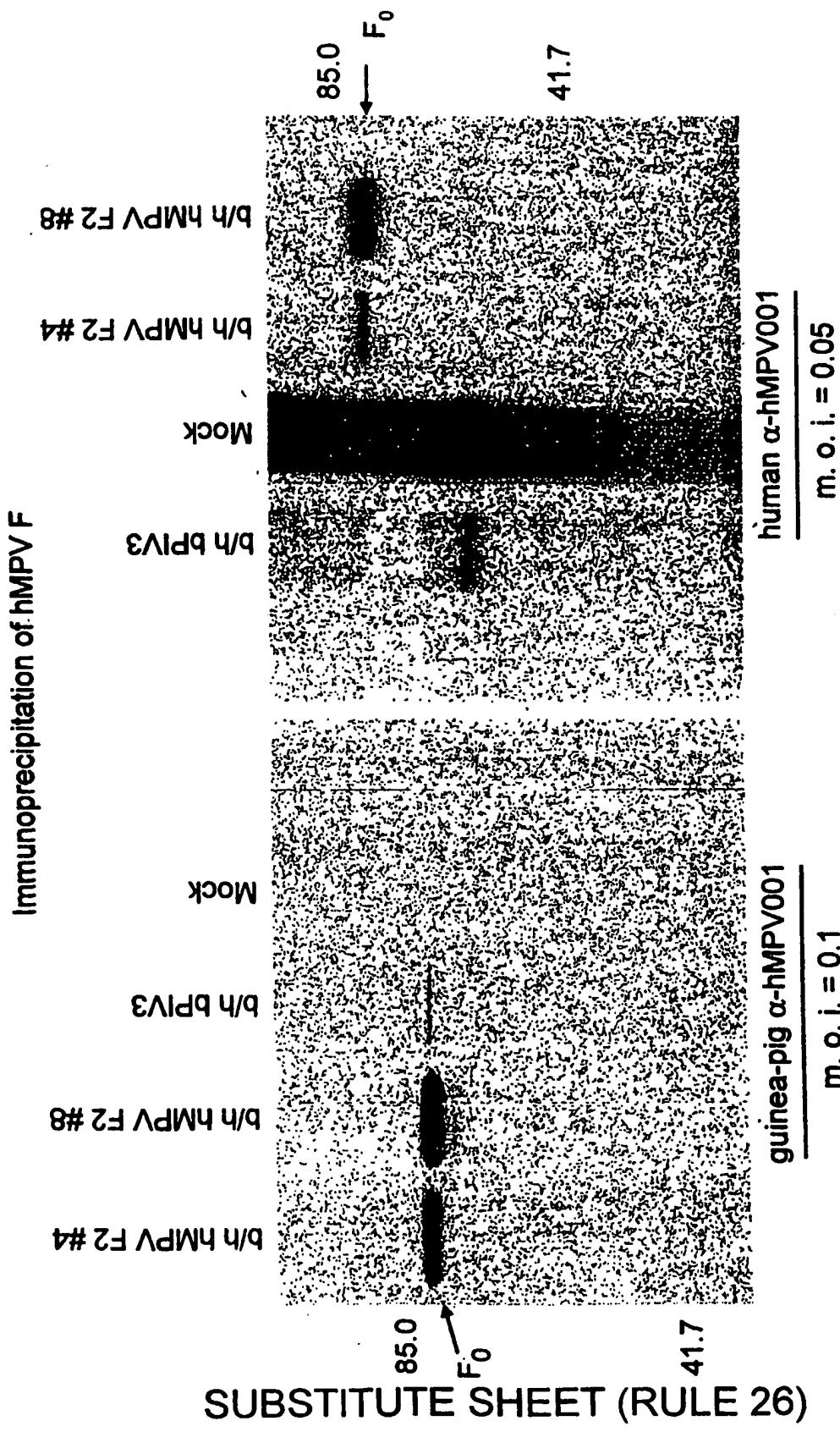


FIG. 13(A)

19/27

Growth Curve of b/h PIV3/ hMPV F2 in Vero Cells,

MOI = 0.1

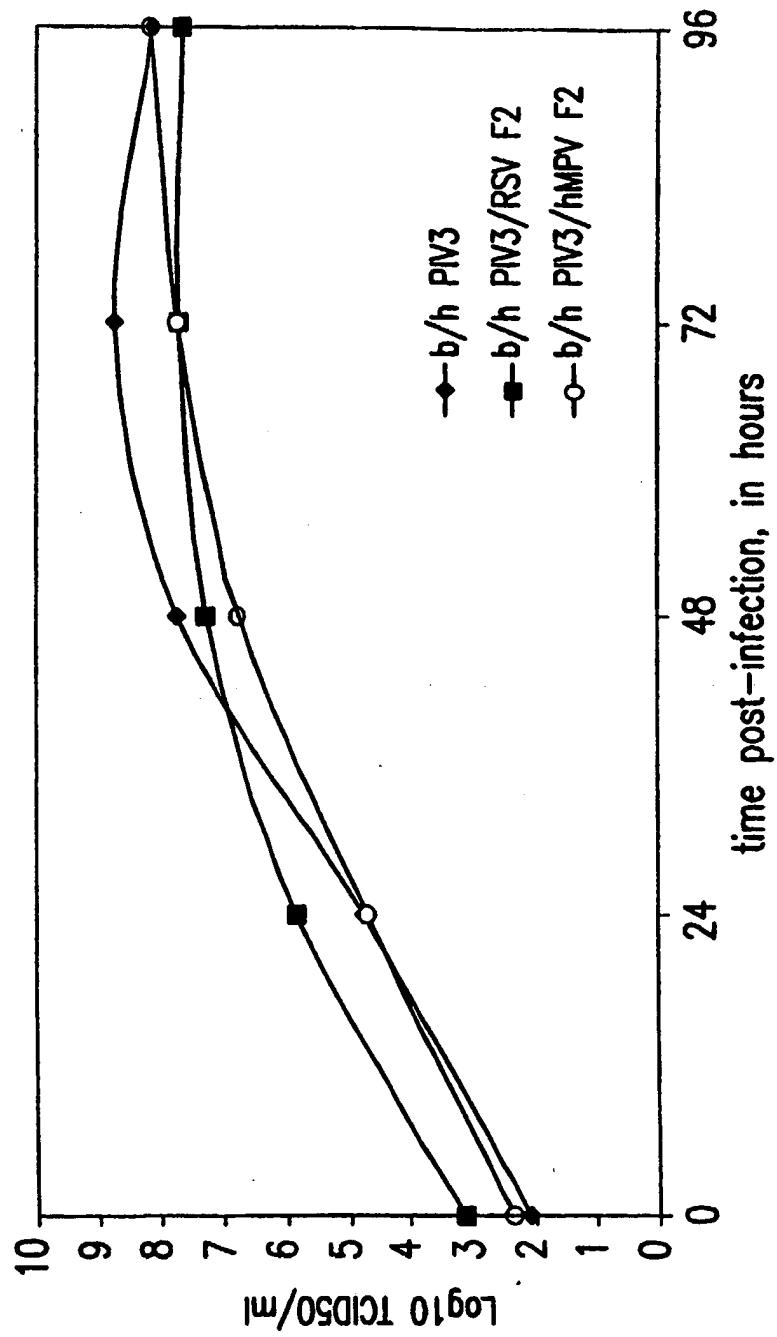


FIG. 13(B)

20/27

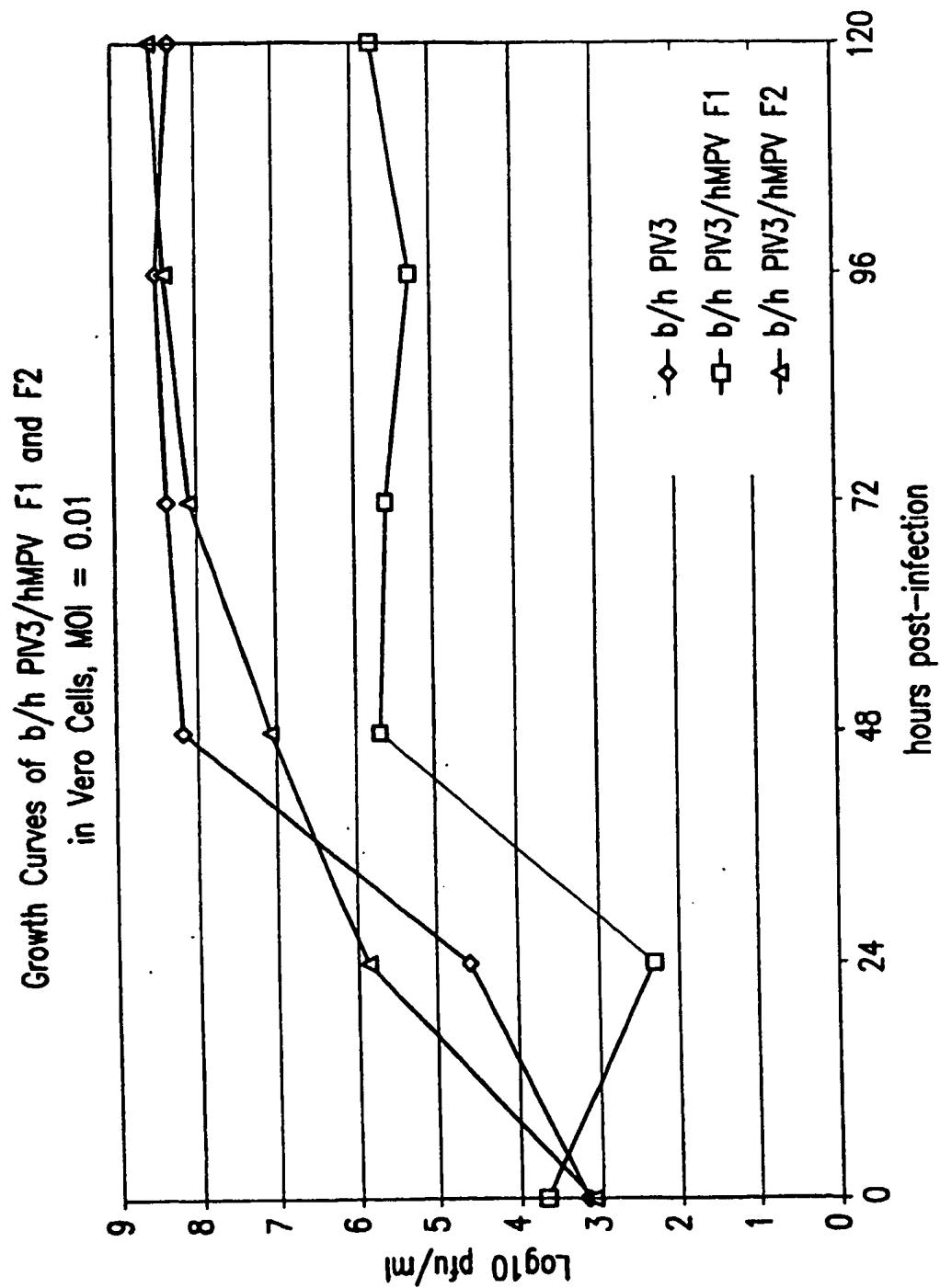
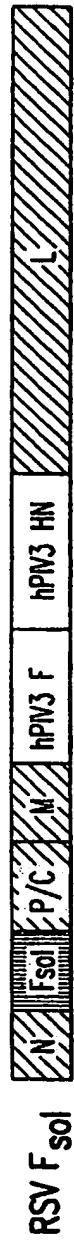


FIG. 13(C)

SUBSTITUTE SHEET (RULE 26)

21/27

Cloning of the Soluble RSV F Gene



Status: Full-length cDNA is being generated.
Purpose: to study whether a soluble RSV F protein without the trans-membrane and intracellular domains will be immunogenic.

FIG. 14

22/27

b/h PIV3/hMPV F1

- liquid overlay on Vero cells
- limiting dilution from 10^{-2} to 10^{-7}
- immunostained with hMPV gp antiserum

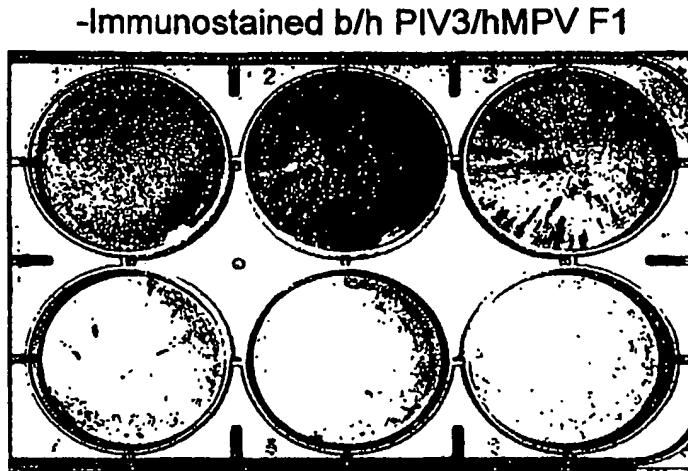


FIG.15(A)

- b/h PIV3/hMPV F2
- methyl cellulose overlay
- on Vero cells
- plaque assay from 10^{-2} to 10^{-7}
- immunostained with hMPV gp antiserum

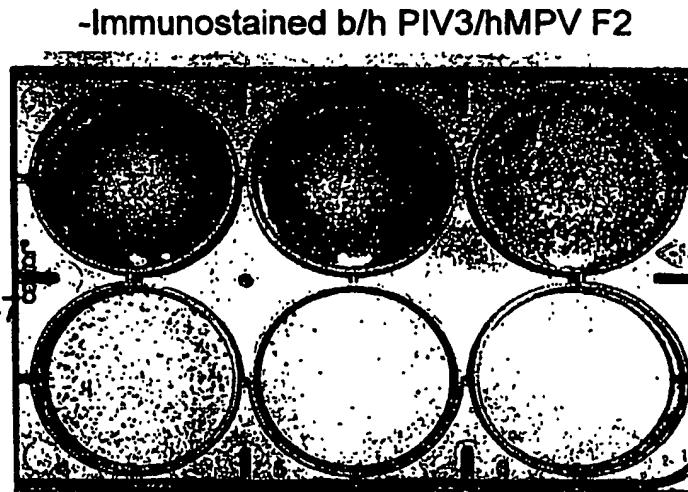


FIG.15(B)

SUBSTITUTE SHEET (RULE 26)

23/27

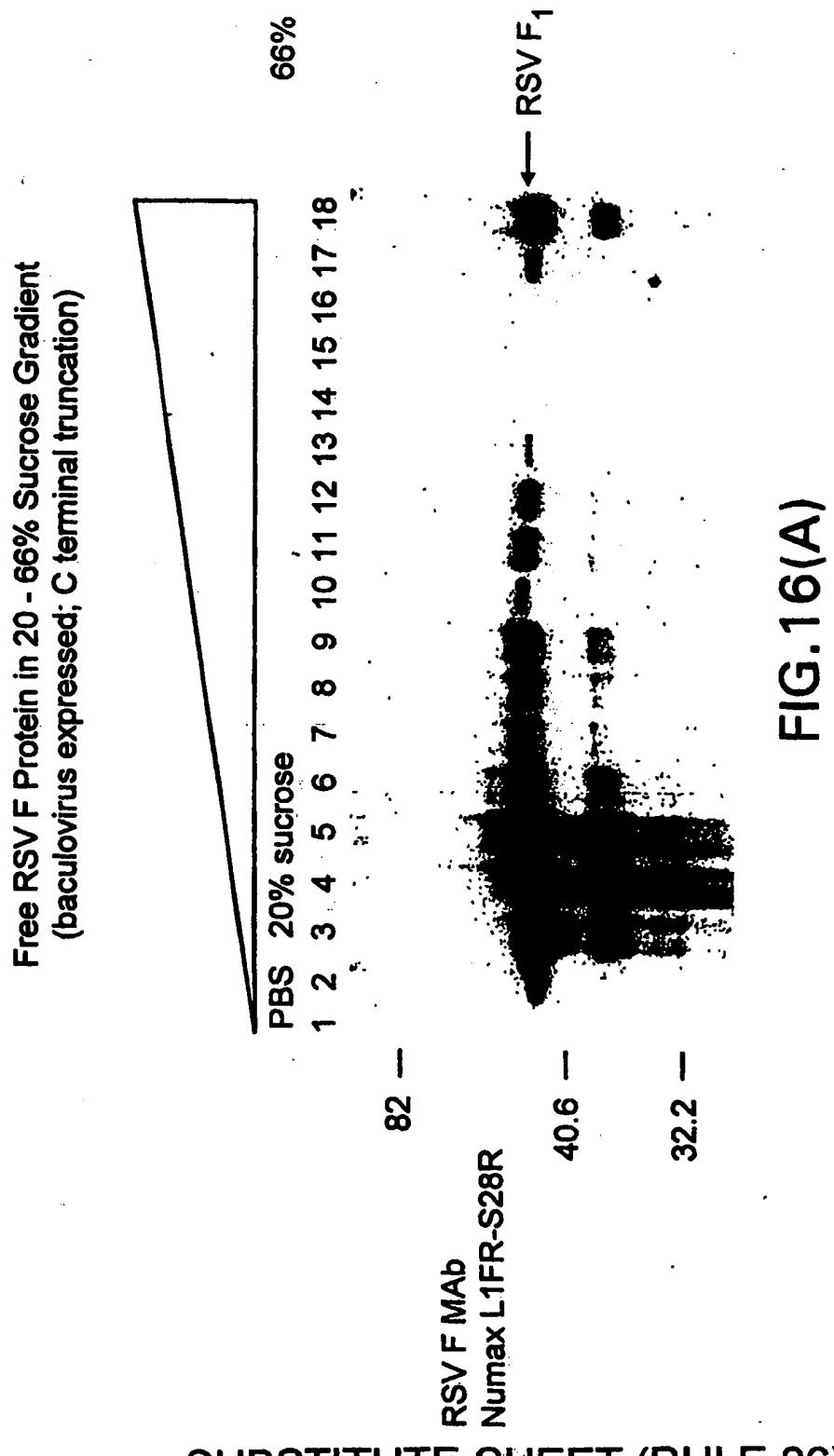
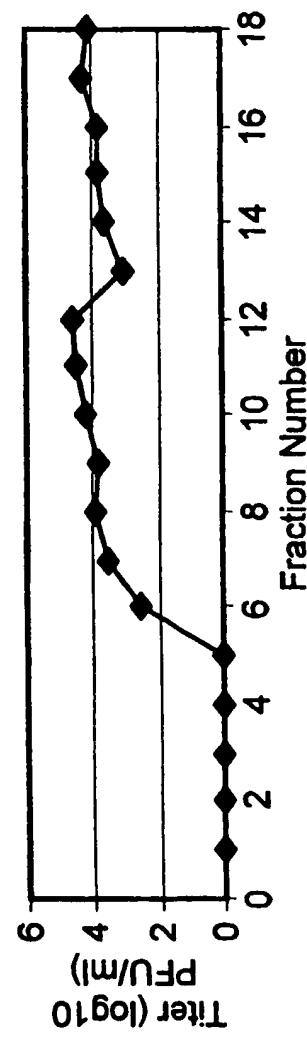


FIG. 16(A)

SUBSTITUTE SHEET (RULE 26)

24/27

**RSV Sucrose Gradient
(spun for 15 hrs @ 25,000 rpm)**

**FIG. 16(B)**

SUBSTITUTE SHEET (RULE 26)

25/27

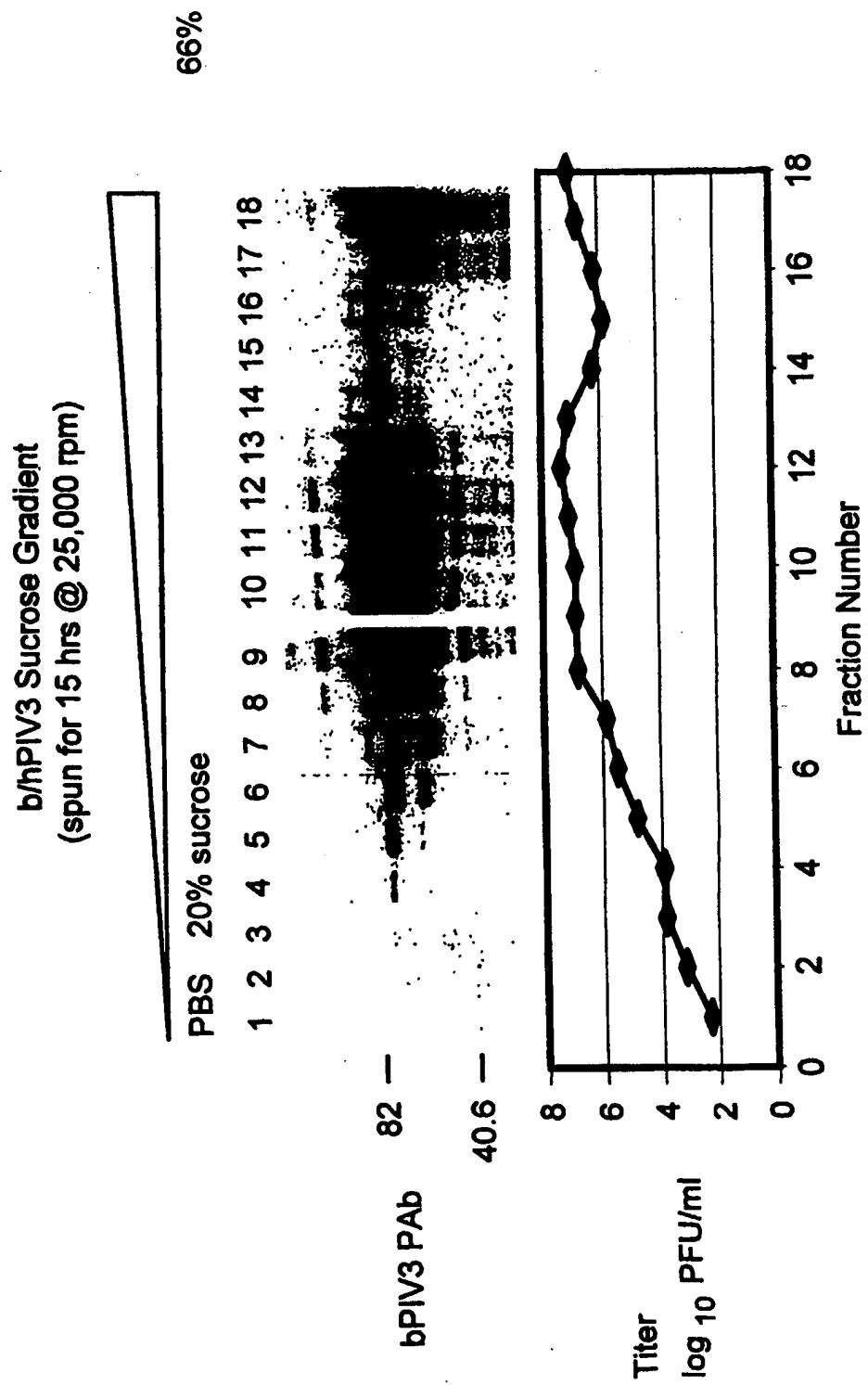
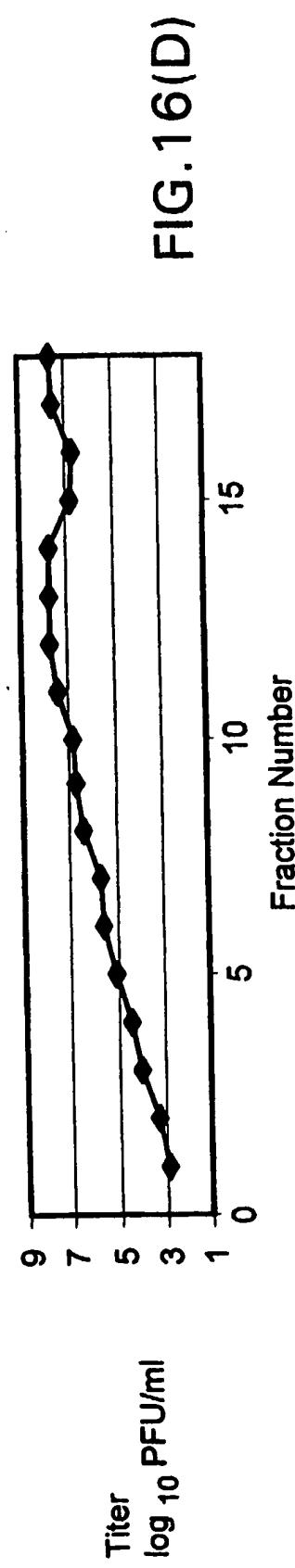
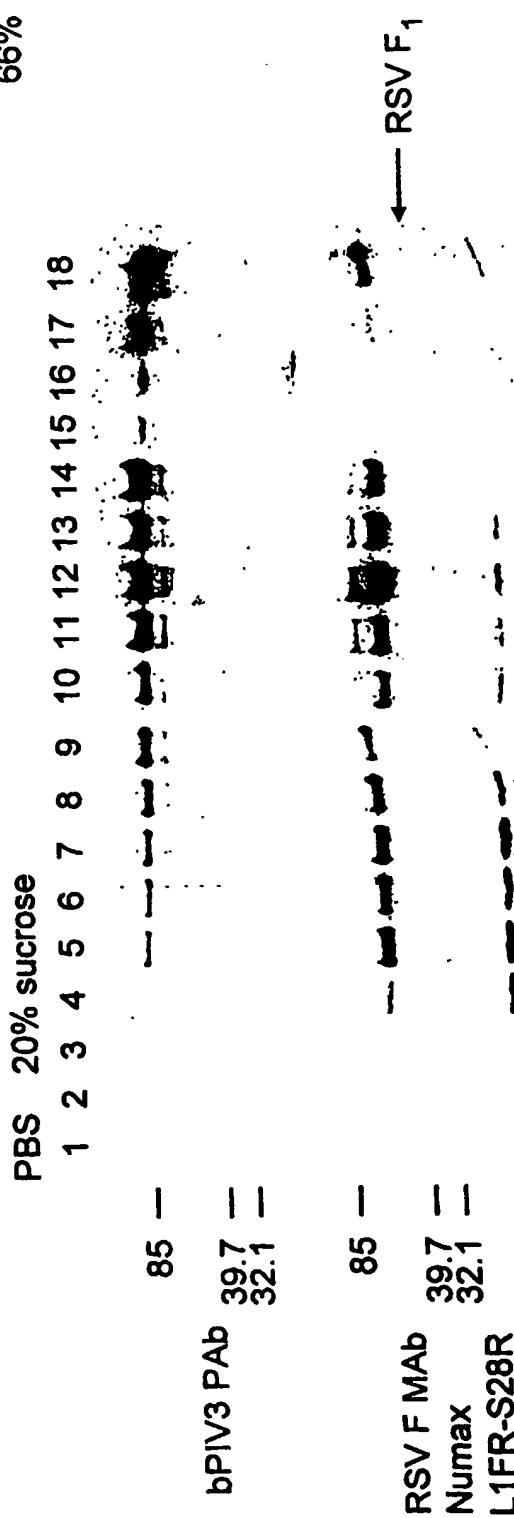


FIG. 16(C)

26/27

b/hPIV3/RSV F2 Sucrose Gradient
(spun for 15 hrs @ 25,000 rpm)



SUBSTITUTE SHEET (RULE 26)

27/27

b/h PIV3/RSV G2 Sucrose Gradient
(spun for 15 hrs @ 25,000 rpm)

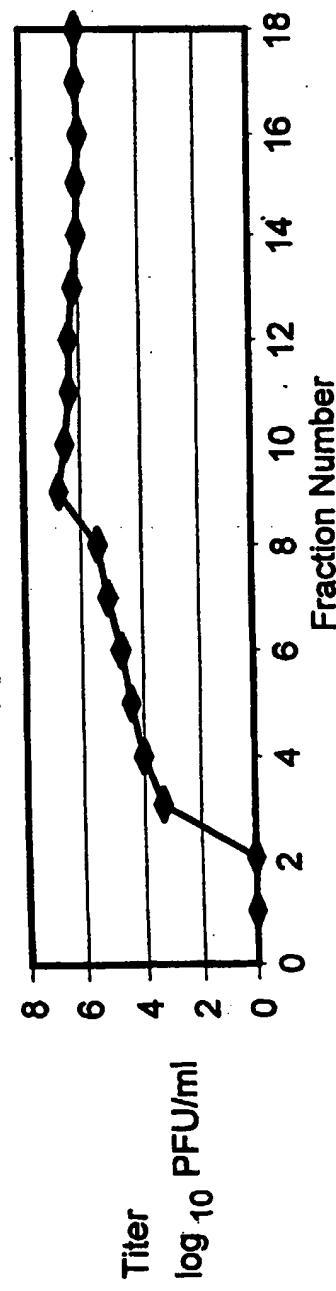
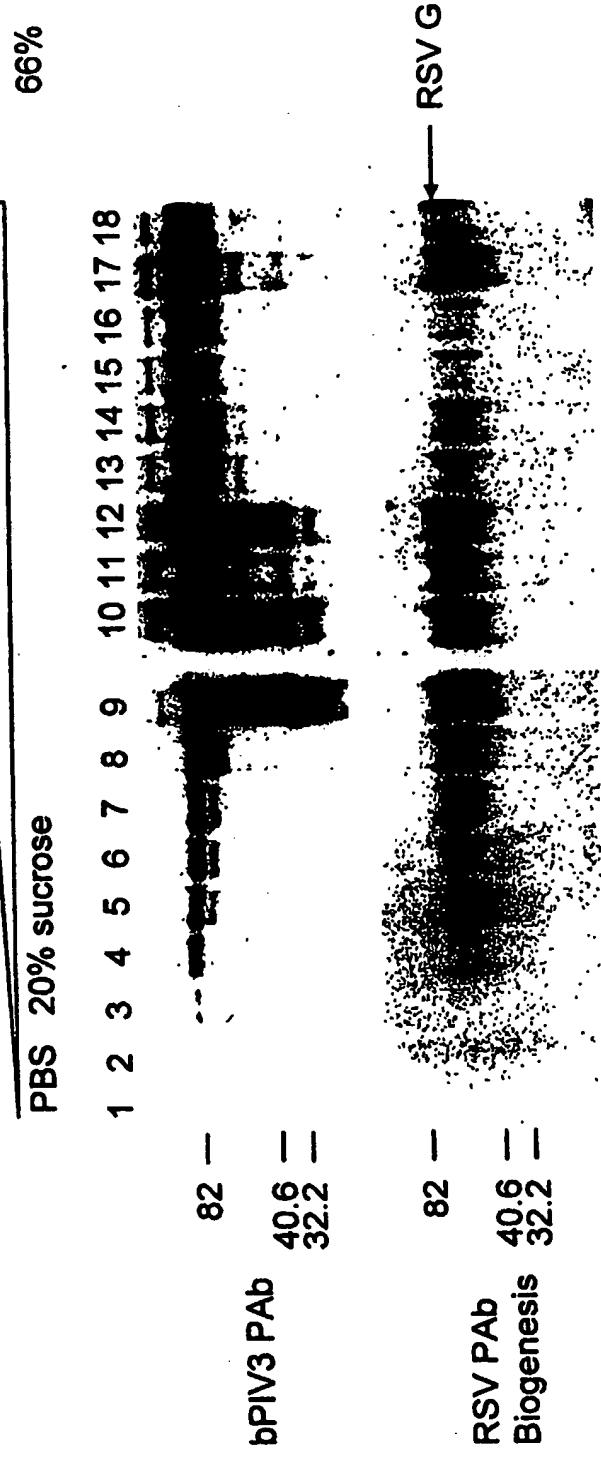


FIG. 16(E)

SUBSTITUTE SHEET (RULE 26)

SEQUENCE LISTING

<110> MedImmune Vaccines, Inc.
ViroNovative BV

<120> RECOMBINANT PARAINFLUENZA VIRUS
EXPRESSION SYSTEMS AND VACCINES
COMPRISING HETEROLOGOUS ANTIGENS
DERIVED FROM METAPNEUMOVIRUS

<130> 7682-061-228

<140> To be assigned

<141> Herewith

<150> 60/358, 934

<151> 2002-02-21

<160> 327

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2507

<212> DNA

<213> metapneumovirus

<220>

<221> CDS

<222> (1) . . . (2507)

<223> Human metapneumovirus isolate 00-1 matrix protein

• (M) and fusion protein (F) genes

<400> 1

atggaggctt	acctagtaga	caccttatcaa	ggcatttcctt	acacagcagc	tgttcaagtt	60
gatctaata	aaaaggac	gttacctgca	agcctaaca	tatggttccc	tttggttcag	120
gccaaacaca	caccagc	gctgctcgat	cagctaaaa	ccctgaca	aaccactctg	180
tatgtctgc	cacaat	tccaaatactc	aaagtgaatg	catcagccca	aggcagca	240
atgtctgtac	ttccccaaa	atttgagtc	aatgcgactg	tagcactg	tgaatata	300
aaactgaa	ttgacaaact	cacagctgt	gaagtaaaa	cagttactt	aacaaccatg	360
aaaccatacg	ggatggtac	aaaatitgt	agctcagcca	aatcagg	aaaaaaaaca	420
catgatctaa	tcgcactatg	tgat	ttttag	gatctagaaa	agaacacacc	480
ccagcattca	tcaaata	ttcaatc	aaa	gagagt	gagactgt	540
ataagcagt	aagcagac	agctcta	aca	caggccaaa	tgcac	600
attatgatca	tgactatgaa	caatcc	aaa	ggcatattc	tgcgggatta	660
caagtcata	tagaactagg	agcatat	gtc	caggctgaaa	agctgggact	720
acttggagcc	atcaagg	aagat	atgtc	ttgaagt	tcc	780
gccaagagct	actaac	cata	ccat	cataa	agg	840
tcaagttaga	acaagaatt	aatcaat	aaat	ggcataa	gca	900
ttgtgtatcat	ttttcatt	ttaataa	acac	ctcaacac	gg	960
aagagtcat	tagactata	actgaagg	at	tctcag	tg	1020
ccaatgttt	ta	acttg	gt	ggag	aggaca	1080
gcttaataaa	aa	caga	gac	taa	gttgg	1140
ctgctgtatca	actgg	caaga	gg	aaaat	gac	1200
taggacaa	at	gactcg	tt	tttcc	tttgg	1260
ccaaaaccat	ccgg	cttgaa	at	tttcc	tttgg	1320
atgaagcagt	at	ttcacatt	gg	ttcgtgt	gt	1380
tgaaagattt	tg	tgagcaag	aa	gtcaat	tg	1440
ctgacctgaa	aa	tggccgtt	ag	tttcaac	tg	1500
ggcaattt	ag	acaacg	tt	tttcaac	tttggactt	1560
ctgaaacta	ca	qactq	tt	tttcaacat	at	1620

tggagaacctg tgcaatggta agaagaaaag ggttcggatt cctgatagga gtttacggaa 1680
 gctccgtaat ttacatggtg caactgc当地 tctttgggt tatagacacg ccttgc当地 1740
 tagtaaaagc agccccctct tgttcaggaa aaaagggaaa ctatgc当地 ctcttaagag 1800
 aagaccaagg atggatttgt caaaatgc当地 ggtcaactgt ttactaccata aatgaaaaaaag 1860
 actgtgaaac aagaggagac catgtctt当地 gc当地 acagac当地 agc当地 agatgtc当地 1920
 agc当地 ct当地 ggagtgc当地 ataaacatata ctactactaa ttaccatgc当地 aaagtttagca 1980
 caggaagaca tc当地 tcatc当地 atgggtc当地 tatctc当地 tgggctt当地 gttgctt当地 2040
 acaaggaggat gagctgtcc attggc当地 acagagtagg gatcatcaag caactgaaca 2100
 aaggctgctc ttatataacc aaccaagac当地 cagacac当地 gacaatagac aacactgtat 2160
 accagctaag caaagttgaa ggc当地 acac当地 atgttataaa aggaaggcca gt当地 caagca 2220
 gcttgc当地 agtcaaggat当地 cctg当地 agat当地 aattcaatgt tgcactt当地 caagttt当地 2280
 agagcattga gaacagtc当地 gc当地 tgggt当地 atcaatcaa当地 cagaatccata agc当地 gt当地 2340
 agaaaaggaaa cactggctt当地 atcattgtaa taattctaat tgctgtc当地 ggctctacca 2400
 tgatccttagt gagttt当地 atcataataa agaaaacaaa gagacccaca ggagcaccc 2460
 cagagctgag tggtgc当地 aacaatggct tc当地 accaca taattag 2507

<210> 2
<211> 1596
<212> DNA
<213> pneumovirus

<220>
<221> CDS
<222> (1)...(1596)
<223> Avian pneumovirus fusion protein gene, partial cds

<400> 2
atgtctt当地 aagtggtaact gctattggta ttgcttagctt ccccaacggg ggggcttagaa 60
gaaaggattatc tagaggagtc atgc当地 ctgactt gttacttagag gatacctgag tttttgagg 120
acaggatggt atacaatgt gttcacactt ggggttggag atgtaaaaaa tctcacatgt 180
accgacgggc ccagcttaat aagaacagaa cttgaaactga caaaaaatgc acttgaggaa 240
ctcaagacag tatcagc当地 tcaattggca aaggaagctt ggataatgtc accaagaaaa 300
gcccggtt当地 ttctgggtgc catagc当地 tttt当地 ggtgtggcaat ctgctgctgc tttt当地 360
ggtagc当地 tagccaaagac aattaggctt gaaaggagaag tggctgcaat caaagggtc当地 420
ctcaggaaaa caaatgaggc tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 480
gctgtgaaatg atctcaagga ct当地 tataatgtt aaaaatgtt cacctgcaat aaacaggaaac 540
aagtgtgaca tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 600
ctcaatgtgg taagacagtt ttctgacaat gc当地 aggtt当地 tttt当地 tttt当地 tttt当地 660
ttaatgactg acgctgagct tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 720
atcaatctga tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 780
ggaggtt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 840
acaccgtt当地 ggagggtgaa ggctgtccat tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 900
tgtctctt当地 gagaggacca aggtt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 960
ccaaatgagg aggactgtgaa agt当地 aagaatgtt gatcatgtt tttt当地 tttt当地 tttt当地 1020
ataaaatgttag caaaggagtc agaaggatgtc aacaggaaata tttt当地 tttt当地 tttt当地 tttt当地 1080
tgcaaggtaa gt当地 acagggtt当地 tc当地 acccaata agcatgtt当地 cttt当地 tttt当地 1140
ttgttagc当地 gttatgtc当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 1200
agacctt当地 ggaaagggtt当地 tt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 1260
gacaacacag tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 1320
ccagtatctt当地 gcaatttt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 1380
gatcagggtt当地 ttgaaatgtt tgagaagatgtt cagaatgtgaa tagaccatgtc aaacaagata 1440
ttggatagca ttgaaaaggaa gaatgtc当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 1500
ctcatgtt当地 cagc当地 agt当地 tt当地 tttt当地 tttt当地 tttt当地 tttt当地 tttt当地 1560
cccaaattt当地 caatggaaat gaatgggtt当地 aacaac 1596

<210> 3
<211> 1666
<212> DNA
<213> pneumovirus

<220>
<221> CDS

<222> (14)...(1627)

<223> Avian pneumovirus isolate 1b fusion protein mRNA,
complete cds

<400> 3

```

gggacaagt gaaaatgtctt gggaaagtgggt actgtctattg gtattgttag ctaccccaac 60
ggggggggcta gaagaaagtt atcttagagga gtcatgcagt actgttacta gaggataacct 120
gagtgtttt aggacaggat ggtatacaaa tggttcaca cttggagggtt gagatgtgga 180
aaatctcaca tgtaccgacg ggcccagctt aataagaaca gaacttgaac tgacaaaaaaa 240
tgcaacttgcg gaactcaaga cagtatcgc agatcaattt gcaaaaggaaat ctaggataat 300
gtcaccaaga aaagcccggt ttgttctggg tgccatagca ttaggtgtgg caactgctgc 360
tgcgtgtacg gctgggttag cgatagccaa gacaatttggg ctagaaggag aagtggctgc 420
aatcaagggt ggcgtcagga aaacaaaatga ggctgtatct acatttaggaa atggcgttag 480
ggtaacttgcg acagctgtga atgatctcaa ggactttata agtaaaaaat tgacacctgc 540
aataaacagg aacaagtgtg acatctcaga ccttaagatg gcagttagt ttggacaata 600
caatcgaggg ttccctcaatg tggtaagaca gttttctgac aatgcaggta ttacgcctgc 660
aatatctcta gatttaatga ctgacgctga gctttaaga gctgttaagca acatgcccac 720
atcttcagga cagatcaatc tggatgttgcg gaatcggca atggtcagaa ggaaaggatt 780
tgggattttt attggagttt atggtagctc tgggtcttat atagtgcagc ttccctat 840
cggtgtgata gatacaccgt gtggaaagggt gaaggctgct ccattatgtt cagggaaaga 900
cggaattat gcatgtctct tgcgagagga ccaagggttgg tattgtcaaa atgctggatc 960
cacagtttat tatccaaatg aggaggactg tgaagtaaga agtgcattatg tgggttgc 1020
cacagcagct gggataaaatg tagcaaaggaa gtcagaagag tgcaacagga atatctcaac 1080
aacaaggatc ccttgcagg taagtacagg gcgtcaccca ataagcatgg tggccttata 1140
accactgggt gctttgttag cctgttatga cggtatgatg tggccattt gaagcaacaa 1200
ggttggata atcagacccctt tggggaaagg gtgttcatac atcagcaatc aagatgtgaa 1260
caactgttaca attgacaaca cagtgttca attgagcaaa gttgaaggag aacaacacac 1320
aattaaaggg aagccagttt ctgcaattt tgaccctata gagttccctg aagatcattt 1380
caacgttagcc ctggatcagg tgggttggaaatg tggtaagatc agtgcattatc 1440
gtcaaaacaaatg atattggata gcaatttggaaatggca ggatttgcg tggtaagatg 1500
ccttatttgcg ctgctcatgc tggcagcgt tgggtgggtt gtcatttttgcg tggtaagaa 1560
gagaaaagct gctccaaat tcccaatggaa aatgaatggt gtcacaaca aaggatttat 1620
cccttaattt tagttattaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1666

```

<210> 4

<211> 1636

<212> DNA

<213> rhinotracheitis virus

<220>

<221> CDS

<222> (13)...(1629)

<223> Turkey rhinotracheitis virus gene for fusion
protein (F1 and F2 subunits), complete cds

<400> 4

```

gggacaagt ggtatggatgt aagaatctgt ctcctattgt tccttatatc taatcctagt 60
agctgcatac aagaaacata caatgaagaa tcctgcagta ctgtacttag aggttataag 120
agtgtttaa ggacagggtt gttatcgatgt gtatataacc tcgaaatagg gaatgttgc 180
aacatcactt gcaatgtatgg acccagcata attgacactg agttgtact cacaagaat 240
gttttgggg agctcaaaac agtgcgtatgt gatcaagtgg ctaaggaaatg cagactatcc 300
tcacccaggaa gacgttagatt tggactgggt gcaatagcac ttgggtttgc gacagctgt 360
gccgtaaacag ctgggttagc acttgcaggaa acaatttagat tagagggaga ggtgaaggca 420
attaagaatg ccctccggaa cacaatgtatgg gcaatgtatccca cattagggaa tgggtgtgagg 480
gtactagcaa ctgcagtcaa tgacctcaaa gaatttataa gtaaaaaatt gactcctgtct 540
attaaccaga acaaattgtatgg tttatgtatggt ataaagatgg caatttagttt tggccaaat 600
aacagaaggat tccctgtatgt ggttggggca ttctctgtata gtcgtatgtt cacatcagct 660
gtgtcttttgcg atttatgtatggt gttttttttttt gttttttttttt gttttttttttt 720
tcattcaggac agattatgtt gatgttgcac aatcgatgc tggtaagatgg gaaagggtttt 780
ggtaatattgtt tgggttttttgcg tttttttttttt gttttttttttt gttttttttttt 840
ggcggttggatggt agacaccccttgcg tttttttttttt gttttttttttt gttttttttttt 900
ggcaattatgtt tgggttttttgcg tttttttttttt gttttttttttt gttttttttttt 960

```

acagcttatt atcctaataa agatgattgt gaggtaaggg atgattatgt attttgtac 1020
 acagcagctg gcattaatgt ggcctagaa gttgaacagt gcaactataa catatcgact 1080
 tctaaatacc catgcaaagt cagcacagg agacaccctg tcagtatggt agcctaacc 1140
 cccctaggg gtcttagtgc ttgttatgag agtgaagtt gctccatagg tagaataaa 1200
 gttagggataa taaaacagct aggaaaggg tgccacccaca ttcccaacaa cgaagctgac 1260
 acgataacca ttgataaacac tggatcacca ttgagcaagg ttgttaggcga acagaggacc 1320
 ataaaaggag ctccagttgt gaacaatttt aacccaatat tattccctga ggatcaggtc 1380
 aatgtgcac ttgaccaagt atttgaggt atagatagat ctcaggactt aatagataag 1440
 tctaacgact tgcttagtgc agatgccaag agcaaggctg gaattgtat agcaatagta 1500
 gtgtcgtca ttcttaggaat cttctttta cttgcagtga tatattactg ttccagagtc 1560
 cggaaagacca aaccaaagca tgattacccg gccacgacag gtcatagcag catggcttat 1620
 gtcagttaaat ttat 1636

<210> 5

<211> 1860

<212> DNA

<213> pneumovirus

<220>

<221> CDS

<222> (1) ... (110)

<223> Avian pneumovirus matrix protein (M) gene, partial
cds

<220>

<221> CDS

<222> (216) ... (1829)

<223> Avian pneumovirus fusion glycoprotein (F) gene,
complete cds

<400> 5

gagttcaggat aatagtggag ttagggcat acgttcaagc agaaagcata agcagaatct 60
 gcaggaactg gagccaccag ggtacgagat atgtcctgaa gtcaagataa acacagagag 120
 tacacttacc aaatcacagt aacaatttcg ttttaaccc tctcatagtt attacctagc 180
 ttgatattat ttagaaaaaa ttggacaag tgaaaatgtc ttgaaaagtg gtactgtat 240
 tggattgtc agtacccca acgggggggc tagaagaaag ttatcttagag gagtcatgca 300
 gtactgttac tagaggatac ctgagtgtt tgaggacagg atggtataca aatgtgtca 360
 cacttgagg tggagatgtg gaaaatctca catgtaccga cgggcccagc ttaataagaa 420
 cagaacttga actgacaaaaa aatgcacttg aggaactcaa gacagtatca gcagatcaat 480
 tggcaagga agctaggata atgtcacca gaaaaggccc gttgttctg ggtgccatag 540
 cattaggtgt ggcaactgtc gctgtgtga cggctgtgt agcgtatgcc aagacaatta 600
 ggctagaagg agaagtggct gcaatacagg gtgcgtctag gaaaacaaat gaggctgtat 660
 ctacattagg aaatggcgtg aggtacttg caacagctgt gaatgtatctc aaggacttta 720
 taagaaaaaa attgacacac gcaataaaca ggaacaagt tgacatctca gacctaaga 780
 tggcagttag cttggacaa tacaatcgga gttcctcaa tggtaaga cagtttctg 840
 acaatgcagg tattacgcct gcaatatctc tagatataat gactgacgtc gagcttgaa 900
 gagctgtaaag caacatgccc acatcttcag gacagatcaa tctgtatgtt gagaatcggg 960
 caatggtcag aaggaaagga tttggatt tgattggagt ttatggtagc tctgtgtct 1020
 atatagtgca gttcctatt ttcgggtgtga tagatacacc gtgttggaa gtgaaggctg 1080
 ctccattatg ttcaggaaa gacgggatt atgcgtgtc cttgcgtagag gaccaagggtt 1140
 ggtattgtca aaatgctgga tccacagttt attatccaa tgaggaggac tgtgaagtaa 1200
 gaagtgtca tggttttgt gacacagcag ctggataaa tggtagcaaag gagtcagaag 1260
 agtcaacac agaatctca acaacaaagt acccttgcaa ggtaaatcaca gggcgtcacc 1320
 caataagcat ggtggccta tcaccactgg gtgccttggt agcgtgttat gacggatgaa 1380
 gttgtccat tggaaacaaac aagttggaa taatcagacc tttggggaaa ggggttcat 1440
 acatcagcaa tcaagatgtc gacactgtt caattgacaa cacagtgtac caattgagca 1500
 aagttgaagg agaacaacac acaattaaag ggaagccagt atctgacat tttgacccta 1560
 tagagttccc tgaagatcag ttcaacatag ccctggatca ggtgtttgaa agtgttgaga 1620
 agagtcagaa tctgtatagac cagtcaaaca agatattggta tagcattgaa aagggaaatg 1680
 caggatttgt catgtgata gtcctcattt tctgtctat gctggcagca gttgggtgtgg 1740
 gtgtcttctt tgggttaag aagagaaaag ctgtccccaa attccaaatg gaaatgaatg 1800
 gtgtgaacaa caaaggattt atcccttaat tttagttact aaaaaattgg gacaagtgaa 1860

<210> 6
<211> 574
<212> PRT
<213> paramyxovirus

<400> 6
Met Glu Leu Leu Ile His Arg Leu Ser Ala Ile Phe Leu Thr Leu Ala
1 5 10 15
Ile Asn Ala Leu Tyr Leu Thr Ser Ser Gln Asn Ile Thr Glu Glu Phe
20 25 30
Tyr Gln Ser Thr Cys Ser Ala Val Ser Arg Gly Tyr Phe Ser Ala Leu
35 40 45
Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60
Lys Glu Thr Lys Cys Asn Gly Thr Asp Thr Lys Val Lys Leu Ile Lys
65 70 75 80
Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
85 90 95
Met Gln Asn Thr Pro Ala Ala Asn Asn Arg Ala Arg Arg Glu Ala Pro
100 105 110
Gln Tyr Met Asn Tyr Thr Ile Asn Thr Thr Lys Asn Leu Asn Val Ser
115 120 125
Ile Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140
Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val Leu His Leu
145 150 155 160
Glu Gly Glu Val Asn Lys Ile Lys Asn Ala Leu Leu Ser Thr Asn Lys
165 170 175
Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
180 185 190
Leu Asp Leu Lys Asn Tyr Ile Asn Asn Gln Leu Leu Pro Ile Val Asn
195 200 205
Gln Gln Ser Cys Arg Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
210 215 220
Gln Lys Asn Ser Arg Leu Leu Glu Ile Asn Arg Glu Phe Ser Val Asn
225 230 235 240
Ala Gly Val Thr Thr Pro Leu Ser Thr Tyr Met Leu Thr Asn Ser Glu
245 250 255
Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
260 265 270
Leu Met Ser Ser Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
275 280 285
Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
290 295 300
Ile Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305 310 315 320
Leu Cys Thr Thr Asn Ile Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
325 330 335
Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
340 345 350
Pro Gln Ala Asp Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
355 360 365
Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Ser Leu Cys Asn Thr
370 375 380
Asp Ile Phe Asn Ser Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385 390 395 400
Asp Ile Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415
Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
420 425 430
Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp

435

440

445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Leu Glu Gly
 450 455 460
 Lys Asn Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Tyr Tyr Asp Pro
 465 470 475 480
 Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
 485 490 495
 Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Arg Ser Asp Glu Leu
 500 505 510
 Leu His Asn Val Asn Thr Gly Lys Ser Thr Thr Asn Ile Met Ile Thr
 515 520 525
 Thr Ile Ile Ile Val Ile Ile Val Val Leu Leu Ser Leu Ile Ala Ile
 530 535 540
 Gly Leu Leu Leu Tyr Cys Lys Ala Lys Asn Thr Pro Val Thr Leu Ser
 545 550 555 560
 Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Lys
 565 570

<210> 7

<211> 574

<212> PRT

<213> paramyxovirus

<400> 7

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
 1 5 10 15
 Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
 20 25 30
 Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
 35 40 45
 Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
 50 55 60
 Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
 65 70 75 80
 Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
 85 90 95
 Met Gln Ser Thr Pro Pro Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
 100 105 110
 Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
 115 120 125
 Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
 130 135 140
 Gly Ser Ala Ile Ala Ser Gly Val Ala Val Ser Val Leu His Leu
 145 150 155 160
 Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
 165 170 175
 Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
 180 185 190
 Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Val Asn
 195 200 205
 Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
 210 215 220
 Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
 225 230 235 240
 Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
 245 250 255
 Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
 260 265 270
 Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
 275 280 285

Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
 290 295 300
 Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
 305 310 315 320
 Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
 325 330 335
 Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
 340 345 350
 Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
 355 360 365
 Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Ile Asn Leu Cys Asn Val
 370 375 380
 Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
 385 390 395 400
 Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
 405 410 415
 Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
 420 425 430
 Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Met Asp
 435 440 445
 Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
 450 455 460
 Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
 465 470 475 480
 Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
 485 490 495
 Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
 500 505 510
 Leu His Asn Val Asn Ala Gly Lys Ser Thr Thr Asn Ile Met Ile Thr
 515 520 525
 Thr Ile Ile Ile Val Ile Ile Val Ile Leu Leu Ser Leu Ile Ala Val
 530 535 540
 Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro Val Thr Leu Ser
 545 550 555 560
 Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Asn
 565 570

<210> 8
 <211> 121
 <212> PRT
 <213> metapneumovirus

<400> 8
 Leu Leu Ile Thr Pro Gln His Gly Leu Lys Glu Ser Tyr Leu Glu Glu
 1 5 10 15
 Ser Cys Ser Thr Ile Thr Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly
 20 25 30
 Trp Tyr Thr Asn Val Phe Thr Leu Glu Val Gly Asp Val Glu Asn Leu
 35 40 45
 Thr Cys Ala Asp Gly Pro Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr
 50 55 60
 Lys Ser Ala Leu Arg Glu Leu Arg Thr Val Ser Ala Asp Gln Leu Ala
 65 70 75 80
 Arg Glu Glu Gln Ile Glu Asn Pro Arg Gln Ser Arg Phe Val Leu Gly
 85 90 95
 Ala Ile Ala Leu Gly Val Ala Thr Ala Ala Val Thr Ala Gly Val
 100 105 110
 Ala Ile Ala Lys Thr Ile Arg Leu Glu
 115 120

<210> 9
<211> 539
<212> PRT
<213> metapneumovirus

<400> 9
Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1 5 10 15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
20 25 30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
35 40 45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ala Asp Gly Pro
50 55 60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65 70 75 80
Leu Arg Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
85 90 95
Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
100 105 110
Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
115 120 125
Arg Leu Glu Ser Glu Val Thr Ala Ile Lys Asn Ala Leu Lys Lys Thr
130 135 140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145 150 155 160
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
165 170 175
Ile Asn Lys Asn Lys Cys Asp Ile Ala Asp Leu Lys Met Ala Val Ser
180 185 190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
195 200 205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
210 215 220
Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225 230 235 240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
245 250 255
Gly Phe Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
260 265 270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
275 280 285
Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
290 295 300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305 310 315 320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
325 330 335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
340 345 350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
355 360 365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
370 375 380
Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385 390 395 400
Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
405 410 415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
420 425 430
Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Phe Asp Pro
435 440 445

Val Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
 450 455 460
 Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
 465 470 475 480
 Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
 485 490 495
 Leu Ile Ala Val Leu Gly Ser Thr Met Ile Leu Val Ser Val Phe Ile
 500 505 510
 Ile Ile Lys Lys Thr Lys Arg Pro Thr Gly Ala Pro Pro Glu Leu Ser
 515 520 525
 Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
 530 535

<210> 10
<211> 532
<212> PRT
<213> Avian pneumovirus

<400> 10
Met Ser Trp Lys Val Val Leu Leu Leu Val Leu Ala Thr Pro Thr
 1 5 10 15
Gly Gly Leu Glu Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Val Thr
 20 25 30
Arg Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35 40 45
Thr Leu Gly Val Gly Asp Val Lys Asn Leu Thr Cys Thr Asp Gly Pro
 50 55 60
Ser Leu Ile Arg Thr Glu Leu Glu Leu Thr Lys Asn Ala Leu Glu Glu
 65 70 75 80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Lys Glu Ala Arg Ile Met
 85 90 95
Ser Pro Arg Lys Ala Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
 100 105 110
Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
 115 120 125
Arg Leu Glu Gly Glu Val Ala Ala Ile Lys Gly Ala Leu Arg Lys Thr
 130 135 140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
 145 150 155 160
Ala Val Asn Asp Leu Lys Asp Phe Ile Ser Lys Lys Leu Thr Pro Ala
 165 170 175
Ile Asn Arg Asn Lys Cys Asp Ile Ser Asp Leu Lys Met Ala Val Ser
 180 185 190
Phe Gly Gln Tyr Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
 195 200 205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
 210 215 220
Ala Glu Leu Val Arg Ala Val Ser Asn Met Pro Thr Ser Ser Gly Gln
 225 230 235 240
Ile Asn Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
 245 250 255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Val Tyr Ile Val Gln
 260 265 270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Arg Val Lys Ala
 275 280 285
Ala Pro Leu Cys Ser Gly Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg
 290 295 300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
 305 310 315 320
Pro Asn Glu Glu Asp Cys Glu Val Arg Ser Asp His Val Phe Cys Asp
 325 330 335

Thr Ala Ala Gly Ile Asn Val Ala Lys Glu Ser Glu Glu Cys Asn Arg
 340 345 350
 Asn Ile Ser Thr Thr Lys Tyr Pro Cys Lys Val Ser Thr Gly Arg His
 355 360 365
 Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
 370 375 380
 Tyr Asp Gly Met Ser Cys Ser Ile Gly Ser Asn Lys Val Gly Ile Ile
 385 390 395 400
 Arg Pro Leu Gly Lys Gly Cys Ser Tyr Ile Ser Asn Gln Asp Ala Asp
 405 410 415
 Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
 420 425 430
 Glu Gln His Thr Ile Lys Gly Lys Pro Val Ser Ser Asn Phe Asp Pro
 435 440 445
 Ile Glu Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
 450 455 460
 Glu Ser Val Glu Lys Ser Gln Asn Leu Ile Asp Gln Ser Asn Lys Ile
 465 470 475 480
 Leu Asp Ser Ile Glu Lys Gly Asn Ala Gly Phe Val Ile Val Ile Val
 485 490 495
 Leu Ile Val Leu Leu Met Leu Ala Ala Val Gly Val Gly Val Phe Phe
 500 505 510
 Val Val Lys Lys Arg Lys Ala Ala Pro Lys Phe Pro Met Glu Met Asn
 515 520 525
 Gly Val Asn Asn
 530

<210> 11
 <211> 537
 <212> PRT
 <213> Avian pneumovirus

<400> 11
 Met Ser Trp Lys Val Val Leu Leu Leu Val Leu Leu Ala Thr Pro Thr
 1 5 10 15
 Gly Gly Leu Glu Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Val Thr
 20 25 30
 Arg Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35 40 45
 Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Thr Asp Gly Pro
 50 55 60
 Ser Leu Ile Arg Thr Glu Leu Glu Leu Thr Lys Asn Ala Leu Glu Glu
 65 70 75 80
 Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Lys Glu Ala Arg Ile Met
 85 90 95
 Ser Pro Arg Lys Ala Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
 100 105 110
 Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
 115 120 125
 Arg Leu Glu Gly Glu Val Ala Ala Ile Lys Gly Ala Leu Arg Lys Thr
 130 135 140
 Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
 145 150 155 160
 Ala Val Asn Asp Leu Lys Asp Phe Ile Ser Lys Lys Leu Thr Pro Ala
 165 170 175
 Ile Asn Arg Asn Lys Cys Asp Ile Ser Asp Leu Lys Met Ala Val Ser
 180 185 190
 Phe Gly Gln Tyr Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
 195 200 205
 Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
 210 215 220

Ala Glu Leu Val Arg Ala Val Ser Asn Met Pro Thr Ser Ser Gly Gln
 225 230 235 240
 Ile Asn Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
 245 250 255
 Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Val Tyr Ile Val Gln
 260 265 270
 Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Lys Val Lys Ala
 275 280 285
 Ala Pro Leu Cys Ser Gly Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg
 290 295 300
 Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
 305 310 315 320
 Pro Asn Glu Glu Asp Cys Glu Val Arg Ser Asp His Val Phe Cys Asp
 325 330 335
 Thr Ala Ala Gly Ile Asn Val Ala Lys Glu Ser Glu Glu Cys Asn Arg
 340 345 350
 Asn Ile Ser Thr Thr Lys Tyr Pro Cys Lys Val Ser Thr Gly Arg His
 355 360 365
 Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
 370 375 380
 Tyr Asp Gly Met Ser Cys Ser Ile Gly Ser Asn Lys Val Gly Ile Ile
 385 390 395 400
 Arg Pro Leu Gly Lys Gly Cys Ser Tyr Ile Ser Asn Gln Asp Ala Asp
 405 410 415
 Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
 420 425 430
 Glu Gln His Thr Ile Lys Gly Lys Pro Val Ser Ser Asn Phe Asp Pro
 435 440 445
 Ile Glu Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
 450 455 460
 Glu Ser Val Glu Lys Ser Gln Asn Leu Ile Asp Gln Ser Asn Lys Ile
 465 470 475 480
 Leu Asp Ser Ile Glu Lys Gly Asn Ala Gly Phe Val Ile Val Ile Val
 485 490 495
 Leu Ile Val Leu Leu Met Leu Ala Ala Val Gly Val Gly Val Phe Phe
 500 505 510
 Val Val Lys Lys Arg Lys Ala Ala Pro Lys Phe Pro Met Glu Met Asn
 515 520 525
 Gly Val Asn Asn Lys Gly Phe Ile Pro
 530 535

<210> 12
 <211> 538
 <212> PRT
 <213> Turkey rhinotracheitis virus

<400> 12
 Met Asp Val Arg Ile Cys Leu Leu Leu Phe Leu Ile Ser Asn Pro Ser
 1 5 10 15
 Ser Cys Ile Gln Glu Thr Tyr Asn Glu Glu Ser Cys Ser Thr Val Thr
 20 25 30
 Arg Gly Tyr Lys Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35 40 45
 Asn Leu Glu Ile Gly Asn Val Glu Asn Ile Thr Cys Asn Asp Gly Pro
 50 55 60
 Ser Leu Ile Asp Thr Glu Leu Val Leu Thr Lys Asn Ala Leu Arg Glu
 65 70 75 80
 Leu Lys Thr Val Ser Ala Asp Gln Val Ala Lys Glu Ser Arg Leu Ser
 85 90 95
 Ser Pro Arg Arg Arg Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
 100 105 110

Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Leu Ala Lys Thr Ile
 115 120 125
 Arg Leu Glu Gly Glu Val Lys Ala Ile Lys Asn Ala Leu Arg Asn Thr
 130 135 140
 Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
 145 150 155 160
 Ala Val Asn Asp Leu Lys Glu Phe Ile Ser Lys Lys Leu Thr Pro Ala
 165 170 175
 Ile Asn Gln Asn Lys Cys Asn Ile Ala Asp Ile Lys Met Ala Ile Ser
 180 185 190
 Phe Gly Gln Asn Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
 195 200 205
 Asp Ser Ala Gly Ile Thr Ser Ala Val Ser Leu Asp Leu Met Thr Asp
 210 215 220
 Asp Glu Leu Val Arg Ala Ile Asn Arg Met Pro Thr Ser Ser Gly Gln
 225 230 235 240
 Ile Ser Leu Met Leu Asn Asn Arg Ala Met Val Arg Arg Lys Gly Phe
 245 250 255
 Gly Ile Leu Ile Gly Val Tyr Asp Gly Thr Val Val Tyr Met Val Gln
 260 265 270
 Leu Pro Ile Phe Gly Val Ile Glu Thr Pro Cys Trp Arg Val Val Ala
 275 280 285
 Ala Pro Leu Cys Arg Lys Glu Lys Gly Asn Tyr Ala Cys Ile Leu Arg
 290 295 300
 Glu Asp Gln Gly Trp Tyr Cys Thr Asn Ala Gly Ser Thr Ala Tyr Tyr
 305 310 315 320
 Pro Asn Lys Asp Asp Cys Glu Val Arg Asp Asp Tyr Val Phe Cys Asp
 325 330 335
 Thr Ala Ala Gly Ile Asn Val Ala Leu Glu Val Glu Gln Cys Asn Tyr
 340 345 350
 Asn Ile Ser Thr Ser Lys Tyr Pro Cys Lys Val Ser Thr Gly Arg His
 355 360 365
 Pro Val Ser Met Val Ala Leu Thr Pro Leu Gly Gly Leu Val Ser Cys
 370 375 380
 Tyr Glu Ser Val Ser Cys Ser Ile Gly Ser Asn Lys Val Gly Ile Ile
 385 390 395 400
 Lys Gln Leu Gly Lys Gly Cys Thr His Ile Pro Asn Asn Glu Ala Asp
 405 410 415
 Thr Ile Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Val Gly
 420 425 430
 Glu Gln Arg Thr Ile Lys Gly Ala Pro Val Val Asn Asn Phe Asn Pro
 435 440 445
 Ile Leu Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
 450 455 460
 Glu Ser Ile Asp Arg Ser Gln Asp Leu Ile Asp Lys Ser Asn Asp Leu
 465 470 475 480
 Leu Gly Ala Asp Ala Lys Ser Lys Ala Gly Ile Ala Ile Ile Val
 485 490 495
 Val Leu Val Ile Leu Gly Ile Phe Phe Leu Leu Ala Val Ile Tyr Tyr
 500 505 510
 Cys Ser Arg Val Arg Lys Thr Lys Pro Lys His Asp Tyr Pro Ala Thr
 515 520 525
 Thr Gly His Ser Ser Met Ala Tyr Val Ser
 530 535

<210> 13
 <211> 537
 <212> PRT
 <213> Avian paramovirus

<400> 13

Met Ser Trp Lys Val Val Leu Leu Leu Val Leu Leu Ala Thr Pro Thr
 1 5 10 15
 Gly Gly Leu Glu Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Val Thr
 20 25 30
 Arg Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35 40 45
 Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Thr Asp Gly Pro
 50 55 60
 Ser Leu Ile Arg Thr Glu Leu Glu Leu Thr Lys Asn Ala Leu Glu Glu
 65 70 75 80
 Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Lys Glu Ala Arg Ile Met
 85 90 95
 Ser Pro Arg Lys Ala Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
 100 105 110
 Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
 115 120 125
 Arg Leu Glu Gly Glu Val Ala Ala Ile Lys Gly Ala Leu Arg Lys Thr
 130 135 140
 Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
 145 150 155 160
 Ala Val Asn Asp Leu Lys Asp Phe Ile Ser Lys Lys Leu Thr Pro Ala
 165 170 175
 Ile Asn Arg Asn Lys Cys Asp Ile Ser Asp Leu Lys Met Ala Val Ser
 180 185 190
 Phe Gly Gln Tyr Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
 195 200 205
 Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
 210 215 220
 Ala Glu Leu Val Arg Ala Val Ser Asn Met Pro Thr Ser Ser Gly Gln
 225 230 235 240
 Ile Asn Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
 245 250 255
 Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Val Tyr Ile Val Gln
 260 265 270
 Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Lys Val Lys Ala
 275 280 285
 Ala Pro Leu Cys Ser Gly Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg
 290 295 300
 Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
 305 310 315 320
 Pro Asn Glu Glu Asp Cys Glu Val Arg Ser Asp His Val Phe Cys Asp
 325 330 335
 Thr Ala Ala Gly Ile Asn Val Ala Lys Glu Ser Glu Glu Cys Asn Arg
 340 345 350
 Asn Ile Ser Thr Thr Lys Tyr Pro Cys Lys Val Ser Thr Gly Arg His
 355 360 365
 Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
 370 375 380
 Tyr Asp Gly Met Ser Cys Ser Ile Gly Ser Asn Lys Val Gly Ile Ile
 385 390 395 400
 Arg Pro Leu Gly Lys Gly Cys Ser Tyr Ile Ser Asn Gln Asp Ala Asp
 405 410 415
 Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
 420 425 430
 Glu Gln His Thr Ile Lys Gly Lys Pro Val Ser Ser Asn Phe Asp Pro
 435 440 445
 Ile Glu Phe Pro Glu Asp Gln Phe Asn Ile Ala Leu Asp Gln Val Phe
 450 455 460
 Glu Ser Val Glu Lys Ser Gln Asn Leu Ile Asp Gln Ser Asn Lys Ile
 465 470 475 480
 Leu Asp Ser Ile Glu Lys Gly Asn Ala Gly Phe Val Ile Val Ile Val
 485 490 495

Leu Ile Val Leu Leu Met Leu Ala Ala Val Gly Val Gly Val Phe Phe
 500 505 510
 Val Val Lys Lys Arg Lys Ala Ala Pro Lys Phe Pro Met Glu Met Asn
 515 520 525
 Gly Val Asn Asn Lys Gly Phe Ile Pro
 530 535

<210> 14
<211> 1193
<212> DNA
<213> rhinotracheitis virus

<220>
<221> CDS
<222> (16) ... (1191)
<223> Turkey rhinotracheitis virus (strain CVL14/1)
attachment protien (G) mRNA, complete cds

<400> 14
gggacaagta tctctatggg gtccaaacta tatatggctc agggcaccag tgcatatcaa 60
actgcagtgg ggttctggct ggacatcgaa agaggatca tattggctat agtcctatca 120
gtttagtggc tgacactgc acgtactatt gcaactactg tttagctcat agttgaacag 180
tcagtgttag aggagtgcag aaactacaat ggaggagata gagattggtg gtcaaccacc 240
caggagcagc caactactgc accaagtgcg actccagcag gaaattatgg aggattacaa 300
acggctcgaa caagaaagtc tgaaagctgt ttgcatgtc aaatttctta tggatgatag 360
tatagccgca gtgatactgt actgggttgtt tttgattgtt tgggttatt gttctttgc 420
aaatcaggac caatttgcgca gcgagataat caagttgacc caacagccct ctgccattgc 480
aggtagatc tttcaagtgt ggactgctgc aaggtgaaca agattagcac taacagcagc 540
accacctctg agccccagaa gaccaacccg gcatggccta gccaaagacaa cacagactcc 600
gatccaaatc cccaaaggcat aaccaccgc acagccactc tgctctcaac aagtctggc 660
ctcatgctca catcgaagac tggcacacaaatcaggcc ccccccacgc cttggccggg 720
agcaacacca acggaaaaaac aaccacagac cgagaaccag gggccacaaa ccaaccaa 780
tcaaccacca atgggcaaca caataaaacac acccaacgaa tgacacccccc gccaagtcac 840
gacaacacaa gaaccatcct ccagcacaca acaccctggg aaaagacatt cagtacatac 900
aagccccacac actctccgac caacgaatca gatcaatccc tccccacac tcaaaacagc 960
atcaactgtg aacattttga cccccaaggc aaggaaaaaaa tctgtacag agtaggttct 1020
tacaactcca atattacaaa gcaatgcaga attgtatgtc ctttgttgc cacttataac 1080
acagtgtgca tgaaaacata ctataccgaa ccattcaact gttggaggcg tatctggcgt 1140
tgcttgcgtg atgacggagt tggctgggtt gagtggtgtt gcaactgtta act 1193

<210> 15
<211> 1260
<212> DNA
<213> rhinotracheitis virus

<220>
<221> CDS
<222> (16) ... (1260)
<223> Turkey rhinotracheitis virus (strain 6574)
attachment protein (G), complete cds

<400> 15
gggacaagta tccagatggg gtcagagctc tacatcatag agggggtagt gtcatctgaa 60
atagtcctca agcaagtctt cagaaggagc caaaaaatac ttttagact ggtgttatca 120
gccttaggtc tgacgctcac tagcactatt gttatctt tttgttattt tttttttttt 180
gtcaaattac gacagtgtgt ggacactttat tggcgaaaa atggatcctt acatccagga 240
cagtcacacca aaaatacttc aacaagaggt aagactacaa caaaagaccc tagaagat 300
caggcactg gaggcagggaa gtttgagac tttttttttt tttttttttt tttttttttt 360
atgcattatgc gcatgttgc tttttttttt tttttttttt tttttttttt tttttttttt 420
tgtgaatcgtt gaccaatttgc tcaggagat acttgggttgc aagacggaaa cttctgcgg 480
tgcactttttt cttccatgg ggtgagttgc tgcaaaaaac ccaaaagacca ggcaaccact 540

gcccagagga actccaaacc agctaacagc aaatcaactc ctccgggtaca ttcagacagg 600
 gccagcaaag aacataatcc ctcctaaggg gagcaacccc gcagggggcc aaccagcagc 660
 aagacaacta ttgcttagcac cccttcaaca gaggacactg ctaaaccAAC gattagcaaa 720
 cctaaactca ccatcaggcc ctcgcaaaga ggtccatccg gcagcacAAA agcagcctcc 780
 agcACCCCA gccacaAGAC caacACCAGA ggcACCCAGA agACGACCGA CCAGAGACCC 840
 cgCACCGGAC ccACTCCCAGA aaggCCCAAGA CAAACCCACA GCACAGCAAC TCCGCCCCC 900
 acaACCCAA tccacaAGGG CGGGCCCCA ACCCCCCAAC CAACAAcAGA CCTCAAGGTc 960
 aACCCAAAGGG aaggcAGCAC aAGCCAACT gcaatacAGA AAAACCCAAc cacacAAAGT 1020
 aATCTTGTG actgcACACT gtCTGATCCA gatgAGGCCAC AAAGGATTG ttaccAGGTA 1080
 ggaACTtaca atcctAGtca atcGGGAACC tgcaACATAG aggttCCAAA atgttCCACT 1140
 tatGGGcatG cttgtatGGC tacattatac gacACCCAT tcaactGCTG gCgCAGGACC 1200
 aggAGATGCA tctgtattc CGGAGGGGAG CTGATTGAGT ggtGCTGTAC tagtcaataa 1260

<210> 16
 <211> 391
 <212> PRT
 <213> Turkey rhinotracheitis virus

<400> 16
 Met Gly Ser Leu Tyr Met Ala Gln Gly Thr Ser Ala Tyr Gln Thr
 1 5 10 15
 Ala Val Gly Phe Trp Leu Asp Ile Gly Arg Arg Tyr Ile Leu Ala Ile
 20 25 30
 Val Leu Ser Ala Phe Gly Leu Thr Cys Thr Val Thr Ile Ala Leu Thr
 35 40 45
 Val Ser Val Ile Val Glu Gln Ser Val Leu Glu Glu Cys Arg Asn Tyr
 50 55 60
 Asn Gly Gly Asp Arg Asp Trp Trp Ser Thr Thr Gln Glu Gln Pro Thr
 65 70 75 80
 Thr Ala Pro Ser Ala Thr Pro Ala Gly Asn Tyr Gly Gly Leu Gln Thr
 85 90 95
 Ala Arg Thr Arg Lys Ser Glu Ser Cys Leu His Val Gln Ile Ser Tyr
 100 105 110
 Gly Asp Met Tyr Ser Arg Ser Asp Thr Val Leu Gly Gly Phe Asp Cys
 115 120 125
 Met Gly Leu Leu Val Leu Cys Lys Ser Gly Pro Ile Cys Gln Arg Asp
 130 135 140
 Asn Gln Val Asp Pro Thr Ala Leu Cys His Cys Arg Val Asp Leu Ser
 145 150 155 160
 Ser Val Asp Cys Cys Lys Val Asn Lys Ile Ser Thr Asn Ser Ser Thr
 165 170 175
 Thr Ser Glu Pro Gln Lys Thr Asn Pro Ala Trp Pro Ser Gln Asp Asn
 180 185 190
 Thr Asp Ser Asp Pro Asn Pro Gln Gly Ile Thr Thr Ser Thr Ala Thr
 195 200 205
 Leu Leu Ser Thr Ser Leu Gly Leu Met Leu Thr Ser Lys Thr Gly Thr
 210 215 220
 His Lys Ser Gly Pro Pro Gln Ala Leu Pro Gly Ser Asn Thr Asn Gly
 225 230 235 240
 Lys Thr Thr Thr Asp Arg Glu Pro Gly Pro Thr Asn Gln Pro Asn Ser
 245 250 255
 Thr Thr Asn Gly Gln His Asn Lys His Thr Gln Arg Met Thr Pro Pro
 260 265 270
 Pro Ser His Asp Asn Thr Arg Thr Ile Leu Gln His Thr Thr Pro Trp
 275 280 285
 Glu Lys Thr Phe Ser Thr Tyr Lys Pro Thr His Ser Pro Thr Asn Glu
 290 295 300
 Ser Asp Gln Ser Leu Pro Thr Thr Gln Asn Ser Ile Asn Cys Glu His
 305 310 315 320
 Phe Asp Pro Gln Gly Lys Glu Lys Ile Cys Tyr Arg Val Gly Ser Tyr
 325 330 335

Asn Ser Asn Ile Thr Lys Gln Cys Arg Ile Asp Val Pro Leu Cys Ser
 340 345 350
 Thr Tyr Ser Thr Val Cys Met Lys Thr Tyr Tyr Thr Glu Pro Phe Asn
 355 360 365
 Cys Trp Arg Arg Ile Trp Arg Cys Leu Cys Asp Asp Gly Val Gly Leu
 370 375 380
 Val Glu Trp Cys Cys Thr Ser
 385 390

<210> 17
 <211> 414
 <212> PRT
 <213> rhinotracheitis virus

<400> 17
 Met Gly Ser Glu Leu Tyr Ile Ile Glu Gly Val Ser Ser Ser Glu Ile
 1 5 10 15
 Val Leu Lys Gln Val Leu Arg Arg Ser Gln Lys Ile Leu Leu Gly Leu
 20 25 30
 Val Leu Ser Ala Leu Gly Leu Thr Leu Thr Ser Thr Ile Val Ile Ser
 35 40 45
 Ile Cys Ile Ser Val Glu Gln Val Lys Leu Arg Gln Cys Val Asp Thr
 50 55 60
 Tyr Trp Ala Glu Asn Gly Ser Leu His Pro Gly Gln Ser Thr Glu Asn
 65 70 75 80
 Thr Ser Thr Arg Gly Lys Thr Thr Thr Lys Asp Pro Arg Arg Leu Gln
 85 90 95
 Ala Thr Gly Ala Gly Lys Phe Glu Ser Cys Gly Tyr Val Gln Val Val
 100 105 110
 Asp Gly Asp Met His Asp Arg Ser Tyr Ala Val Leu Gly Gly Val Asp
 115 120 125
 Cys Leu Gly Leu Leu Ala Leu Cys Glu Ser Gly Pro Ile Cys Gln Gly
 130 135 140
 Asp Thr Trp Ser Glu Asp Gly Asn Phe Cys Arg Cys Thr Phe Ser Ser
 145 150 155 160
 His Gly Val Ser Cys Cys Lys Pro Lys Ser Lys Ala Thr Thr Ala
 165 170 175
 Gln Arg Asn Ser Lys Pro Ala Asn Ser Lys Ser Thr Pro Pro Val His
 180 185 190
 Ser Asp Arg Ala Ser Lys Glu His Asn Pro Ser Gln Gly Glu Gln Pro
 195 200 205
 Arg Arg Gly Pro Thr Ser Ser Lys Thr Thr Ile Ala Ser Thr Pro Ser
 210 215 220
 Thr Glu Asp Thr Ala Lys Pro Thr Ile Ser Lys Pro Lys Leu Thr Ile
 225 230 235 240
 Arg Pro Ser Gln Arg Gly Pro Ser Gly Ser Thr Lys Ala Ala Ser Ser
 245 250 255
 Thr Pro Ser His Lys Thr Asn Thr Arg Gly Thr Ser Lys Thr Thr Asp
 260 265 270
 Gln Arg Pro Arg Thr Gly Pro Thr Pro Glu Arg Pro Arg Gln Thr His
 275 280 285
 Ser Thr Ala Thr Pro Pro Pro Thr Thr Pro Ile His Lys Gly Arg Ala
 290 295 300
 Pro Thr Pro Lys Pro Thr Thr Asp Leu Lys Val Asn Pro Arg Glu Gly
 305 310 315 320
 Ser Thr Ser Pro Thr Ala Ile Gln Lys Asn Pro Thr Thr Gln Ser Asn
 325 330 335
 Leu Val Asp Cys Thr Leu Ser Asp Pro Asp Glu Pro Gln Arg Ile Cys
 340 345 350
 Tyr Gln Val Gly Thr Tyr Asn Pro Ser Gln Ser Gly Thr Cys Asn Ile
 355 360 365

Glu Val Pro Lys Cys Ser Thr Tyr Gly His Ala Cys Met Ala Thr Leu
 370 375 380
 Tyr Asp Thr Pro Phe Asn Cys Trp Arg Arg Thr Arg Arg Cys Ile Cys
 385 390 395 400
 Asp Ser Gly Gly Glu Leu Ile Glu Trp Cys Cys Thr Ser Gln
 405 410

<210> 18
<211> 539
<212> PRT
<213> human Metapneumo virus

<400> 18
Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
 1 5 10 15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
 20 25 30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35 40 45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ala Asp Gly Pro
 50 55 60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
 65 70 75 80
Leu Arg Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
 85 90 95
Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
 100 105 110
Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
 115 120 125
Arg Leu Glu Ser Glu Val Thr Ala Ile Lys Asn Ala Leu Lys Lys Thr
 130 135 140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
 145 150 155 160
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
 165 170 175
Ile Asn Lys Asn Lys Cys Asp Ile Ala Asp Leu Lys Met Ala Val Ser
 180 185 190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
 195 200 205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
 210 215 220
Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
 225 230 235 240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
 245 250 255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
 260 265 270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
 275 280 285
Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
 290 295 300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
 305 310 315 320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
 325 330 335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
 340 345 350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
 355 360 365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
 370 375 380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
 385 390 395 400
 Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
 405 410 415
 Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
 420 425 430
 Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Phe Asp Pro
 435 440 445
 Val Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
 450 455 460
 Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
 465 470 475 480
 Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
 485 490 495
 Leu Ile Ala Val Leu Gly Ser Thr Met Ile Leu Val Ser Val Phe Ile
 500 505 510
 Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
 515 520 525
 Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
 530 535

<210> 19
 <211> 539
 <212> PRT
 <213> human Metapneumo virus

<400> 19
 Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
 1 5 10 15
 His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
 20 25 30
 Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35 40 45
 Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
 50 55 60
 Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
 65 70 75 80
 Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
 85 90 95
 Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
 100 105 110
 Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
 115 120 125
 Arg Leu Glu Ser Glu Val Thr Ala Ile Lys Asn Ala Leu Lys Thr Thr
 130 135 140
 Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
 145 150 155 160
 Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
 165 170 175
 Ile Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
 180 185 190
 Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
 195 200 205
 Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
 210 215 220
 Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
 225 230 235 240
 Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
 245 250 255
 Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Thr Val Gln
 260 265 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
 275 280 285
 Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
 290 295 300
 Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
 305 310 315 320
 Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
 325 330 335
 Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
 340 345 350
 Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
 355 360 365
 Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
 370 375 380
 Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
 385 390 395 400
 Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
 405 410 415
 Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
 420 425 430
 Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Phe Asp Pro
 435 440 445
 Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
 450 455 460
 Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
 465 470 475 480
 Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
 485 490 495
 Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile
 500 505 510
 Ile Ile Lys Lys Thr Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
 515 520 525
 Gly Val Thr Asn Asn Gly Phe Ile Pro His Ser
 530 535

<210> 20
 <211> 539
 <212> PRT
 <213> human Metapneumo virus

<400> 20
 Met Ser Trp Lys Val Met Ile Ile Ser Leu Leu Ile Thr Pro Gln
 1 5 10 15
 His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
 20 25 30
 Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35 40 45
 Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Thr Asp Gly Pro
 50 55 60
 Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
 65 70 75 80
 Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
 85 90 95
 Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
 100 105 110
 Ala Thr Ala Ala Ala Val Thr Ala Gly Ile Ala Ile Ala Lys Thr Ile
 115 120 125
 Arg Leu Glu Ser Glu Val Asn Ala Ile Lys Gly Ala Leu Lys Gln Thr
 130 135 140
 Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
 145 150 155 160

Ala Val Arg Glu Leu Lys Glu Phe Val Ser Lys Asn Leu Thr Ser Ala
 165 170 175
 Ile Asn Arg Asn Lys Cys Asp Ile Ala Asp Leu Lys Met Ala Val Ser
 180 185 190
 Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
 195 200 205
 Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
 210 215 220
 Ala Glu Leu Ala Arg Ala Val Ser Tyr Met Pro Thr Ser Ala Gly Gln
 225 230 235 240
 Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
 245 250 255
 Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
 260 265 270
 Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala
 275 280 285
 Ala Pro Ser Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg
 290 295 300
 Glu Asp Gln Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr
 305 310 315 320
 Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
 325 330 335
 Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile
 340 345 350
 Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
 355 360 365
 Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
 370 375 380
 Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Trp Val Gly Ile Ile
 385 390 395 400
 Lys Gln Leu Pro Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
 405 410 415
 Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
 420 425 430
 Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Phe Asp Pro
 435 440 445
 Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
 450 455 460
 Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Lys Ile
 465 470 475 480
 Leu Asn Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Val Ile
 485 490 495
 Leu Val Ala Val Leu Gly Leu Thr Met Ile Ser Val Ser Ile Ile Ile
 500 505 510
 Ile Ile Lys Lys Thr Arg Lys Pro Thr Gly Ala Pro Pro Glu Leu Asn
 515 520 525
 Gly Val Thr Asn Gly Gly Phe Ile Pro His Ser
 530 535

<210> 21
 <211> 539
 <212> PRT
 <213> human Metapneumo virus

<400> 21
 Met Ser Trp Lys Val Met Ile Ile Ile Ser Leu Leu Ile Thr Pro Gln
 1 5 10 15
 His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
 20 25 30
 Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35 40 45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Thr Asp Gly Pro
 50 55 60
 Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
 65 70 75 80
 Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
 85 90 95
 Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
 100 105 110
 Ala Thr Ala Ala Ala Val Thr Ala Gly Ile Ala Ile Ala Lys Thr Ile
 115 120 125
 Arg Leu Glu Ser Glu Val Asn Ala Ile Lys Gly Ala Leu Lys Thr Thr
 130 135 140
 Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
 145 150 155 160
 Ala Val Arg Glu Leu Lys Glu Phe Val Ser Lys Asn Leu Thr Ser Ala
 165 170 175
 Ile Asn Lys Asn Lys Cys Asp Ile Ala Asp Leu Lys Met Ala Val Ser
 180 185 190
 Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
 195 200 205
 Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
 210 215 220
 Ala Glu Leu Ala Arg Ala Val Ser Tyr Met Pro Thr Ser Ala Gly Gln
 225 230 235 240
 Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
 245 250 255
 Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
 260 265 270
 Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala
 275 280 285
 Ala Pro Ser Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg
 290 295 300
 Glu Asp Gln Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr
 305 310 315 320
 Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
 325 330 335
 Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile
 340 345 350
 Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
 355 360 365
 Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
 370 375 380
 Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
 385 390 395 400
 Lys Gln Leu Pro Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
 405 410 415
 Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
 420 425 430
 Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Phe Asp Pro
 435 440 445
 Ile Arg Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
 450 455 460
 Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Lys Ile
 465 470 475 480
 Leu Asn Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
 485 490 495
 Leu Ile Ala Val Leu Gly Leu Thr Met Ile Ser Val Ser Ile Ile Ile
 500 505 510
 Ile Ile Lys Lys Thr Arg Lys Pro Thr Gly Ala Pro Pro Glu Leu Asn
 515 520 525
 Gly Val Thr Asn Gly Gly Phe Ile Pro His Ser
 530 535

<210> 22
<211> 1620
<212> DNA
<213> human Metapneumo virus

<400> 22
atgtcttggaa aagtgggtat catttttca ttgtaataaa cacctaaca cggcttaaaa 60
gagagctact tagaagagtc atgttagcact ataactgaag gatatctcg ttttctgagg 120
acaggttggt acaccaatgt ttttacactg gaggttaggcg atgttagagaa ctttacatgt 180
gccgatggac ccagcttaat aaaaacagaa ttagacctga cccaaagtgc actaagagag 240
ctcagaacag tttctgtcg tcaactggca agagaggagc aaattgaaaa tcccagacaa 300
tctagattcg ttcttaggagc aatagcactc ggtgttgcgaa ctgcagctgc agttacagca 360
ggtgttgcgaa ttgccaaaac catccggctt gaaagtgaag taacagcaat taagaatgcc 420
ctcaaaaaga ccaatgaagc agtatctaca ttggggatg gagttcgtgt gttggcaact 480
gcagtgagag agctgaaaga ttttgcgac aagaatctaa cacgtgcaat caacaaaaac 540
aagtgcgaca ttgctgaccc gaaaatggcc gttagctca gtcaattcaa cagaagggtc 600
ctaaatgttgc tgccggcaatt ttcagacaac gcttggataaa caccagcaat atctttggac 660
ttaatgacag atgctgaact agccagagct gtttccaaaca tgccaaacatc tgccaggacaa 720
ataaaaactga ttttggagaa ccgtgcaatg gtaagaagaa aagggttcgg aatcctgata 780
ggagtttacg gaagctcgatc aatttacatg gtgcactgc caatctttgg gtttatagac 840
acgccttgcg ggtatgtaaa agcagccccct ttttgcgatc gaaaaaagggg aaactatgt 900
tgccctttaa gagaagacca aggtggat ttttgcgatc cagggtcaac ttttactac 960
ccaaatgaaa aagactgtga aacaagagga gaccatgtct ttttgcgacac agcagcagga 1020
atcaatgttgc ctgagcgtc aaagggtgc aacataaaca tatctactac taattaccca 1080
tgcaaaagtttgc gcacaggaag acatcctatc agtatgggtt cactatctcc ttttgggct 1140
tttgggtcgtt gctacaaggg agtggatgtt ttttgcgatc gcaacagagt agggatcatc 1200
aagcaactga acaaaggctg ctcttatata accaaccaag acgcagacac agtgacaata 1260
gacaacactg tataccagct aagcaaaagtt gaaggcgaac agcatgttat aaaaggaaagg 1320
ccagtgtcaa gcagcttgc cccagtcaag ttttgcgatc atcaattcaa ttttgcgacac 1380
gaccaagtttgc tggatgttgc ttttgcgatc cagggtcaatc aaacagaatc 1440
ctaagcgttgc cagagaaagg aaacactggc ttttgcgatc taataattct aattgtgtc 1500
cttggctcta ccatgtatctt agtggatgtt ttttgcgatc taaagaaaac aaagaaaaccc 1560
acaggagcac ctccagagct gttgggtgc acaaacaatg gtttgcgatc acataattag 1620

<210> 23
<211> 1620
<212> DNA
<213> human Metapneumo virus

<400> 23
atgtcttggaa aagtgggtat catttttca ttgtaataaa cacctaaca cggcttaaaa 60
gagagctacc tagaagaatc atgttagcact ataactgagg gatatcttag ttttctgagg 120
acaggttggt ataccaacgt ttttacatta gaggtgggtg atgttagaaaa ctttacatgt 180
tctgatggac ctgcctaat aaaaacagaa ttagatctga cccaaagtgc actaagagag 240
ctcaaaaacag ttttgcgatc ccaattggca agagaggaaac aaattgagaa tcccagacaa 300
tcttaggtttgc ttcttaggagc aatagcactc ggtgttgcgaa cagcagctgc agtcacagca 360
ggtgttgcgaa ttgccaaaac catccggctt gaggtggatc tcacagcaat taagaatgcc 420
ctcaaaaacgaa ccaatgaagc agtatctaca ttggggatg gagttcgtgt gttggcaact 480
gcagtgagag agctaaaaga ttttgcgatc aagaatttacatc ttttgcgatc caacaaaaac 540
aagtgcgaca ttgatgttgc aaaaatggctt gtttgcgatc gtcaattcaa cagaagggtt 600
ctaaatgttgc tgccggcaatt ttcagacaat gtttgcgatc caccagcaat atctttggac 660
ttaatgacag atgctgaact agccagggcc gtttgcgatc tgccggacatc tgccaggacaa 720
ataaaaattgttgc ttttgcgatc gtttgcgatc gtttgcgatc gtttgcgatc aatcctgata 780
gggttctacg ggagctcgatc aatttacacg gtttgcgatc caatctttgg gtttatagac 840
acgccttgcg ggtatgtaaa agcagccccct ttttgcgatc gaaaaaagggg aaactatgt 900
tgccctttaa gagaagacca aggtggat ttttgcgatc ttttgcgatc cagggtcaac ttttactac 960
ccaaatgaga aagactgtga aacaagagga gaccatgtct ttttgcgatc agcagcagga 1020
atcaatgttgc ctgagcgtc aaagggtgc aacatcaaca ttttgcgatc aaattaccca 1080
tgcaaaagtttgc gcacaggaag acatcctatc agtatgggtt cactatctcc ttttgggct 1140
cttgggtcgtt gctacaaggg agtggatgtt ttttgcgatc gcaacagagt agggatcatc 1200

aagcagctga acaaaggttg ctccttatata accaacaag atgcagacac agtgacata 1260
 gacaacactg tatcatcgat aagcaaagg tgggtgaac agcatgttat aaaaggcaga 1320
 ccagtgtcaa gcagcttga tccaatcaag ttccctgaag atcaattcaa tggtgcatt 1380
 gaccaagttt ttgagaacat taaaacagc caggccttag tagatcaatc aaacagaatc 1440
 ctaagcagtg cagagaaagg gaatactggc ttatcattt taataattct aattgctgtc 1500
 ctgggctcta gcatgatct agtgagcat tcattataa tcaagaaaaac aaagaaacca 1560
 acgggagcac ctccagagct gagtgggtgc acaaacaatg gttcataacc acacagtag 1620

<210> 24

<211> 1620

<212> DNA

<213> human Metapneumo virus

<400> 24

atgtcttggaa aagtgtatcatcatttcg ttactcataa caccctcagca cgggctaaag 60
 gagagttatt tggagaatc atgttagtact ataactgagg gatacctcg tgggtttt 120
 acaggcgttgtt acactaatgt cttcacatta gaagttgggt atgttggaaa tcttacatgt 180
 actgtatggac ctatgtttaat caaaacagaa cttgtatctaa caaaaagtgc tttaagggaa 240
 ctcaaaacag tctctgtga tcagttggcg agagaggagc aaattgaaa tcccagacaa 300
 tcaagatttg tcttagtgc gatagcttc ggagttgcta cagcagcagc agtcacagca 360
 ggcattgcaa tagccaaac cataaggctt gagagtgggg tgaatgcaat taaagggtgt 420
 ctcaaaacaaa ctaatgaagc agtataccaca tttaggaaatg gtgtgcgggt cctagccact 480
 gcagtgagag agctaaaaga atttgtgago aaaaacctga ctatgtcaat caacaggaac 540
 aaatgtgaca ttgctgatct gaagatggct gtcagcttca gtcatttcaa cagaagattt 600
 ctaaatgttg tgcggcagtt ttccagacaat gcagggtt caccaggcaat atcattggac 660
 ctgtatgtc atgtctgatgtt ggcaggatgt gtatcatata tgccaacatc tgcaggcag 720
 ataaaactga ttgtggagaa cccgcgaatgt gtaaggagaa aaggatttgg aatcctgata 780
 ggggtctacg gaagctctgt gatttacatg gttcaatttc cgatctttgg tgcattatgt 840
 acaccttgggtt ggatcatcaa ggcagctccc tcttgcgtcg aaaaaaacgg gaattatgt 900
 tgcctcctaa gagaggatca aggggtggat tgcattttatg caggatctac tgcattttac 960
 ccaaatgaaa aagactgcga aacaagaggat gatcatgttt tttgtgacac agcagcagg 1020
 atcaatgttg ctgagcaatc aagagaatgc aacatcaaca tatctactac caactaccca 1080
 tgcattgtca gcacaggaaac acaccctata agcatgttg cactatcacc tctcggtgt 1140
 ttgggtggctt gctataaagg ggtaaatgtc tcgattggca gcaattgggt tggatcatc 1200
 aacaatttac ccaaaggctg ctcatacata accaaccagg atgcagacac tgtaacaatt 1260
 gacaataccg tgcattcaact aagcaaaggat gaaagggtgaac agcatgtat aaaagggaga 1320
 ccagtttcaa gcagtttga tccaatcaag ttccctgagg atcagttcaa tgcaggcgtt 1380
 gatcaatgtct tcgaaagcat tgaaacatgtt caggactatg tgcaggcgtt aaacaaaatt 1440
 ctaaacatgtt cagaaaaagg aacactggt ttccattatcg tagtaattt ggttgcgtt 1500
 ctgggcttaa ccatgatttca agtgagcatc atcatcataa tcaagaaaaac aaggaagccc 1560
 acaggagcac ctccagagct gaatgggtgc accaacggcg gttcataacc acatagttag 1620

<210> 25

<211> 1620

<212> DNA

<213> human Metapneumo virus

<400> 25

atgtcttggaa aagtgtatcatcatttcg ttactcataa cacctcagca cggactaaaa 60
 gaaaggttatt tagaagaatc atgttagtact ataactgaaatg gatatctcg tgggtttt 120
 acagggttgtt acaccaatgt cttcacatta gaagttgggt atgttggaaa tcttacatgt 180
 actgtatggac ctatgtttaat caaaacagaa cttgtacccaa caaaaagtgc tgcaggagaa 240
 ctcaaaacag tctctgtga tcagttggcg agagaagaac aaattgaaa tcccagacaa 300
 tcaagggtttt tccatgtgc aatagcttc ggagttgcca cagcagcagc agtcacagca 360
 ggcattgcaa tagccaaac cataagactt gagagtgggg tgaatgcaat caaagggtgt 420
 ctcaaaacaaa ccaacccggc agtataccaca ctatgttcaat ggtgcgtt cctagccact 480
 gcagtaagag agctgaaaga atttgtgac gaaaacctga ctatgtcaat caacagaaac 540
 aaatgtgaca ttgctgatct gaagatggct gtcagcttca gtcatttcaa cagaagattt 600
 ctaaatgttg tgcggcagtt ttccagacaat gcagggtt caccaggcaat atcattggac 660
 ctaatgtatgtc atgtctgatgtt ggcaggatgtt gtatcatata tgccaacatc tgcaggcgtt 720

ataaaaactaa tgtagagaaa ccgtgcaatg gtgaggagaa aaggatttgg aatcttgata 780
 ggggtctacg gaagctctgt gatttacatg gtccagctgc cgatcttgg tgcatacat 840
 acaccccttgg ggataatcaa ggcagctccc tcttggtag aaaaagatgg aaattatgtc 900
 tgcctcctaa gagaggatca aggggttat tgcaaaaatg caggatccac tgtttactac 960
 ccaaatgaaa aagactgcga aacaagaggt gatcatgtt ttttgacac agcagcaggg 1020
 atcaatgtt ctgagcaatc aagagaatgc aacatcaaca tatctaccac caactaccca 1080
 tgcaaaagtca gcacaggaag acaccctatc agcatgggtg cactatcacc tctcggtgct 1140
 ttggtagctt gctacaaggg ggttagctgc tcgattggca gtaatcggtt tggataatac 1200
 aaacaactac ctaaaggctg ctcatacata actaaccagg acgcagacac tgtaacaatt 1260
 gacaacactg tttatcaact aagcaagtt gagggtgaac agcatgtaat aaaagggaga 1320
 ccagtttcaa gcagtttga tccaaatcagg tttcctgagg atcagttcaa tggtgcgtt 1380
 gatcaagtct ttgaaaagcat tgaaaacagt caagcactag tggaccagtc aaacaaaatt 1440
 ctgaacagtg cagaaaaagg aaacactggt ttcattattt taataatttt gattgctgtt 1500
 cttgggttaa ccatgattt c agtggcattc atcatcataa tcaaaaaaac aaggaagcccc 1560
 acaggggcac ctccagagct gaatgggtt accaacggcg gttttatacc gcatagttag 1620

<210> 26

<211> 236

<212> PRT

<213> human Metapneumo virus

<400> 26

Met	Glu	Val	Lys	Val	Glu	Asn	Ile	Arg	Thr	Ile	Asp	Met	Leu	Lys	Ala
1							5			10				15	
Arg	Val	Lys	Asn	Arg	Val	Ala	Arg	Ser	Lys	Cys	Phe	Lys	Asn	Ala	Ser
							20			25				30	
Leu	Val	Leu	Ile	Gly	Ile	Thr	Thr	Leu	Ser	Ile	Ala	Leu	Asn	Ile	Tyr
							35			40				45	
Leu	Ile	Ile	Asn	Tyr	Lys	Met	Gln	Lys	Asn	Thr	Ser	Glu	Ser	Glu	His
							50			55				60	
His	Thr	Ser	Ser	Ser	Pro	Met	Glu	Ser	Ser	Arg	Glu	Thr	Pro	Thr	Val
							65			70				75	
Pro	Thr	Asp	Asn	Ser	Asp	Thr	Asn	Ser	Ser	Pro	Gln	His	Pro	Thr	Gln
							85			90				95	
Gln	Ser	Thr	Glu	Gly	Ser	Thr	Leu	Tyr	Phe	Ala	Ala	Ser	Ala	Ser	Ser
							100			105				110	
Pro	Glu	Thr	Glu	Pro	Thr	Ser	Thr	Pro	Asp	Thr	Thr	Asn	Arg	Pro	Pro
							115			120				125	
Phe	Val	Asp	Thr	His	Thr	Thr	Pro	Pro	Ser	Ala	Ser	Arg	Thr	Lys	Thr
							130			135				140	
Ser	Pro	Ala	Val	His	Thr	Lys	Asn	Asn	Pro	Arg	Thr	Ser	Ser	Arg	Thr
							145			150				155	
His	Ser	Pro	Pro	Arg	Ala	Thr	Thr	Arg	Thr	Ala	Arg	Arg	Thr	Thr	Thr
							165			170				175	
Leu	Arg	Thr	Ser	Ser	Thr	Arg	Lys	Arg	Pro	Ser	Thr	Ala	Ser	Val	Gln
							180			185				190	
Pro	Asp	Ile	Ser	Ala	Thr	Thr	His	Lys	Asn	Glu	Glu	Ala	Ser	Pro	Ala
							195			200				205	
Ser	Pro	Gln	Thr	Ser	Ala	Ser	Thr	Thr	Arg	Ile	Gln	Arg	Lys	Ser	Val
							210			215				220	
Glu	Ala	Asn	Thr	Ser	Thr	Thr	Tyr	Asn	Gln	Thr	Ser				
							225			230				235	

<210> 27

<211> 219

<212> PRT

<213> human Metapneumo virus

<400> 27

Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala

1	5	10	15
Arg Val Lys Asn Arg Val Ala Arg Ser	Lys Cys Phe Lys Asn Ala Ser		
20	25	30	
Leu Ile Leu Ile Gly Ile Thr Thr	Leu Ser Ile Ala Leu Asn Ile Tyr		
35	40	45	
Leu Ile Ile Asn Tyr Thr Ile Gln Lys	Thr Thr Ser Glu Ser Glu His		
50	55	60	
His Thr Ser Ser Pro Pro Thr Glu Pro	Asn Lys Glu Ala Ser Thr Ile		
65	70	75	80
Ser Thr Asp Asn Pro Asp Ile Asn Pro	Ser Ser Gln His Pro Thr Gln		
85	90	95	
Gln Ser Thr Glu Asn Pro Thr Leu Asn	Pro Ala Ala Ser Ala Ser Pro		
100	105	110	
Ser Glu Thr Glu Pro Ala Ser Thr Pro	Asp Thr Thr Asn Arg Leu Ser		
115	120	125	
Ser Val Asp Arg Ser Thr Ala Gln	Pro Ser Glu Ser Arg Thr Lys Thr		
130	135	140	
Lys Pro Thr Val His Thr Ile Asn Asn	Pro Asn Thr Ala Ser Ser Thr		
145	150	155	160
Gln Ser Pro Pro Arg Thr Thr Lys	Ala Ile Arg Arg Ala Thr Thr		
165	170	175	
Phe Arg Met Ser Ser Thr Gly Lys	Arg Pro Thr Thr Thr Leu Val Gln		
180	185	190	
Ser Asp Ser Ser Thr Thr Gln Asn His	Glu Glu Thr Gly Ser Ala		
195	200	205	
Asn Pro Gln Ala Ser Ala Ser Thr	Met Gln Asn		
210	215		

<210> 28
<211> 224
<212> PRT
<213> human Metapneumo virus

<400> 28			
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe	Lys Ala		
1	5	10	15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg	Asn Ala Thr		
20	25	30	
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile	Phe		
35	40	45	
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr	Glu Asn		
50	55	60	
Cys Ala Asn Met Pro Ser Ala Glu Pro Ser Lys	Lys Thr Pro Met Thr		
65	70	75	80
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln	Ala Thr Gln		
85	90	95	
Trp Thr Thr Glu Asn Ser Thr Ser Pro Val Ala Thr Pro	Glu Gly His		
100	105	110	
Pro Tyr Thr Gly Thr Thr Gln Thr Ser Asp Thr Thr Ala	Pro Gln Gln		
115	120	125	
Thr Thr Asp Lys His Thr Ala Pro Leu Lys Ser Thr Asn	Glu Gln Ile		
130	135	140	
Thr Gln Thr Thr Glu Lys Lys Thr Ile Arg Ala Thr Thr	Gln Lys		
145	150	155	160
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser	Thr Ala Ala		
165	170	175	
Thr Gln Thr Thr Asn Thr Asn Gln Ile Arg Asn Ala Ser	Glu Thr		
180	185	190	
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Thr Thr Gln	Ser Ser		
195	200	205	
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro Pro	His His Ala		

210

215

220

<210> 29
<211> 236
<212> PRT
<213> human Metapneumo virus

<400> 29

Met	Glu	Val	Arg	Val	Glu	Asn	Ile	Arg	Ala	Ile	Asp	Met	Phe	Lys	Ala	
1					5				10					15		
Lys	Met	Lys	Asn	Arg	Ile	Arg	Ser	Ser	Lys	Cys	Tyr	Arg	Asn	Ala	Thr	
					20			25						30		
Leu	Ile	Leu	Ile	Gly	Leu	Thr	Ala	Leu	Ser	Met	Ala	Leu	Asn	Ile	Phe	
					35			40					45			
Leu	Ile	Ile	Asp	Tyr	Ala	Met	Leu	Lys	Asn	Met	Thr	Lys	Val	Glu	His	
					50			55				60				
Cys	Val	Asn	Met	Pro	Pro	Val	Glu	Pro	Ser	Lys	Lys	Thr	Pro	Met	Thr	
					65		70			75				80		
Ser	Ala	Val	Asp	Leu	Asn	Thr	Lys	Pro	Asn	Pro	Gln	Gln	Ala	Thr	Gln	
					85			90				95				
Leu	Ala	Ala	Glu	Asp	Ser	Thr	Ser	Leu	Ala	Ala	Thr	Ser	Glu	Asp	His	
					100			105				110				
Leu	His	Thr	Gly	Thr	Thr	Pro	Thr	Pro	Asp	Ala	Thr	Val	Ser	Gln	Gln	
					115			120				125				
Thr	Thr	Asp	Glu	Tyr	Thr	Thr	Leu	Leu	Arg	Ser	Thr	Asn	Arg	Gln	Thr	
					130			135				140				
Thr	Gln	Thr	Thr	Thr	Glu	Lys	Lys	Pro	Thr	Gly	Ala	Thr	Thr	Lys	Lys	
					145		150			155				160		
Glu	Thr	Thr	Arg	Thr	Thr	Ser	Thr	Ala	Ala	Thr	Gln	Thr	Leu	Asn		
					165			170				175				
Thr	Thr	Asn	Gln	Thr	Ser	Tyr	Val	Arg	Glu	Ala	Thr	Thr	Ser	Ala		
					180			185				190				
Arg	Ser	Arg	Asn	Ser	Ala	Thr	Thr	Gln	Ser	Ser	Asp	Gln	Thr	Thr	Gln	
					195			200				205				
Ala	Ala	Asp	Pro	Ser	Ser	Gln	Pro	His	His	Thr	Gln	Lys	Ser	Thr	Thr	
					210			215				220				
Thr	Thr	Tyr	Asn	Thr	Asp	Thr	Ser	Ser	Pro	Ser	Ser					
					225			230				235				

<210> 30
<211> 708
<212> DNA
<213> human Metapneumo virus

<400> 30

gagggtgaaag	tggagaacat	tcgaacaata	gatatgctca	aagcaagagt	aaaaaaatcg	60
gtggcacgca	gcaaattgttt	taaaaatgcc	tctttggtcc	tcataggaat	aactacattg	120
agtattgccc	tcaatatatcta	tctgtatcata	aactataaaa	tgcaaaaaaaaa	cacatctgaa	180
tcagaacatc	acaccagctc	atcacccatg	gaatccagca	gagaaactcc	aacggtcccc	240
acagacaact	cagacaccaa	ctcaagccca	cagcatccaa	ctcaacagtc	cacagaaggc	300
tccacactct	actttgcagc	ctcagcaagc	tcaccagaga	cagaaccaac	atcaacacca	360
gatacaacaa	accggccgccc	cttcgtcgac	acacacacaa	caccaccaag	cgcaaggcaga	420
acaaagacaa	gtccggcagt	ccacacaaaa	aacaacccaa	ggacaagctc	tagaacacat	480
tctccaccac	ggcaacgcac	aaggacggca	cgcagaacca	ccactctccg	cacaaggcagc	540
acaagaaga	gaccgtccac	agcatcagtc	caacctgaca	tcagcgaac	aacccacaaa	600
aacaagaag	caagtccagc	gagcccacaa	acatctgcaa	gcacaacaag	aatacaaagg	660
aaaagcgtgg	aggccaacac	atcaacaaca	tacaacccaaa	ctagttaa		708

<210> 31
<211> 660

<212> DNA
<213> human Metapneumo virus

<400> 31

atggagggtga aagttagagaa cattcgagca atagacatgc tcaaagcaag agtaaaaaat 60
cgtgtggcac gtagcaatg cttaaaaat gcttcttta tcctcatagg aataactaca 120
ctgagttatag ctctcaatat ctatctgatc ataaaactaca caatacaaaaa aaccacatcc 180
gaatcagaac accacaccag ctcaccaccc acagaaccca acaaggaagc ttcaacaatc 240
tccacagaca acccagacat caatccaagc tcacagcatc caactcaaca gtccacagaa 300
aaccccacac tcaacccgc agcatcagcg agccccatcag aaacagaacc agcatcaaca 360
ccagacacaa caaaccgcct gtccctcgta gacaggtcca cagcacaacc aagtgaaagc 420
agaacaaaga caaaaaccgac agtccacaca atcaacaacc caaacacagc ttccagttaca 480
caatccccac cacggacaac aacgaaggca atccgcagag ccaccactt ccgcatgagc 540
agcacaggaa aaagaccaac cacaacatta gtccagtccg acagcagcac cacaacccaa 600
aatcatgaag aaacaggttc agcgaaccca caggcgtctg caagcacaat gcaaaaactag 660

<210> 32

<211> 675

<212> DNA

<213> human Metapneumo virus

<400> 32

atggaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaac 60
cgtataagaa gcagcagggtg ctatagaaat gctacactga tccttattgg actaacagcg 120
ttaagcatgg cacttaatat ttcttgcgtc atcgatcatg caacattaag aaacatgatc 180
aaaacagaaa actgtgttaa catgccgtcg gcagaaccaa gcaaaaagac cccaatgacc 240
tcacacagcag gccaaacac caaacccaaat ccacagcaag caacacagtg gaccacagag 300
aactcaacat ccccagttagc aaccccagag ggccatccat acacagggac aactcaaaca 360
tcagacacaa cagctccccca gcaaaccaca gacaaacaca cagcaccgct aaaatcaacc 420
aatgaacaga tcacccagac aaccacagag aaaaagacaa tcagagcaac aacccaaaaa 480
aggaaaaaag gaaaagaaaa cacaacccaa accacaagca cagctgcaac ccaaacaacc 540
aacacccacca accaaatcag aaatgcagt gagacaatca caacatccga cagaccaga 600
actgacacca caacccaaag cagcgaacag acaacccggg caacagaccc aagctcccc 660
ccacaccatg catag 675

<210> 33

<211> 711

<212> DNA

<213> human Metapneumo virus

<400> 33

atggaagtaa gagtggagaa cattcgccc atagacatgt tcaaagcaaa aatgaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttattgg attaacagca 120
ttaagttatgg cacttaatat ttttttaatc attgattatg caatgttaaa aaacatgacc 180
aaagtggAAC actgtgttaa tatgccgcgg gtagaaccaa gcaagaagac cccaatgacc 240
tctgcagtag acttaaacac caaacccaaat ccacagcagg caacacagtg ggccgcagag 300
gattcaacat ctcttagcagc aacctcagag gaccatctac acacagggac aactccaaaca 360
ccagatgcaa cagtctctca gcaaaccaca gacgagtaca caacattgtc gagatcaacc 420
aacagacaga ccacccaaac aaccacagag aaaaagccaa cggagcaac aaccaaaaaa 480
gaaaccacaa ctcgaactac aagcacaagct gcaacccaaa cactcaacac taccaaccaa 540
actagctatg tgagagaggc aaccacaaca tccgcagat ccagaaacag tgccacaact 600
caaagcagcg accaaacaaac ccaggcagca gacccaaagct cccaaaccaca ccatacacag 660
aaaagcacaa caacaacata caacacagac acatcctctc caagtagtt a 711

<210> 34

<211> 2005

<212> PRT

<213> human Metapneumo virus

<400> 34

Met Asp Pro Leu Asn Glu Ser Thr Val Asn Val Tyr Leu Pro Asp Ser

1	5	10	15												
Tyr	Leu	Lys	Gly	Val	Ile	Ser	Phe	Ser	Glu	Thr	Asn	Ala	Ile	Gly	Ser
20	25	30													
Cys	Leu	Leu	Lys	Arg	Pro	Tyr	Leu	Lys	Asn	Asp	Asn	Thr	Ala	Lys	Val
35	40	45													
Ala	Ile	Glu	Asn	Pro	Val	Ile	Glu	His	Val	Arg	Leu	Lys	Asn	Ala	Val
50	55	60													
Asn	Ser	Lys	Met	Lys	Ile	Ser	Asp	Tyr	Lys	Ile	Val	Glu	Pro	Val	Asn
65	70	75	80												
Met	Gln	His	Glu	Ile	Met	Lys	Asn	Val	His	Ser	Cys	Glu	Leu	Thr	Leu
85	90	95													
Leu	Lys	Gln	Phe	Leu	Thr	Arg	Ser	Lys	Asn	Ile	Ser	Thr	Leu	Lys	Leu
100	105	110													
Asn	Met	Ile	Cys	Asp	Trp	Leu	Gln	Leu	Lys	Ser	Thr	Ser	Asp	Asp	Thr
115	120	125													
Ser	Ile	Leu	Ser	Phe	Ile	Asp	Val	Glu	Phe	Ile	Pro	Ser	Trp	Val	Ser
130	135	140													
Asn	Trp	Phe	Ser	Asn	Trp	Tyr	Asn	Leu	Asn	Lys	Ile	Leu	Glu	Phe	
145	150	155	160												
Arg	Lys	Glu	Glu	Val	Ile	Arg	Thr	Gly	Ser	Ile	Leu	Cys	Arg	Ser	Leu
165	170	175													
Gly	Lys	Leu	Val	Phe	Val	Val	Ser	Ser	Tyr	Gly	Cys	Ile	Val	Lys	Ser
180	185	190													
Asn	Lys	Ser	Lys	Arg	Val	Ser	Phe	Phe	Thr	Tyr	Asn	Gln	Leu	Leu	Thr
195	200	205													
Trp	Lys	Asp	Val	Met	Leu	Ser	Arg	Phe	Asn	Ala	Asn	Phe	Cys	Ile	Trp
210	215	220													
Val	Ser	Asn	Ser	Leu	Asn	Glu	Asn	Gln	Glu	Gly	Leu	Gly	Leu	Arg	Ser
225	230	235	240												
Asn	Leu	Gln	Gly	Ile	Leu	Thr	Asn	Lys	Leu	Tyr	Glu	Thr	Val	Asp	Tyr
245	250	255													
Met	Leu	Ser	Leu	Cys	Cys	Asn	Glu	Gly	Phe	Ser	Leu	Val	Lys	Glu	Phe
260	265	270													
Glu	Gly	Phe	Ile	Met	Ser	Glu	Ile	Leu	Arg	Ile	Thr	Glu	His	Ala	Gln
275	280	285													
Phe	Ser	Thr	Arg	Phe	Arg	Asn	Thr	Leu	Leu	Asn	Gly	Leu	Thr	Asp	Gln
290	295	300													
Leu	Thr	Lys	Leu	Lys	Asn	Asn	Arg	Leu	Arg	Val	His	Gly	Thr	Val	
305	310	315	320												
Leu	Glu	Asn	Asn	Asp	Tyr	Pro	Met	Tyr	Glu	Val	Val	Leu	Lys	Leu	
325	330	335													
Gly	Asp	Thr	Leu	Arg	Cys	Ile	Lys	Leu	Leu	Ile	Asn	Lys	Asn	Leu	Glu
340	345	350													
Asn	Ala	Ala	Glu	Leu	Tyr	Tyr	Ile	Phe	Arg	Ile	Phe	Gly	His	Pro	Met
355	360	365													
Val	Asp	Glu	Arg	Asp	Ala	Met	Asp	Ala	Val	Lys	Leu	Asn	Asn	Glu	Ile
370	375	380													
Thr	Lys	Ile	Leu	Arg	Trp	Glu	Ser	Leu	Thr	Glu	Leu	Arg	Gly	Ala	Phe
385	390	395	400												
Ile	Leu	Arg	Ile	Ile	Lys	Gly	Phe	Val	Asp	Asn	Asn	Lys	Arg	Trp	Pro
405	410	415													
Lys	Ile	Lys	Asn	Leu	Lys	Val	Leu	Ser	Lys	Arg	Trp	Thr	Met	Tyr	Phe
420	425	430													
Lys	Ala	Lys	Ser	Tyr	Pro	Ser	Gln	Leu	Glu	Leu	Ser	Glu	Gln	Asp	Phe
435	440	445													
Leu	Glu	Leu	Ala	Ala	Ile	Gln	Phe	Glu	Gln	Glu	Phe	Ser	Val	Pro	Glu
450	455	460													
Lys	Thr	Asn	Leu	Glu	Met	Val	Leu	Asn	Asp	Lys	Ala	Ile	Ser	Pro	Pro
465	470	475	480												
Lys	Arg	Leu	Ile	Trp	Ser	Val	Tyr	Pro	Lys	Asn	Tyr	Leu	Pro	Glu	Lys
485	490	495													
Ile	Lys	Asn	Arg	Tyr	Leu	Glu	Glu	Thr	Phe	Asn	Ala	Ser	Asp	Ser	Leu

500	505	510
Lys Thr Arg Arg Val Leu Glu Tyr	Tyr Leu Lys Asp Asn Lys Phe Asp	
515	520	525
Gln Lys Glu Leu Lys Ser Tyr Val Val Lys Gln Glu Tyr Leu Asn Asp		
530	535	540
Lys Asp His Ile Val Ser Leu Thr Gly Lys Glu Arg Glu Leu Ser Val		
545	550	555
Gly Arg Met Phe Ala Met Gln Pro Gly Lys Gln Arg Gln Ile Gln Ile		560
565	570	575
Leu Ala Glu Lys Leu Leu Ala Asp Asn Ile Val Pro Phe Phe Pro Glu		
580	585	590
Thr Leu Thr Lys Tyr Gly Asp Leu Asp Leu Gln Arg Ile Met Glu Ile		
595	600	605
Lys Ser Glu Leu Ser Ser Ile Lys Thr Arg Arg Asn Asp Ser Tyr Asn		
610	615	620
Asn Tyr Ile Ala Arg Ala Ser Ile Val Thr Asp Leu Ser Lys Phe Asn		
625	630	635
Gln Ala Phe Arg Tyr Glu Thr Thr Ala Ile Cys Ala Asp Val Ala Asp		640
645	650	655
Glu Leu His Gly Thr Gln Ser Leu Phe Cys Trp Leu His Leu Ile Val		
660	665	670
Pro Met Thr Thr Met Ile Cys Ala Tyr Arg His Ala Pro Pro Glu Thr		
675	680	685
Lys Gly Glu Tyr Asp Ile Asp Lys Ile Glu Glu Gln Ser Gly Leu Tyr		
690	695	700
Arg Tyr His Met Gly Gly Ile Glu Gly Trp Cys Gln Lys Leu Trp Thr		
705	710	715
Met Glu Ala Ile Ser Leu Leu Asp Val Val Ser Val Lys Thr Arg Cys		
725	730	735
Gln Met Thr Ser Leu Leu Asn Gly Asp Asn Gln Ser Ile Asp Val Ser		
740	745	750
Lys Pro Val Lys Leu Ser Glu Gly Leu Asp Glu Val Lys Ala Asp Tyr		
755	760	765
Ser Leu Ala Val Lys Met Leu Lys Glu Ile Arg Asp Ala Tyr Arg Asn		
770	775	780
Ile Gly His Lys Leu Lys Glu Gly Glu Thr Tyr Ile Ser Arg Asp Leu		
785	790	795
Gln Phe Ile Ser Lys Val Ile Gln Ser Glu Gly Val Met His Pro Thr		
805	810	815
Pro Ile Lys Lys Ile Leu Arg Val Gly Pro Trp Ile Asn Thr Ile Leu		
820	825	830
Asp Asp Ile Lys Thr Ser Ala Glu Ser Ile Gly Ser Leu Cys Gln Glu		
835	840	845
Leu Glu Phe Arg Gly Glu Ser Ile Ile Val Ser Leu Ile Leu Arg Asn		
850	855	860
Phe Trp Leu Tyr Asn Leu Tyr Met His Glu Ser Lys Gln His Pro Leu		
865	870	875
Ala Gly Lys Gln Leu Phe Lys Gln Leu Asn Lys Thr Leu Thr Ser Val		
885	890	895
Gln Arg Phe Phe Glu Ile Lys Lys Glu Asn Glu Val Val Asp Leu Trp		
900	905	910
Met Asn Ile Pro Met Gln Phe Gly Gly Asp Pro Val Val Phe Tyr		
915	920	925
Arg Ser Phe Tyr Arg Arg Thr Pro Asp Phe Leu Thr Glu Ala Ile Ser		
930	935	940
His Val Asp Ile Leu Leu Arg Ile Ser Ala Asn Ile Arg Asn Glu Ala		
945	950	955
Lys Ile Ser Phe Phe Lys Ala Leu Leu Ser Ile Glu Lys Asn Glu Arg		
965	970	975
Ala Thr Leu Thr Thr Leu Met Arg Asp Pro Gln Ala Val Gly Ser Glu		
980	985	990
Arg Gln Ala Lys Val Thr Ser Asp Ile Asn Arg Thr Ala Val Thr Ser		

995	1000	1005
Ile Leu Ser Leu Ser Pro Asn Gln Leu Phe Ser Asp Ser Ala Ile His		
1010	1015	1020
Tyr Ser Arg Asn Glu Glu Val Gly Ile Ile Ala Asp Asn Ile Thr		
1025	1030	1035
Pro Val Tyr Pro His Gly Léu Arg Val Leu Tyr Glu Ser Leu Pro Phe		1040
1045	1050	1055
His Lys Ala Glu Lys Val Val Asn Met Ile Ser Gly Thr Lys Ser Ile		
1060	1065	1070
Thr Asn Leu Leu Gln Arg Thr Ser Ala Ile Asn Gly Glu Asp Ile Asp		
1075	1080	1085
Arg Ala Val Ser Met Met Leu Glu Asn Leu Gly Leu Leu Ser Arg Ile		
1090	1095	1100
Leu Ser Val Val Val Asp Ser Ile Glu Ile Pro Thr Lys Ser Asn Gly		
1105	1110	1115
Arg Leu Ile Cys Cys Gln Ile Ser Arg Thr Leu Arg Glu Thr Ser Trp		1120
1125	1130	1135
Asn Asn Met Glu Ile Val Gly Val Thr Ser Pro Ser Ile Thr Thr Cys		
1140	1145	1150
Met Asp Val Ile Tyr Ala Thr Ser Ser His Leu Lys Gly Ile Ile Ile		
1155	1160	1165
Glu Lys Phe Ser Thr Asp Arg Thr Thr Arg Gly Gln Arg Gly Pro Lys		
1170	1175	1180
Ser Pro Trp Val Gly Ser Ser Thr Gln Glu Lys Lys Leu Val Pro Val		
1185	1190	1195
Tyr Asn Arg Gln Ile Leu Ser Lys Gln Gln Arg Glu Gln Leu Glu Ala		1200
1205	1210	1215
Ile Gly Lys Met Arg Trp Val Tyr Lys Gly Thr Pro Gly Leu Arg Arg		
1220	1225	1230
Leu Leu Asn Lys Ile Cys Leu Gly Ser Leu Gly Ile Ser Tyr Lys Cys		
1235	1240	1245
Val Lys Pro Leu Leu Pro Arg Phe Met Ser Val Asn Phe Leu His Arg		
1250	1255	1260
Leu Ser Val Ser Ser Arg Pro Met Glu Phe Pro Ala Ser Val Pro Ala		
1265	1270	1275
Tyr Arg Thr Thr Asn Tyr His Phe Asp Thr Ser Pro Ile Asn Gln Ala		1280
1285	1290	1295
Leu Ser Glu Arg Phe Gly Asn Glu Asp Ile Asn Leu Val Phe Gln Asn		
1300	1305	1310
Ala Ile Ser Cys Gly Ile Ser Ile Met Ser Val Val Glu Gln Leu Thr		
1315	1320	1325
Gly Arg Ser Pro Lys Gln Leu Val Leu Ile Pro Gln Leu Glu Ile		
1330	1335	1340
Asp Ile Met Pro Pro Val Phe Gln Gly Lys Phe Asn Tyr Lys Leu		
1345	1350	1355
Val Asp Lys Ile Thr Ser Asp Gln His Ile Phe Ser Pro Asp Lys Ile		1360
1365	1370	1375
Asp Met Leu Thr Leu Gly Lys Met Leu Met Pro Thr Ile Lys Gly Gln		
1380	1385	1390
Lys Thr Asp Gln Phe Leu Asn Lys Arg Glu Asn Tyr Phe His Gly Asn		
1395	1400	1405
Asn Leu Ile Glu Ser Leu Ser Ala Ala Leu Ala Cys His Trp Cys Gly		
1410	1415	1420
Ile Leu Thr Glu Gln Cys Ile Glu Asn Asn Ile Phe Lys Lys Asp Trp		
1425	1430	1435
Gly Asp Gly Phe Ile Ser Asp His Ala Phe Met Asp Phe Lys Ile Phe		1440
1445	1450	1455
Leu Cys Val Phe Lys Thr Lys Leu Leu Cys Ser Trp Gly Ser Gln Gly		
1460	1465	1470
Lys Asn Ile Lys Asp Glu Asp Ile Val Asp Glu Ser Ile Asp Lys Leu		
1475	1480	1485
Leu Arg Ile Asp Asn Thr Phe Trp Arg Met Phe Ser Lys Val Met Phe		

1490	1495	1500
Glu Ser Lys Val Lys Lys Arg Ile Met Leu Tyr Asp Val Lys Phe Leu		
1505	1510	1515
Ser Leu Val Gly Tyr Ile Gly Phe Lys Asn Trp Phe Ile Glu Gln Leu		1520
1525	1530	1535
Arg Ser Ala Glu Leu His Glu Val Pro Trp Ile Val Asn Ala Glu Gly		
1540	1545	1550
Asp Leu Val Glu Ile Lys Ser Ile Lys Ile Tyr Leu Gln Leu Ile Glu		
1555	1560	1565
Gln Ser Leu Phe Leu Arg Ile Thr Val Leu Asn Tyr Thr Asp Met Ala		
1570	1575	1580
His Ala Leu Thr Arg Leu Ile Arg Lys Lys Leu Met Cys Asp Asn Ala		
1585	1590	1595
Leu Leu Thr Pro Ile Pro Ser Pro Met Val Asn Leu Thr Gln Val Ile		1600
1605	1610	1615
Asp Pro Thr Glu Gln Leu Ala Tyr Phe Pro Lys Ile Thr Phe Glu Arg		
1620	1625	1630
Leu Lys Asn Tyr Asp Thr Ser Ser Asn Tyr Ala Lys Gly Lys Leu Thr		
1635	1640	1645
Arg Asn Tyr Met Ile Leu Leu Pro Trp Gln His Val Asn Arg Tyr Asn		
1650	1655	1660
Phe Val Phe Ser Ser Thr Gly Cys Lys Val Ser Leu Lys Thr Cys Ile		
1665	1670	1675
Gly Lys Leu Met Lys Asp Leu Asn Pro Lys Val Leu Tyr Phe Ile Gly		1680
1685	1690	1695
Glu Gly Ala Gly Asn Trp Met Ala Arg Thr Ala Cys Glu Tyr Pro Asp		
1700	1705	1710
Ile Lys Phe Val Tyr Arg Ser Leu Lys Asp Asp Leu Asp His His Tyr		
1715	1720	1725
Pro Leu Glu Tyr Gln Arg Val Ile Gly Glu Leu Ser Arg Ile Ile Asp		
1730	1735	1740
Ser Gly Glu Gly Leu Ser Met Glu Thr Thr Asp Ala Thr Gln Lys Thr		
1745	1750	1755
His Trp Asp Leu Ile His Arg Val Ser Lys Asp Ala Leu Leu Ile Thr		1760
1765	1770	1775
Leu Cys Asp Ala Glu Phe Lys Asp Arg Asp Asp Phe Phe Lys Met Val		
1780	1785	1790
Ile Leu Trp Arg Lys His Val Leu Ser Cys Arg Ile Cys Thr Thr Tyr		
1795	1800	1805
Gly Thr Asp Leu Tyr Leu Phe Ala Lys Tyr His Ala Lys Asp Cys Asn		
1810	1815	1820
Val Lys Leu Pro Phe Phe Val Arg Ser Val Ala Thr Phe Ile Met Gln		
1825	1830	1835
Gly Ser Lys Leu Ser Gly Ser Glu Cys Tyr Ile Leu Leu Thr Leu Gly		1840
1845	1850	1855
His His Asn Asn Leu Pro Cys His Gly Glu Ile Gln Asn Ser Lys Met		
1860	1865	1870
Lys Ile Ala Val Cys Asn Asp Phe Tyr Ala Ala Lys Lys Leu Asp Asn		
1875	1880	1885
Lys Ser Ile Glu Ala Asn Cys Lys Ser Leu Leu Ser Gly Leu Arg Ile		
1890	1895	1900
Pro Ile Asn Lys Lys Glu Leu Asn Arg Gln Arg Arg Leu Leu Thr Leu		
1905	1910	1915
Gln Ser Asn His Ser Ser Val Ala Thr Val Gly Gly Ser Lys Val Ile		1920
1925	1930	1935
Glu Ser Lys Trp Leu Thr Asn Lys Ala Asn Thr Ile Ile Asp Trp Leu		
1940	1945	1950
Glu His Ile Leu Asn Ser Pro Lys Gly Glu Leu Asn Tyr Asp Phe Phe		
1955	1960	1965
Glu Ala Leu Glu Asn Thr Tyr Pro Asn Met Ile Lys Leu Ile Asp Asn		
1970	1975	1980
Leu Gly Asn Ala Glu Ile Lys Lys Leu Ile Lys Val Thr Gly Tyr Met		

1985	1990	1995	2000
Leu Val Ser Lys Lys			
2005			

<210> 35
<211> 2005
<212> PRT
<213> human Metapneumo virus

<400> 35
Met Asp Pro Leu Asn Glu Ser Thr Val Asn Val Tyr Leu Pro Asp Ser
1 5 10 15
Tyr Leu Lys Gly Val Ile Ser Phe Ser Glu Thr Asn Ala Ile Gly Ser
20 25 30
Cys Leu Leu Lys Arg Pro Tyr Leu Lys Asn Asp Asn Thr Ala Lys Val
35 40 45
Ala Ile Glu Asn Pro Val Ile Glu His Val Arg Leu Lys Asn Ala Val
50 55 60
Asn Ser Lys Met Lys Ile Ser Asp Tyr Lys Val Val Glu Pro Val Asn
65 70 75 80
Met Gln His Glu Ile Met Lys Asn Val His Ser Cys Glu Leu Thr Leu
85 90 95
Leu Lys Gln Phe Leu Thr Arg Ser Lys Asn Ile Ser Thr Leu Lys Leu
100 105 110
Asn Met Ile Cys Asp Trp Leu Gln Leu Lys Ser Thr Ser Asp Asp Thr
115 120 125
Ser Ile Leu Ser Phe Ile Asp Val Glu Phe Ile Pro Ser Trp Val Ser
130 135 140
Asn Trp Phe Ser Asn Trp Tyr Asn Leu Asn Lys Leu Ile Leu Glu Phe
145 150 155 160
Arg Arg Glu Glu Val Ile Arg Thr Gly Ser Ile Leu Cys Arg Ser Leu
165 170 175
Gly Lys Leu Val Phe Ile Val Ser Ser Tyr Gly Cys Ile Val Lys Ser
180 185 190
Asn Lys Ser Lys Arg Val Ser Phe Phe Thr Tyr Asn Gln Leu Leu Thr
195 200 205
Trp Ilys Asp Val Met Leu Ser Arg Phe Asn Ala Asn Phe Cys Ile Trp
210 215 220
Val Ser Asn Ser Leu Asn Glu Asn Gln Glu Gly Leu Gly Leu Arg Ser
225 230 235 240
Asn Leu Gln Gly Met Leu Thr Asn Lys Leu Tyr Glu Thr Val Asp Tyr
245 250 255
Met Leu Ser Leu Cys Cys Asn Glu Gly Phe Ser Leu Val Lys Glu Phe
260 265 270
Glu Gly Phe Ile Met Ser Glu Ile Leu Arg Ile Thr Glu His Ala Gln
275 280 285
Phe Ser Thr Arg Phe Arg Asn Thr Leu Leu Asn Gly Leu Thr Asp Gln
290 295 300
Leu Thr Lys Leu Lys Asn Lys Asn Arg Leu Arg Val His Gly Thr Val
305 310 315 320
Leu Glu Asn Asn Asp Tyr Pro Met Tyr Glu Val Val Leu Lys Leu Leu
325 330 335
Gly Asp Thr Leu Arg Cys Ile Lys Leu Leu Ile Asn Lys Asn Leu Glu
340 345 350
Asn Ala Ala Glu Leu Tyr Tyr Ile Phe Arg Ile Phe Gly His Pro Met
355 360 365
Val Asp Glu Arg Asp Ala Met Asp Ala Val Lys Leu Asn Asn Glu Ile
370 375 380
Thr Lys Ile Leu Arg Leu Glu Ser Leu Thr Glu Leu Arg Gly Ala Phe
385 390 395 400
Ile Leu Arg Ile Ile Lys Gly Phe Val Asp Asn Asn Lys Arg Trp Pro

	405	410	415
Lys Ile Lys Asn Leu Ile Val Leu Ser	Lys Arg Trp Thr Met	Tyr Phe	
420	425	430	
Lys Ala Lys Asn Tyr Pro Ser Gln Leu Glu Leu Ser Glu Gln Asp Phe			
435	440	445	
Leu Glu Leu Ala Ala Ile Gln Phe Glu Gln Glu Phe Ser Val Pro Glu			
450	455	460	
Lys Thr Asn Leu Glu Met Val Leu Asn Asp Lys Ala Ile Ser Pro Pro			
465	470	475	480
Lys Arg Leu Ile Trp Ser Val Tyr Pro Lys Asn Tyr Leu Pro Glu Thr			
485	490	495	
Ile Lys Asn Arg Tyr Leu Glu Glu Thr Phe Asn Ala Ser Asp Ser Leu			
500	505	510	
Lys Thr Arg Arg Val Leu Glu Tyr Tyr Leu Lys Asp Asn Lys Phe Asp			
515	520	525	
Gln Lys Glu Leu Lys Ser Tyr Val Val Arg Gln Glu Tyr Leu Asn Asp			
530	535	540	
Lys Glu His Ile Val Ser Leu Thr Gly Lys Glu Arg Glu Leu Ser Val			
545	550	555	560
Gly Arg Met Phe Ala Met Gln Pro Gly Lys Gln Arg Gln Ile Gln Ile			
565	570	575	
Leu Ala Glu Lys Leu Ala Asp Asn Ile Val Pro Phe Pro Glu			
580	585	590	
Thr Leu Thr Lys Tyr Gly Asp Leu Asp Leu Gln Arg Ile Met Glu Ile			
595	600	605	
Lys Ser Glu Leu Ser Ser Ile Lys Thr Arg Arg Asn Asp Ser Tyr Asn			
610	615	620	
Asn Tyr Ile Ala Arg Ala Ser Ile Val Thr Asp Leu Ser Lys Phe Asn			
625	630	635	640
Gln Ala Phe Arg Tyr Glu Thr Thr Ala Ile Cys Ala Asp Val Ala Asp			
645	650	655	
Glu Leu His Gly Thr Gln Ser Leu Phe Cys Trp Leu His Leu Ile Val			
660	665	670	
Pro Met Thr Thr Met Ile Cys Ala Tyr Arg His Ala Pro Pro Glu Thr			
675	680	685	
Lys Gly Glu Tyr Asp Ile Asp Lys Ile Glu Glu Gln Ser Gly Leu Tyr			
690	695	700	
Arg Tyr His Met Gly Gly Ile Glu Gly Trp Cys Gln Lys Leu Trp Thr			
705	710	715	720
Met Glu Ala Ile Ser Leu Leu Asp Val Val Ser Val Lys Thr Arg Cys			
725	730	735	
Gln Met Thr Ser Leu Leu Asn Gly Asp Asn Gln Ser Ile Asp Val Ser			
740	745	750	
Lys Pro Val Lys Leu Ser Glu Gly Leu Asp Glu Val Lys Ala Asp Tyr			
755	760	765	
Arg Leu Ala Ile Lys Met Leu Lys Glu Ile Arg Asp Ala Tyr Arg Asn			
770	775	780	
Ile Gly His Lys Leu Lys Glu Gly Glu Thr Tyr Ile Ser Arg Asp Leu			
785	790	795	800
Gln Phe Ile Ser Lys Val Ile Gln Ser Glu Gly Val Met His Pro Thr			
805	810	815	
Pro Ile Lys Lys Val Leu Arg Val Gly Pro Trp Ile Asn Thr Ile Leu			
820	825	830	
Asp Asp Ile Lys Thr Ser Ala Glu Ser Ile Gly Ser Leu Cys Gln Glu			
835	840	845	
Leu Glu Phe Arg Gly Glu Ser Ile Ile Val Ser Leu Ile Leu Arg Asn			
850	855	860	
Phe Trp Leu Tyr Asn Leu Tyr Met His Glu Ser Lys Gln His Pro Leu			
865	870	875	880
Ala Gly Lys Gln Leu Phe Lys Gln Leu Asn Lys Thr Leu Thr Ser Val			
885	890	895	

Gln Arg Phe Phe Glu Ile Lys Lys Glu Asn Glu Val Val Asp Leu Trp
 900 905 910
 Met Asn Ile Pro Met Gln Phe Gly Gly Gly Asp Pro Val Val Phe Tyr
 915 920 925
 Arg Ser Phe Tyr Arg Arg Thr Pro Asp Phe Leu Thr Glu Ala Ile Ser
 930 935 940
 His Val Asp Ile Leu Leu Lys Ile Ser Ala Asn Ile Lys Asn Glu Thr
 945 950 955 960
 Lys Val Ser Phe Phe Lys Ala Leu Leu Ser Ile Glu Lys Asn Glu Arg
 965 970 975
 Ala Thr Leu Thr Thr Leu Met Arg Asp Pro Gln Ala Val Gly Ser Glu
 980 985 990
 Arg Gln Ala Lys Val Thr Ser Asp Ile Asn Arg Thr Ala Val Thr Ser
 995 1000 1005
 Ile Leu Ser Leu Ser Pro Asn Gln Leu Phe Ser Asp Ser Ala Ile His
 1010 1015 1020
 Tyr Ser Arg Asn Glu Glu Val Gly Ile Ile Ala Glu Asn Ile Thr
 1025 1030 1035 1040
 Pro Val Tyr Pro His Gly Leu Arg Val Leu Tyr Glu Ser Leu Pro Phe
 1045 1050 1055
 His Lys Ala Glu Lys Val Val Asn Met Ile Ser Gly Thr Lys Ser Ile
 1060 1065 1070
 Thr Asn Leu Leu Gln Arg Thr Ser Ala Ile Asn Gly Glu Asp Ile Asp
 1075 1080 1085
 Arg Ala Val Ser Met Met Leu Glu Asn Leu Gly Leu Leu Ser Arg Ile
 1090 1095 1100
 Leu Ser Val Val Val Asp Ser Ile Glu Ile Pro Ile Lys Ser Asn Gly
 1105 1110 1115 1120
 Arg Leu Ile Cys Cys Gln Ile Ser Arg Thr Leu Arg Glu Thr Ser Trp
 1125 1130 1135
 Asn Asn Met Glu Ile Val Gly Val Thr Ser Pro Ser Ile Thr Thr Cys
 1140 1145 1150
 Met Asp Val Ile Tyr Ala Thr Ser Ser His Leu Lys Gly Ile Ile Ile
 1155 1160 1165
 Glu Lys Phe Ser Thr Asp Arg Thr Thr Arg Gly Gln Arg Gly Pro Lys
 1170 1175 1180
 Ser Pro Trp Val Gly Ser Ser Thr Gln Glu Lys Lys Leu Val Pro Val
 1185 1190 1195 1200
 Tyr Asn Arg Gln Ile Leu Ser Lys Gln Gln Arg Glu Gln Leu Glu Ala
 1205 1210 1215
 Ile Gly Lys Met Arg Trp Val Tyr Lys Gly Thr Pro Gly Leu Arg Arg
 1220 1225 1230
 Leu Leu Asn Lys Ile Cys Leu Gly Ser Leu Gly Ile Ser Tyr Lys Cys
 1235 1240 1245
 Val Lys Pro Leu Leu Pro Arg Phe Met Ser Val Asn Phe Leu His Arg
 1250 1255 1260
 Leu Ser Val Ser Ser Arg Pro Met Glu Phe Pro Ala Ser Val Pro Ala
 1265 1270 1275 1280
 Tyr Arg Thr Thr Asn Tyr His Phe Asp Thr Ser Pro Ile Asn Gln Ala
 1285 1290 1295
 Leu Ser Glu Arg Phe Gly Asn Glu Asp Ile Asn Leu Val Phe Gln Asn
 1300 1305 1310
 Ala Ile Ser Cys Gly Ile Ser Ile Met Ser Val Val Glu Gln Leu Thr
 1315 1320 1325
 Gly Arg Ser Pro Lys Gln Leu Val Leu Ile Pro Gln Leu Glu Glu Ile
 1330 1335 1340
 Asp Ile Met Pro Pro Val Phe Gln Gly Lys Phe Asn Tyr Lys Leu
 1345 1350 1355 1360
 Val Asp Lys Ile Thr Ser Asp Gln His Ile Phe Ser Pro Asp Lys Ile
 1365 1370 1375
 Asp Met Leu Thr Leu Gly Lys Met Leu Met Pro Thr Ile Lys Gly Gln
 1380 1385 1390

Lys Thr Asp Gln Phe Leu Asn Lys Arg Glu Asn Tyr Phe His Gly Asn
 1395 1400 1405
 Asn Leu Ile Glu Ser Leu Ser Ala Ala Leu Ala Cys His Trp Cys Gly
 1410 1415 1420
 Ile Leu Thr Glu Gln Cys Ile Glu Asn Asn Ile Phe Lys Lys Asp Trp
 1425 1430 1435 1440
 Gly Asp Gly Phe Ile Ser Asp His Ala Phe Met Asp Phe Lys Ile Phe
 1445 1450 1455
 Leu Cys Val Phe Lys Thr Lys Leu Leu Cys Ser Trp Gly Ser Gln Gly
 1460 1465 1470
 Lys Asn Ile Lys Asp Glu Asp Ile Val Asp Glu Ser Ile Asp Lys Leu
 1475 1480 1485
 Leu Arg Ile Asp Asn Thr Phe Trp Arg Met Phe Ser Lys Val Met Phe
 1490 1495 1500
 Glu Pro Lys Val Lys Lys Arg Ile Met Leu Tyr Asp Val Lys Phe Leu
 1505 1510 1515 1520
 Ser Leu Val Gly Tyr Ile Gly Phe Lys Asn Trp Phe Ile Glu Gln Leu
 1525 1530 1535
 Arg Ser Ala Glu Leu His Glu Ile Pro Trp Ile Val Asn Ala Glu Gly
 1540 1545 1550
 Asp Leu Val Glu Ile Lys Ser Ile Lys Ile Tyr Leu Gln Leu Ile Glu
 1555 1560 1565
 Gln Ser Leu Phe Leu Arg Ile Thr Val Leu Asn Tyr Thr Asp Met Ala
 1570 1575 1580
 His Ala Leu Thr Arg Leu Ile Arg Lys Lys Leu Met Cys Asp Asn Ala
 1585 1590 1595 1600
 Leu Leu Thr Pro Ile Ser Ser Pro Met Val Asn Leu Thr Gln Val Ile
 1605 1610 1615
 Asp Pro Thr Thr Gln Leu Asp Tyr Phe Pro Lys Ile Thr Phe Glu Arg
 1620 1625 1630
 Leu Lys Asn Tyr Asp Thr Ser Ser Asn Tyr Ala Lys Gly Lys Leu Thr
 1635 1640 1645
 Arg Asn Tyr Met Ile Leu Leu Pro Trp Gln His Val Asn Arg Tyr Asn
 1650 1655 1660
 Phe Val Phe Ser Ser Thr Gly Cys Lys Val Ser Leu Lys Thr Cys Ile
 1665 1670 1675 1680
 Gly Lys Leu Met Lys Asp Leu Asn Pro Lys Val Leu Tyr Phe Ile Gly
 1685 1690 1695
 Glu Gly Ala Gly Asn Trp Met Ala Arg Thr Ala Cys Glu Tyr Pro Asp
 1700 1705 1710
 Ile Lys Phe Val Tyr Arg Ser Leu Lys Asp Asp Leu Asp His His Tyr
 1715 1720 1725
 Pro Leu Glu Tyr Gln Arg Val Ile Gly Glu Leu Ser Arg Ile Ile Asp
 1730 1735 1740
 Ser Gly Glu Gly Leu Ser Met Glu Thr Thr Asp Ala Thr Gln Lys Thr
 1745 1750 1755 1760
 His Trp Asp Leu Ile His Arg Val Ser Lys Asp Ala Leu Leu Ile Thr
 1765 1770 1775
 Leu Cys Asp Ala Glu Phe Lys Asp Arg Asp Asp Phe Phe Lys Met Val
 1780 1785 1790
 Ile Leu Trp Arg Lys His Val Leu Ser Cys Arg Ile Cys Thr Thr Tyr
 1795 1800 1805
 Gly Thr Asp Leu Tyr Leu Phe Ala Lys Tyr His Ala Lys Asp Cys Asn
 1810 1815 1820
 Val Lys Leu Pro Phe Phe Val Arg Ser Val Ala Thr Phe Ile Met Gln
 1825 1830 1835 1840
 Gly Ser Lys Leu Ser Gly Ser Glu Cys Tyr Ile Leu Leu Thr Leu Gly
 1845 1850 1855
 His His Asn Ser Leu Pro Cys His Gly Glu Ile Gln Asn Ser Lys Met
 1860 1865 1870
 Lys Ile Ala Val Cys Asn Asp Phe Tyr Ala Ala Lys Lys Leu Asp Asn
 1875 1880 1885

Lys Ser Ile Glu Ala Asn Cys Lys Ser Leu Leu Ser Gly Leu Arg Ile
 1890 1895 1900
 Pro Ile Asn Lys Lys Glu Leu Asp Arg Gln Arg Arg Leu Leu Thr Leu
 1905 1910 1915 1920
 Gln Ser Asn His Ser Val Ala Thr Val Gly Gly Ser Lys Ile Ile
 1925 1930 1935
 Glu Ser Lys Trp Leu Thr Asn Lys Ala Ser Thr Ile Ile Asp Trp Leu
 1940 1945 1950
 Glu His Ile Leu Asn Ser Pro Lys Gly Glu Leu Asn Tyr Asp Phe Phe
 1955 1960 1965
 Glu Ala Leu Glu Asn Thr Tyr Pro Asn Met Ile Lys Leu Ile Asp Asn
 1970 1975 1980
 Leu Gly Asn Ala Glu Ile Lys Lys Leu Ile Lys Val Thr Gly Tyr Met
 1985 1990 1995 2000
 Leu Val Ser Lys Lys
 2005

<210> 36

<211> 2005

<212> PRT

<213> human Metapneumo virus

<400> 36

Met Asp Pro Phe Cys Glu Ser Thr Val Asn Val Tyr Leu Pro Asp Ser
 1 5 10 15
 Tyr Leu Lys Gly Val Ile Ser Phe Ser Glu Thr Asn Ala Ile Gly Ser
 20 25 30
 Cys Leu Leu Lys Arg Pro Tyr Leu Lys Asn Asp Asn Thr Ala Lys Val
 35 40 45
 Ala Val Glu Asn Pro Val Val Glu His Val Arg Leu Arg Asn Ala Val
 50 55 60
 Met Thr Lys Met Lys Ile Ser Asp Tyr Lys Val Val Glu Pro Val Asn
 65 70 75 80
 Met Gln His Glu Ile Met Lys Asn Ile His Ser Cys Glu Leu Thr Leu
 85 90 95
 Leu Lys Gln Phe Leu Thr Arg Ser Lys Asn Ile Ser Ser Leu Lys Leu
 100 105 110
 Asn Met Ile Cys Asp Trp Leu Gln Leu Lys Ser Thr Ser Asp Asn Thr
 115 120 125
 Ser Ile Leu Asn Phe Ile Asp Val Glu Phe Ile Pro Val Trp Val Ser
 130 135 140
 Asn Trp Phe Ser Asn Trp Tyr Asn Leu Asn Lys Leu Ile Leu Glu Phe
 145 150 155 160
 Arg Arg Glu Glu Val Ile Arg Thr Gly Ser Ile Leu Cys Arg Ser Leu
 165 170 175
 Gly Lys Leu Val Phe Ile Val Ser Ser Tyr Gly Cys Val Val Lys Ser
 180 185 190
 Asn Lys Ser Lys Arg Val Ser Phe Phe Thr Tyr Asn Gln Leu Leu Thr
 195 200 205
 Trp Lys Asp Val Met Leu Ser Arg Phe Asn Ala Asn Phe Cys Ile Trp
 210 215 220
 Val Ser Asn Asn Leu Asn Lys Asn Gln Glu Gly Leu Gly Leu Arg Ser
 225 230 235 240
 Asn Leu Gln Gly Met Leu Thr Asn Lys Leu Tyr Glu Thr Val Asp Tyr
 245 250 255
 Met Leu Ser Leu Cys Cys Asn Glu Gly Phe Ser Leu Val Lys Glu Phe
 260 265 270
 Glu Gly Phe Ile Met Ser Glu Ile Leu Lys Ile Thr Glu His Ala Gln
 275 280 285
 Phe Ser Thr Arg Phe Arg Asn Thr Leu Leu Asn Gly Leu Thr Glu Gln
 290 295 300

Leu Ser Val Leu Lys Ala Lys Asn Arg Ser Arg Val Leu Gly Thr Ile
 305 310 315 320
 Leu Glu Asn Asn Asn Tyr Pro Met Tyr Glu Val Val Leu Lys Leu Leu
 325 330 335
 Gly Asp Thr Leu Lys Ser Ile Lys Leu Leu Ile Asn Lys Asn Leu Glu
 340 345 350
 Asn Ala Ala Glu Leu Tyr Tyr Ile Phe Arg Ile Phe Gly His Pro Met
 355 360 365
 Val Asp Glu Arg Glu Ala Met Asp Ala Val Lys Leu Asn Asn Glu Ile
 370 375 380
 Thr Lys Ile Leu Lys Leu Glu Ser Leu Thr Glu Leu Arg Gly Ala Phe
 385 390 395 400
 Ile Leu Arg Ile Ile Lys Gly Phe Val Asp Asn Asn Lys Arg Trp Pro
 405 410 415
 Lys Ile Lys Asn Leu Lys Val Leu Ser Lys Arg Trp Ala Met Tyr Phe
 420 425 430
 Lys Ala Lys Ser Tyr Pro Ser Gln Leu Glu Leu Ser Val Gln Asp Phe
 435 440 445
 Leu Glu Leu Ala Ala Val Gln Phe Glu Gln Glu Phe Ser Val Pro Glu
 450 455 460
 Lys Thr Asn Leu Glu Met Val Leu Asn Asp Lys Ala Ile Ser Pro Pro
 465 470 475 480
 Lys Lys Leu Ile Trp Ser Val Tyr Pro Lys Asn Tyr Leu Pro Glu Thr
 485 490 495
 Ile Lys Asn Gln Tyr Leu Glu Glu Ala Phe Asn Ala Ser Asp Ser Gln
 500 505 510
 Arg Thr Arg Arg Val Leu Glu Phe Tyr Leu Lys Asp Cys Lys Phe Asp
 515 520 525
 Gln Lys Glu Leu Lys Arg Tyr Val Ile Lys Gln Glu Tyr Leu Asn Asp
 530 535 540
 Lys Asp His Ile Val Ser Leu Thr Gly Lys Glu Arg Glu Leu Ser Val
 545 550 555 560
 Gly Arg Met Phe Ala Met Gln Pro Gly Lys Gln Arg Gln Ile Gln Ile
 565 570 575
 Leu Ala Glu Lys Leu Ala Asp Asn Ile Val Pro Phe Phe Pro Glu
 580 585 590
 Thr Leu Thr Lys Tyr Gly Asp Leu Asp Leu Gln Arg Ile Met Glu Ile
 595 600 605
 Lys Ser Glu Leu Ser Ser Ile Lys Thr Arg Lys Asn Asp Ser Tyr Asn
 610 615 620
 Asn Tyr Ile Ala Arg Ala Ser Ile Val Thr Asp Leu Ser Lys Phe Asn
 625 630 635 640
 Gln Ala Phe Arg Tyr Glu Thr Thr Ala Ile Cys Ala Asp Val Ala Asp
 645 650 655
 Glu Leu His Gly Thr Gln Ser Leu Phe Cys Trp Leu His Leu Ile Val
 660 665 670
 Pro Met Thr Thr Met Ile Cys Ala Tyr Arg His Ala Pro Pro Glu Thr
 675 680 685
 Lys Gly Glu Tyr Asp Ile Asp Lys Ile Gln Glu Gln Ser Gly Leu Tyr
 690 695 700
 Arg Tyr His Met Gly Gly Ile Glu Gly Trp Cys Gln Lys Leu Trp Thr
 705 710 715 720
 Met Glu Ala Ile Ser Leu Leu Asp Val Val Ser Val Lys Thr Arg Cys
 725 730 735
 Gln Met Thr Ser Leu Leu Asn Gly Asp Asn Gln Ser Ile Asp Val Ser
 740 745 750
 Lys Pro Val Lys Leu Ser Glu Gly Ile Asp Glu Val Lys Ala Asp Tyr
 755 760 765
 Ser Leu Ala Ile Arg Met Leu Lys Glu Ile Arg Asp Ala Tyr Lys Asn
 770 775 780
 Ile Gly His Lys Leu Lys Glu Gly Glu Thr Tyr Ile Ser Arg Asp Leu
 785 790 795 800

Gln Phe Ile Ser Lys Val Ile Gln Ser Glu Gly Val Met His Pro Thr
 805 810 815
 Pro Ile Lys Lys Ile Leu Arg Val Gly Pro Trp Ile Asn Thr Ile Leu
 820 825 830
 Asp Asp Ile Lys Thr Ser Ala Glu Ser Ile Gly Ser Leu Cys Gln Glu
 835 840 845
 Leu Glu Phe Arg Gly Glu Ser Ile Leu Val Ser Leu Ile Leu Arg Asn
 850 855 860
 Phe Trp Leu Tyr Asn Leu Tyr Met Tyr Glu Ser Lys Gln His Pro Leu
 865 870 875 880
 Ala Gly Lys Gln Leu Phe Lys Gln Leu Asn Lys Thr Leu Thr Ser Val
 885 890 895
 Gln Arg Phe Phe Glu Leu Lys Lys Glu Asn Asp Val Val Asp Leu Trp
 900 905 910
 Met Asn Ile Pro Met Gln Phe Gly Gly Asp Pro Val Val Phe Tyr
 915 920 925
 Arg Ser Phe Tyr Arg Arg Thr Pro Asp Phe Leu Thr Glu Ala Ile Ser
 930 935 940
 His Val Asp Leu Leu Leu Lys Val Ser Asn Asn Ile Lys Asp Glu Thr
 945 950 955 960
 Lys Ile Arg Phe Phe Lys Ala Leu Leu Ser Ile Glu Lys Asn Glu Arg
 965 970 975
 Ala Thr Leu Thr Thr Leu Met Arg Asp Pro Gln Ala Val Gly Ser Glu
 980 985 990
 Arg Gln Ala Lys Val Thr Ser Asp Ile Asn Arg Thr Ala Val Thr Ser
 995 1000 1005
 Ile Leu Ser Leu Ser Pro Asn Gln Leu Phe Cys Asp Ser Ala Ile His
 1010 1015 1020
 Tyr Ser Arg Asn Glu Glu Val Gly Ile Ile Ala Asp Asn Ile Thr
 1025 1030 1035 1040
 Pro Val Tyr Pro His Gly Leu Arg Val Leu Tyr Glu Ser Leu Pro Phe
 1045 1050 1055
 His Lys Ala Glu Lys Val Val Asn Met Ile Ser Gly Thr Lys Ser Ile
 1060 1065 1070
 Thr Asn Leu Leu Gln Arg Thr Ser Ala Ile Asn Gly Glu Asp Ile Asp
 1075 1080 1085
 Arg Ala Val Ser Met Met Leu Glu Asn Leu Gly Leu Leu Ser Arg Ile
 1090 1095 1100
 Leu Ser Val Ile Ile Asn Ser Ile Glu Ile Pro Ile Lys Ser Asn Gly
 1105 1110 1115 1120
 Arg Leu Ile Cys Cys Gln Ile Ser Lys Thr Leu Arg Glu Lys Ser Trp
 1125 1130 1135
 Asn Asn Met Glu Ile Val Gly Val Thr Ser Pro Ser Ile Val Thr Cys
 1140 1145 1150
 Met Asp Val Val Tyr Ala Thr Ser Ser His Leu Lys Gly Ile Ile Ile
 1155 1160 1165
 Glu Lys Phe Ser Thr Asp Lys Thr Thr Arg Gly Gln Arg Gly Pro Lys
 1170 1175 1180
 Ser Pro Trp Val Gly Ser Ser Thr Gln Glu Lys Lys Leu Val Pro Val
 1185 1190 1195 1200
 Tyr Asn Arg Gln Ile Leu Ser Lys Gln Gln Lys Glu Gln Leu Glu Ala
 1205 1210 1215
 Ile Gly Lys Met Arg Trp Val Tyr Lys Gly Thr Pro Gly Leu Arg Arg
 1220 1225 1230
 Leu Leu Asn Lys Ile Cys Ile Gly Ser Leu Gly Ile Ser Tyr Lys Cys
 1235 1240 1245
 Val Lys Pro Leu Leu Pro Arg Phe Met Ser Val Asn Phe Leu His Arg
 1250 1255 1260
 Leu Ser Val Ser Ser Arg Pro Met Glu Phe Pro Ala Ser Val Pro Ala
 1265 1270 1275 1280
 Tyr Arg Thr Thr Asn Tyr His Phe Asp Thr Ser Pro Ile Asn Gln Ala
 1285 1290 1295

Leu Ser Glu Arg Phe Gly Asn Glu Asp Ile Asn Leu Val Phe Gln Asn
 1300 1305 1310
 Ala Ile Ser Cys Gly Ile Ser Ile Met Ser Val Val Glu Gln Leu Thr
 1315 1320 1325
 Gly Arg Ser Pro Lys Gln Leu Val Leu Ile Pro Gln Leu Glu Glu Ile
 1330 1335 1340
 Asp Ile Met Pro Pro Val Phe Gln Gly Lys Phe Asn Tyr Lys Leu
 1345 1350 1355 1360
 Val Asp Lys Ile Thr Ser Asp Gln His Ile Phe Ser Pro Asp Lys Ile
 1365 1370 1375
 Asp Ile Leu Thr Leu Gly Lys Met Leu Met Pro Thr Ile Lys Gly Gln
 1380 1385 1390
 Lys Thr Asp Gln Phe Leu Asn Lys Arg Glu Asn Tyr Phe His Gly Asn
 1395 1400 1405
 Asn Leu Ile Glu Ser Leu Ser Ala Ala Leu Ala Cys His Trp Cys Gly
 1410 1415 1420
 Ile Leu Thr Glu Gln Cys Ile Glu Asn Asn Ile Phe Arg Lys Asp Trp
 1425 1430 1435 1440
 Gly Asp Gly Phe Ile Ser Asp His Ala Phe Met Asp Phe Lys Val Phe
 1445 1450 1455
 Leu Cys Val Phe Lys Thr Lys Leu Leu Cys Ser Trp Gly Ser Gln Gly
 1460 1465 1470
 Lys Asn Val Lys Asp Glu Asp Ile Ile Asp Glu Ser Ile Asp Lys Leu
 1475 1480 1485
 Leu Arg Ile Asp Asn Thr Phe Trp Arg Met Phe Ser Lys Val Met Phe
 1490 1495 1500
 Glu Ser Lys Val Lys Lys Arg Ile Met Leu Tyr Asp Val Lys Phe Leu
 1505 1510 1515 1520
 Ser Leu Val Gly Tyr Ile Gly Phe Lys Asn Trp Phe Ile Glu Gln Leu
 1525 1530 1535
 Arg Val Val Glu Leu His Glu Val Pro Trp Ile Val Asn Ala Glu Gly
 1540 1545 1550
 Glu Leu Val Glu Ile Lys Ser Ile Lys Ile Tyr Leu Gln Leu Ile Glu
 1555 1560 1565
 Gln Ser Leu Ser Leu Arg Ile Thr Val Leu Asn Tyr Thr Asp Met Ala
 1570 1575 1580
 His Ala Leu Thr Arg Leu Ile Arg Lys Lys Leu Met Cys Asp Asn Ala
 1585 1590 1595 1600
 Leu Phe Asn Pro Ser Ser Ser Pro Met Phe Asn Leu Thr Gln Val Ile
 1605 1610 1615
 Asp Pro Thr Thr Gln Leu Asp Tyr Phe Pro Arg Ile Ile Phe Glu Arg
 1620 1625 1630
 Leu Lys Ser Tyr Asp Thr Ser Ser Asp Tyr Asn Lys Gly Lys Leu Thr
 1635 1640 1645
 Arg Asn Tyr Met Thr Leu Leu Pro Trp Gln His Val Asn Arg Tyr Asn
 1650 1655 1660
 Phe Val Phe Ser Ser Thr Gly Cys Lys Val Ser Leu Lys Thr Cys Ile
 1665 1670 1675 1680
 Gly Lys Leu Ile Lys Asp Leu Asn Pro Lys Val Leu Tyr Phe Ile Gly
 1685 1690 1695
 Glu Gly Ala Gly Asn Trp Met Ala Arg Thr Ala Cys Glu Tyr Pro Asp
 1700 1705 1710
 Ile Lys Phe Val Tyr Arg Ser Leu Lys Asp Asp Leu Asp His His Tyr
 1715 1720 1725
 Pro Leu Glu Tyr Gln Arg Val Ile Gly Asp Leu Asn Arg Val Ile Asp
 1730 1735 1740
 Ser Gly Glu Gly Leu Ser Met Glu Thr Thr Asp Ala Thr Gln Lys Thr
 1745 1750 1755 1760
 His Trp Asp Leu Ile His Arg Ile Ser Lys Asp Ala Leu Leu Ile Thr
 1765 1770 1775
 Leu Cys Asp Ala Glu Phe Lys Asn Arg Asp Asp Phe Phe Lys Met Val
 1780 1785 1790

<210> 37
<211> 2005
<212> PRT
<213> human Metapneumo virus

<400> 37
 Met Asp Pro Phe Cys Glu Ser Thr Val Asn Val Tyr Leu Pro Asp Ser
 1 5 10 15
 Tyr Leu Lys Gly Val Ile Ser Phe Ser Glu Thr Asn Ala Ile Gly Ser
 20 25 30
 Cys Leu Leu Lys Arg Pro Tyr Leu Lys Lys Asp Asn Thr Ala Lys Val
 35 40 45
 Ala Val Glu Asn Pro Val Val Glu His Val Arg Leu Arg Asn Ala Val
 50 55 60
 Met Thr Lys Met Lys Ile Ser Asp Tyr Lys Val Val Glu Pro Ile Asn
 65 70 75 80
 Met Gln His Glu Ile Met Lys Asn Ile His Ser Cys Glu Leu Thr Leu
 85 90 95
 Leu Lys Gln Phe Leu Thr Arg Ser Lys Asn Ile Ser Ser Leu Lys Leu
 100 105 110
 Ser Met Ile Cys Asp Trp Leu Gln Leu Lys Ser Thr Ser Asp Asn Thr
 115 120 125
 Ser Ile Leu Asn Phe Ile Asp Val Glu Phe Ile Pro Val Trp Val Ser
 130 135 140
 Asn Trp Phe Ser Asn Trp Tyr Asn Leu Asn Lys Leu Ile Leu Glu Phe
 145 150 155 160
 Arg Arg Glu Glu Val Ile Arg Thr Gly Ser Ile Leu Cys Arg Ser Leu
 165 170 175
 Gly Lys Leu Val Phe Ile Val Ser Ser Tyr Gly Cys Val Val Lys Ser
 180 185 190
 Asn Lys Ser Lys Arg Val Ser Phe Phe Thr Tyr Asn Gln Leu Leu Thr
 195 200 205

Trp Lys Asp Val Met Leu Ser Arg Phe Asn Ala Asn Phe Cys Ile Trp
 210 215 220
 Val Ser Asn Asn Leu Asn Lys Asn Gln Glu Gly Leu Gly Phe Arg Ser
 225 230 235 240
 Asn Leu Gln Gly Met Leu Thr Asn Lys Leu Tyr Glu Thr Val Asp Tyr
 245 250 255
 Met Leu Ser Leu Cys Ser Asn Glu Gly Phe Ser Leu Val Lys Glu Phe
 260 265 270
 Glu Gly Phe Ile Met Ser Glu Ile Leu Lys Ile Thr Glu His Ala Gln
 275 280 285
 Phe Ser Thr Arg Phe Arg Asn Thr Leu Leu Asn Gly Leu Thr Glu Gln
 290 295 300
 Leu Ser Met Leu Lys Ala Lys Asn Arg Ser Arg Val Leu Gly Thr Ile
 305 310 315 320
 Leu Glu Asn Asn Asp Tyr Pro Met Tyr Glu Val Val Leu Lys Leu Leu
 325 330 335
 Gly Asp Thr Leu Lys Ser Ile Lys Leu Leu Ile Asn Lys Asn Leu Glu
 340 345 350
 Asn Ala Ala Glu Leu Tyr Tyr Ile Phe Arg Ile Phe Gly His Pro Met
 355 360 365
 Val Asp Glu Arg Glu Ala Met Asp Ala Val Lys Leu Asn Asn Glu Ile
 370 375 380
 Thr Lys Ile Leu Lys Leu Glu Ser Leu Thr Glu Leu Arg Gly Ala Phe
 385 390 395 400
 Ile Leu Arg Ile Ile Lys Gly Phe Val Asp Asn Asn Lys Arg Trp Pro
 405 410 415
 Lys Ile Lys Asn Leu Lys Val Leu Ser Lys Arg Trp Val Met Tyr Phe
 420 425 430
 Lys Ala Lys Ser Tyr Pro Ser Gln Leu Glu Leu Ser Val Gln Asp Phe
 435 440 445
 Leu Glu Leu Ala Ala Val Gln Phe Glu Gln Glu Phe Ser Val Pro Glu
 450 455 460
 Lys Thr Asn Leu Glu Met Val Leu Asn Asp Lys Ala Ile Ser Pro Pro
 465 470 475 480
 Lys Lys Leu Ile Trp Ser Val Tyr Pro Lys Asn Tyr Leu Pro Glu Ile
 485 490 495
 Ile Lys Asn Gln Tyr Leu Glu Glu Val Phe Asn Ala Ser Asp Ser Gln
 500 505 510
 Arg Thr Arg Arg Val Leu Glu Phe Tyr Leu Lys Asp Cys Lys Phe Asp
 515 520 525
 Gln Lys Asp Leu Lys Arg Tyr Val Leu Lys Gln Glu Tyr Leu Asn Asp
 530 535 540
 Lys Asp His Ile Val Ser Leu Thr Gly Lys Glu Arg Glu Leu Ser Val
 545 550 555 560
 Gly Arg Met Phe Ala Met Gln Pro Gly Lys Gln Arg Gln Ile Gln Ile
 565 570 575
 Leu Ala Glu Lys Leu Leu Ala Asp Asn Ile Val Pro Phe Phe Pro Glu
 580 585 590
 Thr Leu Thr Lys Tyr Gly Asp Leu Asp Leu Gln Arg Ile Met Glu Met
 595 600 605
 Lys Ser Glu Leu Ser Ser Ile Lys Thr Arg Lys Asn Asp Ser Tyr Asn
 610 615 620
 Asn Tyr Ile Ala Arg Ala Ser Ile Val Thr Asp Leu Ser Lys Phe Asn
 625 630 635 640
 Gln Ala Phe Arg Tyr Glu Thr Thr Ala Ile Cys Ala Asp Val Ala Asp
 645 650 655
 Glu Leu His Gly Thr Gln Ser Leu Phe Cys Trp Leu His Leu Ile Val
 660 665 670
 Pro Met Thr Thr Met Ile Cys Ala Tyr Arg His Ala Pro Pro Glu Thr
 675 680 685
 Lys Gly Glu Tyr Asp Ile Asp Lys Ile Glu Glu Gln Ser Gly Leu Tyr
 690 695 700

Arg Tyr His Met Gly Gly Ile Glu Gly Trp Cys Gln Lys Leu Trp Thr
 705 710 715 720
 Met Glu Ala Ile Ser Leu Leu Asp Val Val Ser Val Lys Thr Arg Cys
 725 730 735
 Gln Met Thr Ser Leu Leu Asn Gly Asp Asn Gln Ser Ile Asp Val Ser
 740 745 750
 Lys Pro Val Lys Leu Ser Glu Gly Ile Asp Glu Val Lys Ala Asp Tyr
 755 760 765
 Ser Leu Ala Ile Lys Met Leu Lys Glu Ile Arg Asp Ala Tyr Lys Asn
 770 775 780
 Ile Gly His Lys Leu Lys Glu Gly Glu Thr Tyr Ile Ser Arg Asp Leu
 785 790 795 800
 Gln Phe Ile Ser Lys Val Ile Gln Ser Glu Gly Val Met His Pro Thr
 805 810 815
 Pro Ile Lys Lys Ile Leu Arg Val Gly Pro Trp Ile Asn Thr Ile Leu
 820 825 830
 Asp Asp Ile Lys Thr Ser Ala Glu Ser Ile Gly Ser Leu Cys Gln Glu
 835 840 845
 Leu Glu Phe Arg Gly Glu Ser Met Leu Val Ser Leu Ile Leu Arg Asn
 850 855 860
 Phe Trp Leu Tyr Asn Leu Tyr Met His Glu Ser Lys Gln His Pro Leu
 865 870 875 880
 Ala Gly Lys Gln Leu Phe Lys Gln Leu Asn Lys Thr Leu Thr Ser Val
 885 890 895
 Gln Arg Phe Phe Glu Leu Lys Lys Glu Asn Asp Val Val Asp Leu Trp
 900 905 910
 Met Asn Ile Pro Met Gln Phe Gly Gly Asp Pro Val Val Phe Tyr
 915 920 925
 Arg Ser Phe Tyr Arg Arg Thr Pro Asp Phe Leu Thr Glu Ala Ile Ser
 930 935 940
 His Val Asp Leu Leu Leu Lys Val Ser Asn Asn Ile Lys Asn Glu Thr
 945 950 955 960
 Lys Ile Arg Phe Phe Lys Ala Leu Leu Ser Ile Glu Lys Asn Glu Arg
 965 970 975
 Ala Thr Leu Thr Thr Leu Met Arg Asp Pro Gln Ala Val Gly Ser Glu
 980 985 990
 Arg Gln Ala Lys Val Thr Ser Asp Ile Asn Arg Thr Ala Val Thr Ser
 995 1000 1005
 Ile Leu Ser Leu Ser Pro Asn Gln Leu Phe Cys Asp Ser Ala Ile His
 1010 1015 1020
 Tyr Ser Arg Asn Glu Glu Glu Val Gly Ile Ile Ala Asp Asn Ile Thr
 1025 1030 1035 1040
 Pro Val Tyr Pro His Gly Leu Arg Val Leu Tyr Glu Ser Leu Pro Phe
 1045 1050 1055
 His Lys Ala Glu Lys Val Val Asn Met Ile Ser Gly Thr Lys Ser Ile
 1060 1065 1070
 Thr Asn Leu Leu Gln Arg Thr Ser Ala Ile Asn Gly Glu Asp Ile Asp
 1075 1080 1085
 Arg Ala Val Ser Met Met Leu Glu Asn Leu Gly Leu Leu Ser Arg Ile
 1090 1095 1100
 Leu Ser Val Ile Ile Asn Ser Ile Glu Ile Pro Ile Lys Ser Asn Gly
 1105 1110 1115 1120
 Arg Leu Ile Cys Cys Gln Ile Ser Lys Thr Leu Arg Glu Lys Ser Trp
 1125 1130 1135
 Asn Asn Met Glu Ile Val Gly Val Thr Ser Pro Ser Ile Val Thr Cys
 1140 1145 1150
 Met Asp Val Val Tyr Ala Thr Ser Ser His Leu Lys Gly Ile Ile Ile
 1155 1160 1165
 Glu Lys Phe Ser Thr Asp Lys Thr Thr Arg Gly Gln Arg Gly Pro Lys
 1170 1175 1180
 Ser Pro Trp Val Gly Ser Ser Thr Gln Glu Lys Lys Leu Val Pro Val
 1185 1190 1195 1200

Tyr Asn Arg Gln Ile Leu Ser Lys Gln Gln Lys Glu Gln Leu Glu Ala
 1205 1210 1215
 Ile Gly Lys Met Arg Trp Val Tyr Lys Gly Thr Pro Gly Leu Arg Arg
 1220 1225 1230
 Leu Leu Asn Lys Ile Cys Ile Gly Ser Leu Gly Ile Ser Tyr Lys Cys
 1235 1240 1245
 Val Lys Pro Leu Leu Pro Arg Phe Met Ser Val Asn Phe Leu His Arg
 1250 1255 1260
 Leu Ser Val Ser Ser Arg Pro Met Glu Phe Pro Ala Ser Val Pro Ala
 1265 1270 1275 1280
 Tyr Arg Thr Thr Asn Tyr His Phe Asp Thr Ser Pro Ile Asn Gln Ala
 1285 1290 1295
 Leu Ser Glu Arg Phe Gly Asn Glu Asp Ile Asn Leu Val Phe Gln Asn
 1300 1305 1310
 Ala Ile Ser Cys Gly Ile Ser Ile Met Ser Val Val Glu Gln Leu Thr
 1315 1320 1325
 Gly Arg Ser Pro Lys Gln Leu Val Leu Ile Pro Gln Leu Glu Glu Ile
 1330 1335 1340
 Asp Ile Met Pro Pro Val Phe Gln Gly Lys Phe Asn Tyr Lys Leu
 1345 1350 1355 1360
 Val Asp Lys Ile Thr Ser Asp Gln His Ile Phe Ser Pro Asp Lys Ile
 1365 1370 1375
 Asp Ile Leu Thr Leu Gly Lys Met Leu Met Pro Thr Ile Lys Gln
 1380 1385 1390
 Lys Thr Asp Gln Phe Leu Asn Lys Arg Glu Asn Tyr Phe His Gly Asn
 1395 1400 1405
 Asn Leu Ile Glu Ser Leu Ser Ala Ala Leu Ala Cys His Trp Cys Gly
 1410 1415 1420
 Ile Leu Thr Glu Gln Cys Val Glu Asn Asn Ile Phe Arg Lys Asp Trp
 1425 1430 1435 1440
 Gly Asp Gly Phe Ile Ser Asp His Ala Phe Met Asp Phe Lys Ile Phe
 1445 1450 1455
 Leu Cys Val Phe Lys Thr Lys Leu Leu Cys Ser Trp Gly Ser Gln Gly
 1460 1465 1470
 Lys Asn Val Lys Asp Glu Asp Ile Ile Asp Glu Ser Ile Asp Lys Leu
 1475 1480 1485
 Leu Arg Ile Asp Asn Thr Phe Trp Arg Met Phe Ser Lys Val Met Phe
 1490 1495 1500
 Glu Ser Lys Val Lys Arg Ile Met Leu Tyr Asp Val Lys Phe Leu
 1505 1510 1515 1520
 Ser Leu Val Gly Tyr Ile Gly Phe Lys Asn Trp Phe Ile Glu Gln Leu
 1525 1530 1535
 Arg Val Val Glu Leu His Glu Val Pro Trp Ile Val Asn Ala Glu Gly
 1540 1545 1550
 Glu Leu Val Glu Ile Lys Pro Ile Lys Ile Tyr Leu Gln Leu Ile Glu
 1555 1560 1565
 Gln Ser Leu Ser Leu Arg Ile Thr Val Leu Asn Tyr Thr Asp Met Ala
 1570 1575 1580
 His Ala Leu Thr Arg Leu Ile Arg Lys Lys Leu Met Cys Asp Asn Ala
 1585 1590 1595 1600
 Leu Phe Asn Pro Ser Ser Ser Pro Met Phe Ser Leu Thr Gln Val Ile
 1605 1610 1615
 Asp Pro Thr Thr Gln Leu Asp Tyr Phe Pro Lys Val Ile Phe Glu Arg
 1620 1625 1630
 Leu Lys Ser Tyr Asp Thr Ser Ser Asp Tyr Asn Lys Gly Lys Leu Thr
 1635 1640 1645
 Arg Asn Tyr Met Thr Leu Leu Pro Trp Gln His Val Asn Arg Tyr Asn
 1650 1655 1660
 Phe Val Phe Ser Ser Thr Gly Cys Lys Ile Ser Leu Lys Thr Cys Ile
 1665 1670 1675 1680
 Gly Lys Leu Ile Lys Asp Leu Asn Pro Lys Val Leu Tyr Phe Ile Gly
 1685 1690 1695

Glu Gly Ala Gly Asn Trp Met Ala Arg Thr Ala Cys Glu Tyr Pro Asp
 1700 1705 1710
 Ile Lys Phe Val Tyr Arg Ser Leu Lys Asp Asp Leu Asp His His Tyr
 1715 1720 1725
 Pro Leu Glu Tyr Gln Arg Val Ile Gly Asp Leu Asn Arg Val Ile Asp
 1730 1735 1740
 Gly Gly Glu Gly Leu Ser Met Glu Thr Thr Asp Ala Thr Gln Lys Thr
 1745 1750 1755 1760
 His Trp Asp Leu Ile His Arg Ile Ser Lys Asp Ala Leu Leu Ile Thr
 1765 1770 1775
 Leu Cys Asp Ala Glu Phe Lys Asn Arg Asp Asp Phe Phe Lys Met Val
 1780 1785 1790
 Ile Leu Trp Arg Lys His Val Leu Ser Cys Arg Ile Cys Thr Ala Tyr
 1795 1800 1805
 Gly Thr Asp Leu Tyr Leu Phe Ala Lys Tyr His Ala Thr Asp Cys Asn
 1810 1815 1820
 Ile Lys Leu Pro Phe Phe Val Arg Ser Val Ala Thr Phe Ile Met Gln
 1825 1830 1835 1840
 Gly Ser Lys Leu Ser Gly Ser Glu Cys Tyr Ile Leu Leu Thr Leu Gly
 1845 1850 1855
 His His Asn Asn Leu Pro Cys His Gly Glu Ile Gln Asn Ser Lys Met
 1860 1865 1870
 Arg Ile Ala Val Cys Asn Asp Phe His Ala Ser Lys Lys Leu Asp Asn
 1875 1880 1885
 Lys Ser Ile Glu Ala Asn Cys Lys Ser Leu Leu Ser Gly Leu Arg Ile
 1890 1895 1900
 Pro Ile Asn Lys Lys Glu Leu Asn Arg Gln Lys Lys Leu Leu Thr Leu
 1905 1910 1915 1920
 Gln Ser Asn His Ser Ser Ile Ala Thr Val Gly Gly Ser Lys Ile Ile
 1925 1930 1935
 Glu Ser Lys Trp Leu Lys Asn Lys Ala Ser Thr Ile Ile Asp Trp Leu
 1940 1945 1950
 Glu His Ile Leu Asn Ser Pro Lys Gly Glu Leu Asn Tyr Asp Phe Phe
 1955 1960 1965
 Glu Ala Leu Glu Asn Thr Tyr Pro Asn Met Ile Lys Leu Ile Asp Asn
 1970 1975 1980
 Leu Gly Asn Ala Glu Ile Lys Lys Leu Ile Lys Val Pro Gly Tyr Met
 1985 1990 1995 2000
 Leu Val Ser Lys Lys
 2005

<210> 38
 <211> 6018
 <212> DNA
 <213> human Metapneumo virus

<400> 38
 atggatcctc tcaatgaatc cactgttaat gtcttatcttc ctgactcata tcttaaagga 60
 gtgatttctt ttagtgagac taatgcatt ggttcatgtc tctaaaaag accttaccta 120
 aaaaatgaca acactgaaa agttgccata gagaatccctg ttatcgagca tgtagactc 180
 aaaaatgcag tcaattctaa gatggaaaata tcagattaca agatagtaga gccagtaaac 240
 atgcaacatg aaattatgaa gaatgtacac agttgtgagc tcacattttt aaaacagttt 300
 ttaacaagga gtaaaaatat tagcaactctc aaattaaata tgatatgtga ttggctgcag 360
 ttaaaagtcta catcagatga tacctcaatc ctaagttta tagatgtaga atttataacct 420
 agctgggtaa gcaattgggt tagtaattgg tacaatctca acaagttgat tctggattc 480
 agggaaagaag aagaataaaag aactggttca atcttgttga ggtcattggg taaatttagtt 540
 ttttgttat catcatatgg atgtatagtc aagagcaaca aaagcaaaag agtgagcttc 600
 ttcacatata atcaactgtt aacatggaaa gatgtgatgt taatgtgatt caatgcaaat 660
 ttttgtatat gggtaagcaa cagtctgaat gaaaatcaag aaggctttagg gttgagaagt 720
 aatctgcaag gcatattaaac taataagcta tatgaaaacty tagatttatat gcttagtttta 780
 tggatcatttca acttgtgaaa gagttcgaag gctttattat gagtggaaattt 840

cttaggatata ctgaacatgc tcaattcagt actagattta gaaataactt attaaaatgg 900
ttaactgatc aattaacaaa attaaaaaat aaaaacagac tcagaggta tggtaccgtg 960
tttagaaaaata atgattatcc aatgtacgaa gtttactta agttattagg agataacttg 1020
agatgtatta aattattaat caataaaaac ttagagaatg ctgctgaatt atactatata 1080
tttagaaat tcggtcaccc aatggtagat gaaagagatg ctgctgaatt atactatata 1080
aacaatgaaa tcacaaaaat ccttaggtgg gagagcttga caatggatgc tgtcaaatta 1140
atattaagga ttatcaaagg attttagac aacaacaaaaa cagaactaag aggggcattc 1200
ttaaaagtgc ttagtaagag atggactatg tacttcaaag gatggccca aattaaaaac 1260
cttgaattaa gcgaacaaga ttttttagag cttgctgcaa caaaaagttt ccccagtcaa 1320
tctgtccctg aaaaaaccaa ctttgagatg gtattaaatg tacatggatgc tgtcaaatta 1140
aaaagattaa tatgttctgt gtatccaaa aattacttac ataaagctat atcacctcct 1440
tatctagaag agactttcaa tgcaagtgt agtctcaaaa ctgagaaat aaaaatcg 1500
tatttgaag ataataaatt cgaccaaaaaa gaactaaaaa caagaagagt actagagtc 1560
tatttaatg ataaggatca tattgtctcg ctaactggaa gttatgttgc tttttttt 1620
ggttagatgt ttgtatgc accagggaaa cagcgacaaa tacaaatatt ggctgaaaaa 1740
ttgttagctg ataatatgtt acctttttc ccagaaacct taacaaagta tggtgatcta 1800
gatcttcaga gaataatgg aatcaaatcg gaactttttt ctattaaac tagaagaaat 1860
gatagttata ataattacat tgcaagagca tccatagtaa cagatggatgc tttttttt 1920
caagcctta ggtatgaaac tacagcgatc tggcgatg tagcagatga actacatgg 1980
acacaaagcc tattctgtt gttacatctt atctccctt tgacaacaat gatatgtcc 2040
tatagacatg caccaccaga aacaaaaaggta gaatgtataa tagatggatgc tttttttt 2100
agtggtttat atagatatca tattttttt attagaggat ggtgtcaaaa actctggaca 2160
atggaagctt atatcttattt agatgttga tctgtaaaaaa cacatgttca aatgacatct 2220
ttttaaacgc gtgacaaacca atcaatagat gtaatgttgc cttttttt 2280
tttagatgaag tggaaagcaga ttagatgttgc tttttttt 2340
gcatacagaa atataggcca cttttttt 2400
cagtttataa gtaaggtgtt atcttaagag tttttttt 2460
atcttaagag tgggaccatg tcaataggga gtctatgtca acattaaacac 2520
tcaataggga gtctatgtca atattaagga atttttggct aaagcataat agttatgtctg 2580
gcagggaaagc agttattcaa gaaataaaaaa agggaaatgtt aatcaaagca acaccccccta 2640
ggaggagatc cttttttt 2700
cagttatcata gtaatgttgc tttttttt 2760
ctatagatct ttctatagaa ggacccctga ttttttaact 2820
gaagcaatca gtcatgttgc tttttttt 2880
aaaataagtt tcttcaaagc tttttttt 2940
acactaatga gagatccca tttttttt 3000
atcaatagaa cagcagttac gctattaatgttgc tttttttt 3060
agtgtatatac actacagtag cttttttt 3120
cctgttatac ctcatggact aaagttgtga atatgtatc tttttttt 3180
aaagttgtga atatgtatc tttttttt 3240
gctattaatg gtgaagatata tttttttt 3300
ttatctagaa tattgtcagt agttgttgc tttttttt 3360
aggctgatata gtttgcataat tttttttt 3420
atagttggag taacatcccc tttttttt 3480
tctcatatgc aagggataat tttttttt 3540
agaggtccaa agagcccttgc tttttttt 3600
tataacacagc aaatttttgc aaaaacaaacca agagaacagc tagaagcaat tggaaaaatgt 3660
agatggatataa aaaaagggtt accagggttca tttttttt 3720
agtttaggc ttagttacaa tttttttt 3780
ttcttacaca ggttatctgt tttttttt 3840
tatagaacaa caaattacca ttttgacact agtcttata tcccgacatc agttccagct 3900
tttggaaatg aagatattaa tttggcttca caaaatgc tttttttt 3960
atagatgttag tagaacaatt aactggtagg agtccaaaac atcaagcact aagtggagaga 4020
ttagaagaaa tagacattat gcccacca gtttcaag gttttttt 4080
gtagataaga taacttctga tcaacatata tttttttt 4140
ctggggaaaaa tgctcatgcc cactataaaa ggtcagaaaaa cagatcagtt cctgaacaag 4200
agagagaattt attccatgg gaataatctt attgtatgtt tttttttt 4260
cattgggtgtt ggtatattaaac agagcaatgt atagaaaata tttttttt 4320
ggtagacgggt tcatatcggt tttttttt 4380
aaaactaaac tttttatgttgc ttgggggtcc caagggaaaaa acattaaaga tgaagatata 4440
gtagatgaat caatagataa actgttaagg attgataata tttttttt 4500
aagggttatgtt tttttttt 4560

tcatttagtag gttatataagg gtttaagaat tggttttag aacagtttag atcagcttag 4620
 ttgcattgagg taccttgat tgcataatgcc gaaggtgatc tgggttagat caagtcaatt 4680
 aaaatctatt tgcaactgat agagcaaagt ttatTTTaa gaataactgt tttgaactat 4740
 acagatatgg cacatgcct cacaagatta atcagaaaaga agttgatgt tgataatgca 4800
 ctattaactc cgattccatc cccaaatggtt aatttaactc aagttattga tcctacagaa 4860
 caatttagctt atttccctaa gataacattt gaaaggctaa aaaattatga cactagttca 4920
 aattatgcta aaggaaagct aacaaggaat tacatgatac tggttgcattt gcaacatgtt 4980
 aatagatata actttgtctt tagttctact ggatgtaaag ttatgtctaa aacatgcatt 5040
 ggaaaactta taaaaagatct aaaccctaaa gttctgtact ttattggaga aggggcagga 5100
 aattggatgg ccagaacagc atgtgaatat cctgacatca aatttgtata cagaagttta 5160
 aaagatgacc ttgtatcatca ttatcccttga gataaccaga gagttatagg agaattaagc 5220
 aggataatag atagcggtga agggcttca atggaaacaa cagatgcaac tcaaaaaact 5280
 cattgggatt tgatacacag agtaagcaaa gatgttttat taataactt atgtgatgca 5340
 gaatttaagg acagagatga ttttttaag atggttaattc tatggaggaa acatgtattta 5400
 tcatgcagaa ttgcactac ttatggaca gacctctatt tattgcataa gtatcatgt 5460
 aaagactgca atgtaaaattt acctttttt gtgagatcg tagccacctt tattatgca 5520
 ggttagaaac tgcaggctc agaatgctac atactcttaa cactaggcca ccacaacaat 5580
 ttaccctgccc atggagaaat acaaattctt aagatgaaaa tagcagtgtg taatgatttt 5640
 tatgctgcaa aaaaacttga caataaatctt attgaagcca actgtttatc acttttatca 5700
 gggctaaagaa taccgataaa taagaaagaa ttaaatagac agagaaggtt attaacaacta 5760
 caaagcaacc attcttcgtt agcaacagtt ggaggttagca aggtcataga gtctaaatgg 5820
 ttaacaaaca aggcaaacac aataattgtat tggtagaaac atatttaaa ttctccaaaa 5880
 ggtgaattaa attatgattt ttttgaagca ttagaaaattt cttaccctaa tatgattaaa 5940
 ctaatagata atcttagggaa tgcagagata aaaaaacttga tcaaagtaac tggatataatg 6000
 cttgtaaatgaa aaaaatgtt 6018

<210> 39

<211> 6018

<212> DNA

<213> human Metapneumo virus

<400> 39

atggatccctc ttaatgaatc cactgttaat gtctatctcc ctgattcgta ctttaaaggaa 60
 gtaatttctt ttagtgaac taatgcaatt gttcatgtc tctaaaaag accttactta 120
 aaaaatgaca acactgcaaa agttgcata gagaatcttgc ttatggaca tggagactc 180
 aaaaatgcag tcaattctaa aatggaaaata tcagattaca aggttagtaga gccagtaac 240
 atgcaacatg aaataatgaa gaatgtcac agttgtgagc tcacactt gaaacagttt 300
 ttaacaaggaa gtaaaaacat tagcacttca aatggaaaata-tgatgtgtt tggtgcata 360
 ttaaagtctt catcagatga tacctcaatc ctaagttca tagatgttaga atttataacct 420
 agttggtaa gcaactgggtt tagtaattgg tacaatctca ataagttat tttgaaattc 480
 agaagagagg aagtaataag aaccgggtca atcttatgca ggtcattggg taaattagtt 540
 ttatgttat catcatacgg atgtatgtc aagagcaaca aaagcaaaag agtgagctt 600
 ttcacatatac atcaactgtt aacatggaaa gatgtatgtt taatgttagatt taatgcgaat 660
 tttgtatata gggtaagca tagtctgaat gaaaatcagg aagggtctagg gttaaagaaatg 720
 aatctacaag gtatgttaac taatggaaaata tatggaaactg tagatttat gctaagttta 780
 tggcaatg aagggttctc actgtttaaa gagttcgaag gtttattat gagtgaatc 840
 cttaggatta ctgaacatgc tcaattcagt actagattt gaaatacttt attaaatgg 900
 ttaacagatc aattaacaaa attggaaaata aaaaacagac tcagagttca tggtagctt 960
 ttagaaaata atgattatcc aatgtatgaa gttgtactt aatttttagg agataacttg 1020
 agatgtatca aatttataat caataaaaac ttagagaatg ctgcagaattt atactatata 1080
 ttcaaaatggaa ttggcatcc aatggtagat gaaagagatg caatggatgc tgcataatgg 1140
 aacaatgaaa tcacaaaaat cctaaagggtt gagagcttgc cagaactaag aggagcatc 1200
 atattaaggaa ttatcaaaagg attgtggac aacaacaaaaa ggtggcccaaa attaaaaat 1260
 ttaatgtgc ttagcaaaag atggactatg tacttcaaaatg tcccaatggaa 1320
 ctcaattaa gtgaacaaga ctttcttagag cttgtcttgc tacaatttgc acaagagttt 1380
 tctgttccctg aaaaaccaa tcttggatgt gtatggaaaatg acaaagccat atcaccctt 1440
 aaaagattaa tatggctgtt gtatccaaag aattacttac ctgagacgt aaaaatcgaa 1500
 tatttggaaatg aaactttca tgcggatgtt agtctcaaaa caagaagagt actagagttac 1560
 tattttaaatg acaataaaattt tgatcaaaaatg gaaatggaaa gttatgttagt tagacaagaa 1620
 tattttaaatg ataggagca cttgtctca ttaactggaa aagaaagaga attaagtgtt 1680

ggtagaatgt ttgctatgca accagggaaaa cagcgacaaa tacaatatt ggcagaaaaaa 1740
tttgttagctg ataacattgt acctttcttc cggaaacct taacaaagta tggatcta 1800
gatcttcaga gaataatgga aatcaaatacga aacttttctt ctatcaaacc cagaagaaat 1860
gacagtata ataattacat tgcaagagca tccatagtaa cagatttgag caagttcaac 1920
caagcctta gatatgaaac tacagcgatc tggcgatg tagcagacga attacatgga 1980
acacaaagct tattctgtt gttacatctt atcgatcata tgactacaat gatatgtgcc 2040
tatagacatg caccaccaga aacaaaaggt gaatatgata tagataagat agaagagcaa 2100
agtggcttat atagatatac catggcggt attgaaggat ggtgtcaaaa actctggaca 2160
atggaagcta tatctttatt ggtgttgta tctgtaaaga cacgggtca aatgacatct 2220
ttattaaacg gtgataacca atcaatagat gtaagtaaac cagtcaagtt atctgaagg 2280
tttagatgaag tgaaggcaga ttatcgctt gcaataaaaaa tgctaaaaga aataagagat 2340
gcatacagaa atataggcca taaactaaa gaagggaaa catatatatac aaggatctt 2400
caatttataa gcaaggtgat tcaatctgaa ggagtgtatgc atcctacccc tataaaaaaag 2460
gtcttgagag taggaccatg gataaacaca atattagatg acattaaaac tagtgcgtag 2520
tcaatagggta gtctatgtca agaattagaa tttaggggag aaagcataat agttagtctg 2580
atattaagaa acttctggct gtataactt tacatgcata aatcaaagca acatcctt 2640
gcaggaaaac agtattcaa acaactaaat aaaacattaa catcgtcga gagattttt 2700
gaaattaaaaa aggaaaatga ggttagtagat ctatggatga acataccat gcaatttgg 2760
ggaggagatc cagtagtctt ctatagatct ttctatagaa ggaccctga ttttttaact 2820
gaggcaatca gccatgtga tattctgtt aaaatatcag ctaacataaa aatgaaacg 2880
aaagtaatttcttcaaggc cttactatca atagaaaaaa atgaacgtgc tacactgaca 2940
acgctaatacga gagatcctca agctgttggc tcagaacgc aagcaaaagt aacaagtgc 3000
atcaatagaa cagcagttac cagtatctt agtcttccc caaatcaact ttcatgtat 3060
agtgcataac actatagcag gaatgaagaa gaagtggaa tcattgcaga aacataaaca 3120
cctgtttatc ctcatgggtc gagagtatta tatgaatcat tgcccttca caaagctgaa 3180
aaagttgtaa acatgatatac agggacaaaaa tctataacca acttattaca gagaacatcc 3240
gcttataatg gtgaagatatac tgacaggct gtagtctatga tggggagaa tctaggatta 3300
ttatctagaa tattgtcagt agttgttgc agttagagaaa ttcaatcaa atctaattgt 3360
aggctgatatac gttgtcaaat ctcttaggact ttaagagaga catcatggaa taatatggaa 3420
atagttggag taacatctcc tagcatcaat acatgtatgg atgtcatata tgcaactagt 3480
tctcatgttga aggggataat tatagaaaag tttagcactg acagaactac aaggggtcaa 3540
agaggtccaa aaagcccttgc ggttagggctg agtactcaag agaaaaaatt agtacctgtt 3600
tataacagac aaattcttcaaaaaccaaa agagaacacgc tagaagcaat tggaaaatg 3660
agatgggtgt ataaagggac accaggcttgc ctagcattac tcaacaagat ctgtcttggg 3720
agtttaggca ttatgtacaa atgtttaaaa ctttattac cttaggtt gatgttaat 3780
ttcttacata gtttatctgt cagtagtata cctatggaa tcccagcatc agtccagct 3840
tatagaacaa caaattacca ttgcacact agtcttattata atcaagcaact aagtgagaga 3900
tttggaaatg aagatattaa cttggcttc caaaatgcga tcagctgtgg aattagcata 3960
atgagtgttag tagaacaatt aacaggtaga agccccaaac agttagttt aataccctaa 4020
ttagaagaaa tagacattat gccaccacca gtgtttcaag gggaaattcaa ttataattaa 4080
gtagataaga taacttctgtcaacatatac tttagtccgg acaaaataga tatgttaaca 4140
ctaggaaaaa tgctcatgccc tactataaa ggtcagaaaaa cagatcagttt cttaaataa 4200
agagagaatt attccatgg gaacaatctt attgagtctt tatcagcgc attagcatgt 4260
cattgggtgt ggtatattaaac agaacaatgc atagaaaaaaat atatttcaaa gaaggactgg 4320
ggtgacgggtt ttatctgca tcatgtttt atggacttca aaatattccct atgtgtctt 4380
aaaactaaac ttatgttag ttggggatcc caaggaaaaaa acattaaaga tgaagatata 4440
gtagatgaat caatagataa atgtttaagg attgacaata cttttggag aatgttcagc 4500
aaagttagt ttgaacccaa agttaagaaa aggataatgt tataatgtt aaaaattccta 4560
tcactatgt gctacatagg gtttaagaac tggtttatag agcagttgag atcagctgaa 4620
ttgcatgaaa taccttggat tgcaatgccc gaagggtattt tggttggat caagtcaatt 4680
aaaatctatt tcaactgtat agaacaatgc ttatctttaa gaataactgt tttgaactat 4740
acagatatacgtt ccatgctt cacaacgatca atcagaaaga agttaatgtg tgataatgca 4800
ctgttaaccc caatttcatc cccaaatggtt aacttaactc aagttattga tcccacaaca 4860
caatttagatt acttccccaa gataacattc gaaaggctaa aaaattatga cacaagttca 4920
aattatgtca aaggaaaagct aacaagaaaat tacatgatac tattggccatg gcagcatgtt 4980
aattatgtca actttgtctt tagttctact ggatgttaag ttatgtctgaa aacatgtatt 5040
ggaaaacttca tggaaagactt aaatctaaa gttttgtact ttatggaga aggagcagg 5100
aattggatgg coagaacacgc atgtgaatatac cctgtatattaa aatttgtata tagaagtctg 5160
aaagatgacc ttgatcatca ttatctctg gaataccaga ggtgtatagg tgaattaagc 5220
agaatcatag atagtgggtga aggacttca atggaaacaa cagacgcac tcaaaaaact 5280
cattgggatt tgatcacacag ggtaaacaa gatgtttat taataactt atgtgtatgca 5340
qaatttaagg acagagatga ttttttaag atggtatcc tatggagaaa acatgttata 5400

tcatgcagaa	tttgcactac	ttatgggacg	gacctctatt	tattcgcaaa	gtatcatgtc	5460
aaagactgca	atgtaaaatt	acctttttt	gtgagatcag	ttgctacttt	cattatgcag	5520
ggtagtaagc	tgtcagggttc	agaatgtcac	atactcttaa	cactaggcca	ccacaacagt	5580
ttaccttgcc	atggagaaaat	acaaaattct	aagatgaaaaa	tagcagtgtg	taatgatttt	5640
tatgctgcaa	aaaaactcga	caataaatca	attgaagcta	attgtaaaatc	acttttgtca	5700
gggctaagaa	tacctataaa	taagaaggaa	ctagatagac	agagaagatt	attaacacta	5760
caaagcaatc	attttctgt	ggcaacagtt	ggcggtagca	agatcataga	gtctaaatgg	5820
ttaacaaaca	aagcaagtac	aataattgtat	tggtagaaac	atattttaaa	ttctccaaag	5880
ggcgaattaa	attatgattt	ttttgaagca	ttggagaaca	cttaccctaa	tatgattaaa	5940
ctaatacgata	acttagggaa	tgcagagatt	aaaaaaactta	tcaaagtaac	aggatacagt	6000
cttgtaaagta	aaaaatgta					6018

<210> 40
<211> 6018
<212> DNA
<213> human Metapneumo virus

tcaataggaa gtctatgtca agaactagaa ttccagagggg agagtatact agtttagcttg 2580
 atattaagga atttctggct gtataactg tacatgtatg agtcaaaaaca gcacccatta 2640
 gctgggaagc aactgtcaa gcaattgaac aaaacattaa cattgtgca gagattttt 2700
 gaactgaaga aagaaaatga tgggtgtac ctatggatga atataccaat gcagtttgg 2760
 gggggagatc cagtagttt ttacagatct ttttacagaa ggactcccga ttcctaact 2820
 gaagcaatca gccatgtgaa ttactgtta aaagtgtcaa acaatataa agatgagact 2880
 aagatacgat tttcaaaagc cttattatct atagaaaaa atgaacgtgc tacattaaca 2940
 acactaatga gagaccctca ggcagtagga tcagaacgac aagctaagg aacaagtgt 3000
 ataaaatagaa cagcagttac cagcatactg agtctatctc cgaatcagct cttctgtat 3060
 agtgctatac attatagtag aataggagaa gaagttggg tcaattgcaga caacataaca 3120
 cctgtctatc ctcatggct gagagtgctc tatgaatcac tacctttca taaggctgaa 3180
 aagggttgtca atatgatatac aggcacaaag tctataacta atctattaca gagaacatct 3240
 gctatcaatg gtgaagatat tgatagagca gtgtctatga tggtagagaa cttagggtt 3300
 ttatctagaa tattgtcagt aataattaat agtataaaaa taccaatcaa gtccaatggc 3360
 agattgatatac gctgtcaaatttccaagacc ttgagagaaa aatcatggaa caatatggaa 3420
 atatgaggag tgacatctcc tagtattgtg acatgtatgg atgttgtgta tgcaactagt 3480
 tctcatttaa aaggaataat tattaaaaaa ttcaagttactg acaagaccac aagaggtcag 3540
 aggggaccaa aaagccccgt ggttaggatca agcactcaag agaaaaaaatt gttccctgtt 3600
 tataatagac aaattcttc aaaacaacaa aaagagacaac tggaaagcaat agggaaaaatg 3660
 aggtgggtgt acaaagaac tccagggtca agaagattgc tcaacaagat ttgcatacg 3720
 agcttaggtt ttagctataa atgtgtgaaa ccttattttac caagattcat ggtgtaaac 3780
 ttcttacata ggttatctgt tagtagttaga cccatggaaat tcccaagttc tggccagct 3840
 tacaggacaa caaattacca ttgtacact agtccatca accaagacc aagtgagagg 3900
 ttcgggaaacg aagacattaa tttagtgttca caaaatgcaat tcaagctgcgg aatttagata 3960
 atagatgttg tagaacagtt aactggtaga agcccaaaac aatttagtctt aatccctaa 4020
 ttagaagaga tagatattat gcctccctt gtatttcaag gaaaattcaa ttataaacta 4080
 gttgataaga taaccccgaa tcaacacatc ttcaagttc tcaaaataga catattaaca 4140
 cttagggaaagta gctttagtgc taccataaaaa ggtcaaaaaa ctgatcagtt cttaaataag 4200
 agaaaaaaacttatttcatgg aaataattta attgaatctt tatctgcagc acttgcattgc 4260
 cactgggtgtt ggatattaaac agaacagtgc atagaaaaaca atatctttag gaaagattgg 4320
 ggtgatgggt tcatctcaga tcatgcctt atggattca aggtatttctt atgtgtattt 4380
 aaaacccaaac tttttagttag ttgggatctt caagggaaatg atgtaaaaga tgaagatata 4440
 atagatgaat ccattgacaa attattaaga attgacacaa cctttggag aatgttcagc 4500
 aaagtcatgt ttgaatcaaa agtcaaaaaa agaataatgt tatatgtatg gaaattccct 4560
 tcatttagtag gtttatatagg attaaaaac tggtttatag aacagttaaag agtggtagaa 4620
 ttgcattgagg taccttggat tgcataatgtt gaaggagagt tagttgaaat taaatcaatc 4680
 aaaatttatac tgcagttaat agaacaaatg ctatcttgc tgcataatgtt attgaattat 4740
 acagacatgg cacatgtct tacacgatta attagaaaaa aattgtatgt tgataatgc 4800
 ctcttaatc caagttcattc accaatgtttt aatctaactc aggttatttgc tcccacaaca 4860
 caacttagact attttcttag gataatattt gagaggttac aaagttatgc taccaggatc 4920
 gactacaaca aagggaagtt aacaaggaaat tacatgacat tattaccatg gcaacacgt 4980
 aacaggtaca attttgtctt tagttctaca ggttggaaatg tcaagtttgc gacatgcattc 5040
 gggaaattga taaaggattt aaatcttcaa gttctttact ttattggaga aggagcagg 5100
 aactggatgg caagaacacgc atgtgaatat cctgatataa aatttgatata taggagttt 5160
 aaggatgacc ttgatcaccatc ttaccatcataa gaatataaaa ggttaatagg tgatctaaat 5220
 agggtgatag atagtggta aggattatca atggaaacca cagatgcac tcaaaaaact 5280
 cattgggact tgcatacag aataagttt gatgtttat tgcataatgtt gtgtgtatgc 5340
 gaattcaaaa acagagatgtt ttcttttaag atggtaatcc ttggagaaa acatgtatca 5400
 ttctgttagaa tctgtacacgc ttatggaaaca gatctttact tatttgcacaa gtatcatgc 5460
 gtggactgc atataaaaattt accatttttt gtaagatctg tagctacttt tattatgcac 5520
 ggaagcaat tatcagggtc agaatgttac atactttaa cattaggtca tcacaataat 5580
 ctaccctgtc atggagaaaatc accaaaattcc aaaatgagaa tagcagtgtg taatgattc 5640
 tatgcctca agaaactgga caacaaatca attgaacaa actgcaatc tcttctatca 5700
 ggattgagaa tacctataaa caaaaaggag ttaaatagac aaaagaaaattt gttiacacta 5760
 caaaagtaacc attcttctat agcaacagttt ggcggcagta agattataga atccaaatgg 5820
 ttaaaagaata aagcaagtac aataattgtat ggttagagc atattttgaa ttctccaaaa 5880
 ggtgaattaa actatgattt ctttgaagca ttagagaaca cataccccaa tatgatcaag 5940
 cttatagata atttggaaa tgcagaaata aagaaactaa tcaaggtcac tgggtatatg 6000
 cttgtgagta agaagttaa 6018

<210> 41
<211> 6018
<212> DNA
<213> human Metapneumo virus

<400> 41
atggatccat tttgtgaatc cactgtcaat gtttatcttc ctgactcata tctcaaagga 60
gtaatatctt tcagtgaac caatgcattt ggctcatgcc ttttggaaaag accctatcta 120
aaaaaaagata acactgctaa agttgctgtt gaaaaccctg ttgttgaaca tgtcaggcgtt 180
agaaatgcag tcatgaccaa aatgaagata tcagattata aagtgggttga accaattaat 240
atgcagcatg aaataatgaa aaatatacac agttgtgagc tcacattattt aaaacaattc 300
ttaacaagaa gtaaaaaacat tagctctcta aaattaagta tgatatgtga ttgggttacag 360
ttaaaaatcca cctcagataa cacatcaattt ctttttttta tagatgtgga gtttataacct 420
gtttgggtga gcaatttggtt tagtaactgg tataatctca ataaaattaat ctttagagttt 480
agaagagagg aagtaataag aactgggtca attttatgtt gatcacttagg caagtttagt 540
ttcattgtat catcttatgg gtgtgttagt aaaaagcaaca aaagtaaaaag agtaagtttt 600
ttcacatata accaactgtt aacatggaaa gatgtgtatgt taatgttagtt caatgcaaac 660
ttttgtatata gggtaagtaa caacctgaac aaaaatcaag aaggactagg atttagaaagt 720
aatotgcaag gtatgtttaac caataaaatta tatgaaaactg ttgatttatat tttaagtctt 780
tgttagtaatg aagggttctc actagtggaa gagttcgaag gcttttattt ggttggaaattt 840
cttaaaaatta ctgagcatgc tcaattcagt actaggtt ggaatactttt attaaatggg 900
ttgactgaac aattatcaat gttgaaagct aaaaacagat cttagtttct tggcactata 960
tttagaaaaca atgattaccc catgtatgg ttagactttaa aattattagg ggacactttg 1020
aaaagtataa aattatcaat taacaagaat tttagaaaatg ctgcagaattt atattatata 1080
ttcagaattt ttggcacaccc tatggtagat gagagggaag caatggatgc tttttttttt 1140
aataatgaga ttacaaaaat tctttttttt tttttttttt tttttttttt tttttttttt 1200
atactaagaa ttataaaaagg gttttagat aataataaaa gatggccttaa aattaagaat 1260
ttaaaaagtgc tcagtaaaag atgggttatg tatttcaaaag cccaaaagttt ccctagccaa 1320
cttgagctaa gtgtacaaga tttttttttt tttttttttt tttttttttt tttttttttt 1380
tctgtccctg aaaaacccaa ccttggatgtt gtattttttttt ataaagcaat atctccttcca 1440
aaaaagttaa tatggctggt atatccaaa aattatctac ctgaaatttat aaaaatccaa 1500
tatttagaaag aggtcttcaa tgcaagtgc agtcaagaa cgaggagagt tttagaaattt 1560
tacttaaaag attgcaaaattt tgatcaaaaaa gaccttaaac gttatgtact taaacaagag 1620
tatctaaatg acaaagacca cattgtctca ttaactggg aggaaagaga attaagtgtt 1680
ggcaggatgt ttgcaatgca accaggccaa caaagacaaa tacagatact agctgagaaa 1740
cttctagctg ataataatgtt acccttttttcc ccagaaaactt taacaaagttt tggtgacttg 1800
gatctccaaa gaattatggaa aatgaaatca gaaactttttt ccattttttt taggaagaat 1860
gatagttaca acaatttatat tcaagagcc tccatagttt cagacccatg taaattttttt 1920
caaggcccttta gatatgaaac cacagcttcc tttttttttt tttttttttt tttttttttt 1980
acgcaaaagct tttttttttt gtttacatctt tttttttttt tttttttttt tttttttttt 2040
tacagacatg caccaccaga aacaaaggggg gtttacatctt tttttttttt tttttttttt 2100
agtgggccttta acagatataca tttttttttt tttttttttt tttttttttt tttttttttt 2160
atggaaagcgaa tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2220
ctattaaacg gagacaatca atcaatagat gtttacatctt tttttttttt tttttttttt 2280
atagatgaag taaaagcaga ttatagctt gtttacatctt tttttttttt tttttttttt 2340
gcctataaaa acattggccaa taaactcaaa gtttacatctt tttttttttt tttttttttt 2400
caattttataa gtttacatctt tttttttttt tttttttttt tttttttttt tttttttttt 2460
atattaagggg taggtccctg gataaaataca tttttttttt tttttttttt tttttttttt 2520
tcaataggga gtttacatctt tttttttttt tttttttttt tttttttttt tttttttttt 2580
atattaaggga tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2640
gctggaaaac aactgtttttaa gtttacatctt tttttttttt tttttttttt tttttttttt 2700
gagctgaaga aagaaaatgtt gtttacatctt tttttttttt tttttttttt tttttttttt 2760
gggggagacc cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2820
gaagcaatca gtttacatctt tttttttttt tttttttttt tttttttttt tttttttttt 2880
aagatacgt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2940
acactaatgtt gtttacatctt tttttttttt tttttttttt tttttttttt tttttttttt 3000
ataaaatagaa cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 3060
agtgcatac actatagcag aaatgaagaa gtttacatctt tttttttttt tttttttttt 3120
cctgtttatc cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 3180
aagggttgcatac atatgtatc aggtacaaag tttttttttt tttttttttt tttttttttt 3240
gttatcaatg gtgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt 3300
ttatcttagga tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 3360

aggttgcataat	gctgtcaaat	ttctaagact	ttgagagaaa	aatcatggaa	caatatggaa	3420
atagtagggag	tgacatctcc	aagtattgt	acatgtatgg	atgttgtta	tgcaactagt	3480
tctcatttaa	aaggaaataat	tattaaaaaa	ttcagtactg	acaagaccac	aagaggctcg	3540
aggggaccaa	aaagccccctg	ggtaggatca	agcactcaag	agaaaaaatt	agttccttgtt	3600
tataatagac	aaattcttc	aaaacaacaa	aaggagcaac	tggaagcaat	agggaaaatg	3660
aggtgggtgt	ataaaaggaac	tccagggcta	agaagattgc	tcaataagat	ttgcata>tagga	3720
agtttaggtt	ttagctataa	atgtgtaaaa	ccttctattac	caagattcat	gagtgtaaac	3780
tcttacata	ggtatctgt	tagtagcaga	cccattgaaat	tcccagcttc	tgttccagct	3840
tataggacaa	caaattacca	ctttgacact	agtccaaatca	accaagcatt	aagtgagagg	3900
ttcgggAACG	aagacattaa	tctagtgtt	caaaatgcaa	tcagctgcgg	aattagtata	3960
atgagtgtt	tagaacagtt	aactggtaga	agccaaaac	aattagtctt	aatcccccaa	4020
ttagaagaga	tagatattat	gcctccctct	gtatttcaag	gaaaattcaa	ttataaacta	4080
gttataaaaa	taacctctga	tcaacacatc	ttcagtccctg	acaaaataga	cattaaca	4140
ctagggaaaga	tgtttatgcc	tactataaaa	ggtcaaaaaaa	ctgatcatgtt	cttaaataag	4200
agagaaaact	atttccatgg	aaataattha	atgaatctt	tatctgcagc	acttgcattc	4260
cactgggtg	gaatattaac	agaacagtgt	gtagaaaaaca	atatctttag	gaaagactgg	4320
ggtgcgttgtt	tcatatcaga	tcatgccttc	atgatttca	agatatttct	atgtgtatTT	4380
aaaaccaaaaac	ttttatgttag	ttggggatcc	caaggaaaaaa	atgtaaaaga	tgaagatata	4440
atagtagaat	ccattgacaa	attattaaga	attgacaaca	ctttttggag	aatgttcagc	4500
aaagtcatgt	ttgaatcaaa	ggtcaaaaaaa	agaataatgt	tatatgatgt	aaaattccta	4560
tcattatgt	gttatataagg	attttttttt	tggttttag	agcagttaa	agtagtagaa	4620
ttgcataag	tgccctggat	tgtcaatgt	gaaggggagc	tagttgaaat	taaaccatc	4680
aaaattttatt	tgcatgttaat	agaacaagt	ctatctttaa	gaataactgt	tttgaattat	4740
acagacatgg	cacatgctct	tacacgatta	attaggaaga	aattgtatgt	tgataatgc	4800
ctcttcaatc	caagttcatc	accaatgttt	agtctaaatc	aagttatcga	tcctacaaca	4860
cagctagact	atttccttaa	ggtgatattt	gaaaggttaa	aaagttatga	taccagttc	4920
gactacaaca	aaggaaagtt	aacaagaaat	tacatgacat	tattaccatg	gcagcacgt	4980
aacagggtata	atttgtctt	tagttcaaca	ggatgtaaaaa	tcagcttga	gacatgcac	5040
gggaaattga	taaaggactt	aaacccttaag	gttctttact	ttattggaga	aggagcagg	5100
aactggatgg	caagaacacg	atgtgagttt	cctgacataaa	aatttgtata	taggagttt	5160
aaggatgatc	ttgatcatca	ttacccatta	gaatatcaaa	gggtatagg	tgattttaaat	5220
agggtatata	atgggtgtga	aggactatca	atggagacca	cagatgcac	tcaaaagact	5280
cattgggact	taatacacag	aataagtaaa	gatgttttat	tgataacatt	gtgtgtatgc	5340
gaattcaaaa	acagagatga	tttttttttt	atgttaatcc	tttggagaaa	acatgtatta	5400
tcatgtatgg	tctgtacagc	ttatggaaaca	gatctttact	tatttgcataa	gtatcatgc	5460
acggactgca	atataaaatt	accatttttt	gtaaggctgt	tagtacttt	tattatgca	5520
ggaagcaaat	tgtcaggatc	agaatgttac	atacttttaa	cattaggtca	tcacaataat	5580
ctggcatgcc	atggagaaaat	acaaaattcc	aaaatgagaa	tagcagttg	taatgattc	5640
catgcctcaa	aaaaactaga	caacaaatca	atgaaagcta	actgtaaatc	tcttctatca	5700
ggattaagaa	taccaataaa	caaaaaagag	ttaaatagac	aaaagaaact	gttaacacta	5760
caaagcaatc	attcttccat	agcaacagtt	ggccggcagta	agattataga	atccaaatgg	5820
ttaaaagaata	aagcaagttac	aataattgtat	tggtagagc	atatcttga	ttctccaaaa	5880
ggtgaattaa	actatgattt	ctttgaagca	ttagagaaca	catacccaa	tatgtatcaag	5940
cttatacgata	acctggggaaa	tgcagagata	aaaaaaactaa	tcaaagtcc	tgggtatatg	6000
cttgcgtatgt	agaagttaa					6018

<210> 42
<211> 187
<212> PRT
<213> human Metapneumo virus

```

<400> 42
Met Ser Arg Lys Ala Pro Cys Lys Tyr Glu Val Arg Gly Lys Cys Asn
      5          10          15
      1
Arg Gly Ser Glu Cys Lys Phe Asn His Asn Tyr Trp Ser Trp Pro Asp
      20         25          30
      35
Arg Tyr Leu Leu Ile Arg Ser Asn Tyr Leu Leu Asn Gln Leu Leu Arg
      40          45
      50
Asn Thr Asp Arg Ala Asp Gly Leu Ser Ile Ile Ser Gly Ala Gly Arg
      55          60

```

Glu Asp Arg Thr Gln Asp Phe Val Leu Gly Ser Thr Asn Val Val Gln
 65 70 75 80
 Gly Tyr Ile Asp Asp Asn Gln Ser Ile Thr Lys Ala Ala Ala Cys Tyr
 85 90 95
 Ser Leu His Asn Ile Ile Lys Gln Leu Gln Glu Val Glu Val Arg Gln
 100 105 110
 Ala Arg Asp Asn Lys Leu Ser Asp Ser Lys His Val Ala Leu His Asn
 115 120 125
 Leu Val Leu Ser Tyr Met Glu Met Ser Lys Thr Pro Ala Ser Leu Ile
 130 135 140
 Asn Asn Leu Lys Arg Leu Pro Arg Glu Lys Leu Lys Lys Leu Ala Lys
 145 150 155 160
 Leu Ile Ile Asp Leu Ser Ala Gly Ala Glu Asn Asp Ser Ser Tyr Ala
 165 170 175
 Leu Gln Asp Ser Glu Ser Thr Asn Gln Val Gln
 180 185

<210> 43

<211> 187

<212> PRT

<213> human Metapneumo virus

<400> 43

Met Ser Arg Lys Ala Pro Cys Lys Tyr Glu Val Arg Gly Lys Cys Asn
 1 5 10 15
 Arg Gly Ser Glu Cys Lys Phe Asn His Asn Tyr Trp Ser Trp Pro Asp
 20 25 30
 Arg Tyr Leu Leu Ile Arg Ser Asn Tyr Leu Leu Asn Gln Leu Leu Arg
 35 40 45
 Asn Thr Asp Arg Ala Asp Gly Leu Ser Ile Ile Ser Gly Ala Gly Arg
 50 55 60
 Glu Asp Arg Thr Gln Asp Phe Val Leu Gly Ser Thr Asn Val Val Gln
 65 70 75 80
 Gly Tyr Ile Asp Asp Asn Gln Ser Ile Thr Lys Ala Ala Ala Cys Tyr
 85 90 95
 Ser Leu His Asn Ile Ile Lys Gln Leu Gln Glu Val Glu Val Arg Gln
 100 105 110
 Ala Arg Asp Ser Lys Leu Ser Asp Ser Lys His Val Ala Leu His Asn
 115 120 125
 Leu Ile Leu Ser Tyr Met Glu Met Ser Lys Thr Pro Ala Ser Leu Ile
 130 135 140
 Asn Asn Leu Lys Arg Leu Pro Arg Glu Lys Leu Lys Lys Leu Ala Lys
 145 150 155 160
 Leu Ile Ile Asp Leu Ser Ala Gly Ala Asp Asn Asp Ser Ser Tyr Ala
 165 170 175
 Leu Gln Asp Ser Glu Ser Thr Asn Gln Val Gln
 180 185

<210> 44

<211> 187

<212> PRT

<213> human Metapneumo virus

<400> 44

Met Ser Arg Lys Ala Pro Cys Lys Tyr Glu Val Arg Gly Lys Cys Asn
 1 5 10 15
 Arg Gly Ser Asp Cys Lys Phe Asn His Asn Tyr Trp Ser Trp Pro Asp
 20 25 30
 Arg Tyr Leu Leu Arg Ser Asn Tyr Leu Leu Asn Gln Leu Leu Arg
 35 40 45

Asn Thr Asp Lys Ala Asp Gly Leu Ser Ile Ile Ser Gly Ala Gly Arg
 50 55 60
 Glu Asp Arg Thr Gln Asp Phe Val Leu Gly Ser Thr Asn Val Val Gln
 65 70 75 80

 Gly Tyr Ile Asp Asp Asn Gln Gly Ile Thr Lys Ala Ala Ala Cys Tyr
 85 90 95
 Ser Leu His Asn Ile Ile Lys Gln Leu Gln Glu Thr Glu Val Arg Gln
 100 105 110
 Ala Arg Asp Asn Lys Leu Ser Asp Ser Lys His Val Ala Leu His Asn
 115 120 125
 Leu Ile Leu Ser Tyr Met Glu Met Ser Lys Thr Pro Ala Ser Leu Ile
 130 135 140
 Asn Asn Leu Lys Lys Leu Pro Arg Glu Lys Leu Lys Lys Leu Ala Arg
 145 150 155 160
 Leu Ile Ile Asp Leu Ser Ala Gly Thr Asp Asn Asp Ser Ser Tyr Ala
 165 170 175
 Leu Gln Asp Ser Glu Ser Thr Asn Gln Val Gln
 180 185

<210> 45
 <211> 187
 <212> PRT
 <213> human Metapneumo virus

<400> 45
 Met Ser Arg Lys Ala Pro Cys Lys Tyr Glu Val Arg Gly Lys Cys Asn
 1 5 10 15
 Arg Gly Ser Glu Cys Lys Phe Asn His Asn Tyr Trp Ser Trp Pro Asp
 20 25 30
 Arg Tyr Leu Leu Leu Arg Ser Asn Tyr Leu Leu Asn Gln Leu Leu Arg
 35 40 45
 Asn Thr Asp Lys Ala Asp Gly Leu Ser Ile Ile Ser Gly Ala Gly Arg
 50 55 60
 Glu Asp Arg Thr Gln Asp Phe Val Leu Gly Ser Thr Asn Val Val Gln
 65 70 75 80
 Gly Tyr Ile Asp Asn Asn Gln Gly Ile Thr Lys Ala Ala Ala Cys Tyr
 85 90 95
 Ser Leu His Asn Ile Ile Lys Gln Leu Gln Glu Ile Glu Val Arg Gln
 100 105 110
 Ala Arg Asp Asn Lys Leu Ser Asp Ser Lys His Val Ala Leu His Asn
 115 120 125
 Leu Ile Leu Ser Tyr Met Glu Met Ser Lys Thr Pro Ala Ser Leu Ile
 130 135 140
 Asn Asn Leu Lys Lys Leu Pro Arg Glu Lys Leu Lys Lys Leu Ala Lys
 145 150 155 160
 Leu Ile Ile Asp Leu Ser Ala Gly Thr Asp Asn Asp Ser Ser Tyr Ala
 165 170 175
 Leu Gln Asp Ser Glu Ser Thr Asn Gln Val Gln
 180 185

<210> 46
 <211> 564
 <212> DNA
 <213> human Metapneumo virus

<400> 46
 atgtctcgca aggctccgtg caaatatgaa gtgcggggca aatgcaatag aggaagttag 60
 tgcaagttta accacaatta ctggagttgg ccagatagat acttattaaat aagatcaaat 120
 tatttattaa atcaacttt aaggaacact gatagagctg atggcttatac aataatatac 180

ggaggcaggca gagaagatag gacacaagat tttgtcctag gttccaccaa tggggttcaa 240
 gtttatgg atgataacca aagcataaca aaagctgcag cctgttacag tctacataat 300
 ataatcaaac aactacaaga agttgaagtt aggccaggcta gagataacaa actatctgac 360
 agcaaacatg tagcacttca caacttagtc ctatcttata tggagatgag caaaaactcct 420
 gcatctttaa tcaacaatct caagagactg ccgagagaga aactaaaaaa attagcaaag 480
 ctcataattg acttatacgc aggtgctgaa aatgacttt catatgcctt gcaagacagt 540
 gaaagcacta atcaagtgca gtga 564

<210> 47
 <211> 564
 <212> DNA
 <213> human Metapneumo virus

<400> 47
 atgtctcgca aggctccatg caaatatgaa gtgcggggca aatgcaacag aggaagttag 60
 tgtaagttt accacaatta ctggagttgg ccagatagat acttattaat aagatcaaac 120
 tatctttaa atcagcttt aaggaacact gataaggctg atggcttgc aataatatca 180
 ggccgaggca gagaagacag aacgcaagat tttgttctag gttccaccaa tggggttcaa 240
 ggttatattg atgataacca aagcataaca aaagctgcag cctgttacag tctacacaac 300
 ataatcaagc aactacaaga agttgaagtt aggccaggcta gagatagcaa actatctgac 360
 agcaagcatg tggcacttca taacttaatc ttatcttata tggagatgag caaaaactccc 420
 gcatctttaa tcaacaatct taaaagactg ccgagagaaa aactaaaaaa attagcaaag 480
 ctgataattg acttatacgc aggcgctgac aatgacttt catatgcctt gcaagacagt 540
 gaaagcacta atcaagtgca gtga 564

<210> 48
 <211> 564
 <212> DNA
 <213> human Metapneumo virus

<400> 48
 atgtctcgta aggctccatg caaatatgaa gtgcggggca aatgcaacag agggagtgtat 60
 tgcaaattca atcacaatta ctggagttgg cctgataat atttattgtt aagatcaaat 120
 tatctttaa atcagcttt aagaaacaca gataaggctg atggtttgc aataatatca 180
 ggagcaggta gagaagatag aactcaagac tttgttcttgc gttctactaa tggggttcaa 240
 gggtacattg atgacaacca aggaataacc aaggctgcag cttgctatag tctacacaac 300
 ataatcaagc aactacaaga aacagaagta agacaggcta gagacaacaa gctttctgtat 360
 agcaaacatg tggcgttcca caacttgata ttatcctata tggagatgag caaaaactcct 420
 gcatctctaa tcaacaacct aaagaaacta ccaaggaaaa aactgaagaa attagcaaga 480
 ttaataattg atttatacgc aggaactgac aatgacttt catatgcctt gcaagacagt 540
 gaaagcacta atcaagtgca gtaa 564

<210> 49
 <211> 564
 <212> DNA
 <213> human Metapneumo virus

<400> 49
 atgtctcgca aagctccatg caaatatgaa gtacggggca agtgcacacag gggaaagttag 60
 tgcaaattca accacaatta ctggagctgg cctgataat atttattgtt aagatcaaat 120
 tatcttctgta atcagcttt aagaaacact gataaggctg atggtttgc aataatatca 180
 ggagcaggta gagaagatag gactcaagac tttgttcttgc gttctactaa tggggttcaa 240
 gggtacattg ataacaatca aggaataaca aaggctgcag cttgctatag tctacataac 300
 ataataaaac agctacaaga aatagaagta agacaggcta gagataataa gctttctgtac 360
 agcaaacatg tggcacttca caacttgata ttatcctata tggagatgag caaaaactcct 420
 gcatccctga ttaataacct aaagaaacta ccaaggaaaa aactgaagaa attagcgaaa 480
 ttaataattg atttatacgc aggaactgat aatgacttt catatgcctt gcaagacagt 540
 gaaagcacta atcaagtgca gtaa 564

<210> 50
 <211> 71
 <212> PRT

<213> human Metapneumo virus

<400> 50
Met Thr Leu His Met Pro Cys Lys Thr Val Lys Ala Leu Ile Lys Cys
1 5 10 15
Ser Glu His Gly Pro Val Phe Ile Thr Ile Glu Val Asp Asp Met Ile
20 25 30
Trp Thr His Lys Asp Leu Lys Glu Ala Leu Ser Asp Gly Ile Val Lys
35 40 45
Ser His Thr Asn Ile Tyr Asn Cys Tyr Leu Glu Asn Ile Glu Ile Ile
50 55 60
Tyr Val Lys Ala Tyr Leu Ser
65 70

<210> 51

<211> 71

<212> PRT

<213> human Metapneumo virus

<400> 51
Met Thr Leu His Met Pro Cys Lys Thr Val Lys Ala Leu Ile Lys Cys
1 5 10 15
Ser Glu His Gly Pro Val Phe Ile Thr Ile Glu Val Asp Glu Met Ile
20 25 30
Trp Thr Gln Lys Glu Leu Lys Glu Ala Leu Ser Asp Gly Ile Val Lys
35 40 45
Ser His Thr Asn Ile Tyr Asn Cys Tyr Leu Glu Asn Ile Glu Ile Ile
50 55 60
Tyr Val Lys Ala Tyr Leu Ser
65 70

<210> 52

<211> 71

<212> PRT

<213> human Metapneumo virus

<400> 52
Met Thr Leu His Met Pro Cys Lys Thr Val Lys Ala Leu Ile Lys Cys
1 5 10 15
Ser Lys His Gly Pro Lys Phe Ile Thr Ile Glu Ala Asp Asp Met Ile
20 25 30
Trp Thr His Lys Glu Leu Lys Glu Thr Leu Ser Asp Gly Ile Val Lys
35 40 45
Ser His Thr Asn Ile Tyr Ser Cys Tyr Leu Glu Asn Ile Glu Ile Ile
50 55 60
Tyr Val Lys Thr Tyr Leu Ser
65 70

<210> 53

<211> 71

<212> PRT

<213> human Metapneumo virus

<400> 53

Met Thr Leu His Met Pro Cys Lys Thr Val Lys Ala Leu Ile Lys Cys
1 5 10 15
Ser Lys His Gly Pro Lys Phe Ile Thr Ile Glu Ala Asp Asp Met Ile
20 25 30
Trp Thr His Lys Glu Leu Lys Glu Thr Leu Ser Asp Gly Ile Val Lys

35	40	45
Ser His Thr Asn Ile Tyr Ser Cys Tyr Leu Glu Asn Ile Glu Ile Ile		
50	55	60
Tyr Val Lys Ala Tyr Leu Ser		
65	70	

<210> 54
<211> 216
<212> DNA
<213> human Metapneumo virus

<400> 54
atgactcttc atatgccttg caagacagtg aaagcactaa tcaagtgcag tgagcatgg 60
ccagtttca ttactataga ggtttagatgc atgatatgg ctcacaagg cttaaaagaa 120
gcttatctg atggatagt gaagtctcat actaacattt acaattgtta ttttagaaaac 180
atagaaatta tatatgtcaa ggcttactta agttag 216

<210> 55
<211> 216
<212> DNA
<213> human Metapneumo virus

<400> 55
atgactcttc atatgccttg caagacagtg aaagcactaa tcaagtgcag tgagcatgg 60
cctgtttca ttactataga ggtttagatgc atgatatgg ctcacaaaaga attaaaagaa 120
gcttgcctg atggatagt gaagtctcac accaacattt acaattgtta ttttagaaaac 180
atagaaatta tatatgtcaa ggcttactta agttag 216

<210> 56
<211> 216
<212> DNA
<213> human Metapneumo virus

<400> 56
atgactcttc atatgccttg caagacagtg aaagcactaa tcaagtgcag taaaacatgg 60
cccaaattca ttaccataga ggcagatgt atgatatgg ctcacaaaaga attaaaagaa 120
acactgtctg atggatagt aaaatcacac accaatattt atagttgtta ctttagaaaat 180
atagaaataa tatatgttaa aacttactta agttag 216

<210> 57
<211> 216
<212> DNA
<213> human Metapneumo virus

<400> 57
atgactcttc atatgccttg caagacagtg aaagcactaa tcaagtgcag taagcatgg 60
cccaaattca ttaccataga ggcagatgt atgatatgg cacacaaaaga attaaaaggag 120
acactgtctg atggatagt aaaatcacac accaatattt acagttgtta ttttagaaaat 180
atagaaataa tatatgttaa agcttactta agttag 216

<210> 58
<211> 727
<212> DNA
<213> human Metapneumo virus

<400> 58
atgtctcgca aggctccgtg caaatatgaa gtgcgggca aatgcaatag aggaagttag 60
tgcaagtttta accacaattt ctggatgttgg ccagatagat acttattaat aagatcaa 120
tatttttttta atcaactttt aaggaacact gatagagctg atggcttatac aataatatca 180
ggagcaggca gagaagatag gacacaagat tttgtccatg gttccaccaa tgggttcaa 240
ggttatatttgc atgataacca aagcataaca aaagctgcag cctgttacag tctacataat 300

ataatcaaac aactacaaga agttgaagtt aggcaggcta gagataacaa actatctgac 360
 agcaaacatg tagcacttca caacttagtc ctatcttata tggagatgag caaaactcct 420
 gcatctttaa tcaacaatct caagagactg ccgagagaga aactgaaaaaa attagcaaag 480
 ctataatttgcg acttattcgc aggtgctgaa aatgactt catatgcctt gcaagacagt 540
 gaaagacta atcaagtgc a gtgagcatgg tccagtttc attactatag aggttgatga 600
 catgatatgg actcacaagg acttaaaaga agcttatct gatggatag tgaagtctca 660
 tactaacatt tacaattgtt atttagaaaa catagaaatt atatatgtca aggcttactt 720
 aagttag 727

<210> 59

<211> 727

<212> DNA

<213> human Metapneumo virus

<400> 59

atgtctcgca aggctccatg caaatatgaa gtgcgggca aatgcaacag aggaagttag 60
 tgtaagttt accacaatta ctggagttgg ccagatagat acttattaat aagatcaaac 120
 tatctttaa atcagcttt aaggaacact gataaggctg atggccttca aataatatca 180
 ggcgcaggca gagaagacag aacgcaagat tttgttctag gtccaccaa tgtggtcaa 240
 gtttatattt atgataacca aagcataaca aaagctgcag cctgctacag tctacacaac 300
 ataatcaagc aactacaaga agttgaagtt aggcaggcta gagatagcaa actatctgac 360
 agcaagcatg tggcactcca taacttata ttatcttca tgagatgag caaaactccc 420
 gcatctttaa tcaacaatct taaaagactg ccgagagaaa aactgaaaaaa attagcaaag 480
 ctgataatttgcg acttattcgc aggcgcgtgaa aatgactt catatgcctt gcaagacagt 540
 gaaagacta atcaagtgc a gtgagcatgg tcccttttcc attactatag aggttgatga 600
 aatgatatgg actcacaagg aattaaaaga agctttgtcc gatggatag tgaagtctca 660
 caccacacatt tacaattgtt atttagaaaa catagaaatt atatatgtca aggcttactt 720
 aagttag 727

<210> 60

<211> 727

<212> DNA

<213> human Metapneumo virus

<400> 60

atgtctcgta aggctccatg caaatatgaa gtgcgggca aatgcaacag agggagtgat 60
 tgcaaattca atcacaatta ctggagttgg cctgatagat atttattgtt aagatcaaat 120
 tatctcttaa atcagcttt aagaaacaca gataaggctg atggtttgc aataatatca 180
 ggagcaggtt gagaagatag aactcaagac tttgttctt gttctactaa tgtggtcaa 240
 ggttacattt atgacaacca aggaataacc aaggctgcag cttgctatag tctacacaac 300
 ataatcaagc aactacaaga aacagaagta agacaggcta gagacaacaa gctttctgat 360
 agcaaacatg tggcgctcca caacttgcata ttatcttata tgagatgag caaaactcct 420
 gcatctcttaa tcaacaacact aagaaacacta ccaaggaaa aactgaagaa attagcaaga 480
 ttataatttgcg atttacatgc aggaactgac aatgactt catatgcctt gcaagacagt 540
 gaaagacta atcaagtgc a gtaaacatgg tcccaaatttcc attaccatag aggcagatga 600
 tatgatatgg actcacaagg aattaaaaga aacactgtct gatggatag taaaatcaca 660
 caccatatttataatttgcg atttacatgg tcccaaatttcc attaccatag aggcagatga 720
 aagttag 727

<210> 61

<211> 727

<212> DNA

<213> human Metapneumo virus

<400> 61

atgtctcgca aagctccatg caaatatgaa gtacgggca agtgcaacag gggagtgag 60
 tgcaaattca accacaatta ctggagctgg cctgatagat atttattgtt aagatcaaat 120
 tatctcttgcg atcagcttt aagaaacact gataaggctg atggtttgc aataatatca 180
 ggagcaggtt gagaagatag gactcaagac tttgttctt gttctactaa tgtggtcaa 240
 ggttacattt ataaacatca aggaataacc aaggctgcag cttgctatag tctacataac 300
 ataataaaac agctacaaga aatagaagta agacaggcta gagataataa gctttctgac 360
 agcaaacatg tggcacttca caacttgcata ttatcttata tgagatgag caaaactcct 420

gcatccctga ttaataaacct aaagaaaacta ccaagagaaaa aactgaagaa attagcgaaa 480
 ttaataattg atttatcgc aggaactgat aatgacttt catatgcctt gcaagacagt 540
 gaaagcacta atcaagtca gtaagcatgg tcccaaattc attaccatag aggcatgta 600
 tatgatatgg acacacaaaag aattaaagga gacactgtct gatgggatag taaaatcaca 660
 caccaattt tacagttgtt atttagaaaa tatagaaaata atatatgtta aagcttactt 720
 aagttag 727

<210> 62
 <211> 254
 <212> PRT
 <213> human Metapneumo virus

<400> 62
 Met Glu Ser Tyr Leu Val Asp Thr Tyr Gln Gly Ile Pro Tyr Thr Ala
 1 5 10 15
 Ala Val Gln Val Asp Leu Ile Glu Lys Asp Leu Leu Pro Ala Ser Leu
 20 25 30
 Thr Ile Trp Phe Pro Leu Phe Gln Ala Asn Thr Pro Pro Ala Val Leu
 35 40 45
 Leu Asp Gln Leu Lys Thr Leu Thr Ile Thr Leu Tyr Ala Ala Ser
 50 55 60
 Gln Asn Gly Pro Ile Leu Lys Val Asn Ala Ser Ala Gln Gly Ala Ala
 65 70 75 80
 Met Ser Val Leu Pro Lys Lys Phe Glu Val Asn Ala Thr Val Ala Leu
 85 90 95
 Asp Glu Tyr Ser Lys Leu Glu Phe Asp Lys Leu Thr Val Cys Glu Val
 100 105 110
 Lys Thr Val Tyr Leu Thr Thr Met Lys Pro Tyr Gly Met Val Ser Lys
 115 120 125
 Phe Val Ser Ser Ala Lys Ser Val Gly Lys Lys Thr His Asp Leu Ile
 130 135 140
 Ala Leu Cys Asp Phe Met Asp Leu Glu Lys Asn Thr Pro Val Thr Ile
 145 150 155 160
 Pro Ala Phe Ile Lys Ser Val Ser Ile Lys Glu Ser Glu Ser Ala Thr
 165 170 175
 Val Glu Ala Ala Ile Ser Ser Glu Ala Asp Gln Ala Leu Thr Gln Ala
 180 185 190
 Lys Ile Ala Pro Tyr Ala Gly Leu Ile Met Ile Met Thr Met Asn Asn
 195 200 205
 Pro Lys Gly Ile Phe Lys Lys Leu Gly Ala Gly Thr Gln Val Ile Val
 210 215 220
 Glu Leu Gly Ala Tyr Val Gln Ala Glu Ser Ile Ser Lys Ile Cys Lys
 225 230 235 240
 Thr Trp Ser His Gln Gly Thr Arg Tyr Val Leu Lys Ser Arg
 245 250

<210> 63
 <211> 254
 <212> PRT
 <213> human Metapneumo virus

<400> 63
 Met Glu Ser Tyr Leu Val Asp Thr Tyr Gln Gly Ile Pro Tyr Thr Ala
 1 5 10 15
 Ala Val Gln Val Asp Leu Val Glu Lys Asp Leu Leu Pro Ala Ser Leu
 20 25 30
 Thr Ile Trp Phe Pro Leu Phe Gln Ala Asn Thr Pro Pro Ala Val Leu
 35 40 45
 Leu Asp Gln Leu Lys Thr Leu Thr Ile Thr Leu Tyr Ala Ala Ser
 50 55 60
 Gln Ser Gly Pro Ile Leu Lys Val Asn Ala Ser Ala Gln Gly Ala Ala

65	70	75	80
Met Ser Val Leu Pro Lys Lys Phe Glu Val Asn Ala Thr Val Ala Leu			
85	90	95	
Asp Glu Tyr Ser Lys Leu Glu Phe Asp Lys Leu Thr Val Cys Glu Val			
100	105	110	
Lys Thr Val Tyr Leu Thr Thr Met Lys Pro Tyr Gly Met Val Ser Lys			
115	120	125	
Phe Val Ser Ser Ala Lys Ser Val Gly Lys Lys Thr His Asp Leu Ile			
130	135	140	
Ala Leu Cys Asp Phe Met Asp Leu Glu Lys Asn Thr Pro Val Thr Ile			
145	150	155	160
Pro Ala Phe Ile Lys Ser Val Ser Ile Lys Glu Ser Ala Thr			
165	170	175	
Val Glu Ala Ala Ile Ser Ser Glu Ala Asp Gln Ala Leu Thr Gln Ala			
180	185	190	
Lys Ile Ala Pro Tyr Ala Gly Leu Ile Met Ile Met Thr Met Asn Asn			
195	200	205	
Pro Lys Gly Ile Phe Lys Lys Leu Gly Ala Gly Thr Gln Val Ile Val			
210	215	220	
Glu Leu Gly Ala Tyr Val Gln Ala Glu Ser Ile Ser Lys Ile Cys Lys			
225	230	235	240
Thr Trp Ser His Gln Gly Thr Arg Tyr Val Leu Lys Ser Ser			
245	250		

<210> 64
<211> 254
<212> PRT
<213> human Metapneumo virus

<400> 64			
Met Glu Ser Tyr Leu Val Asp Thr Tyr Gln Gly Ile Pro Tyr Thr Ala			
1	5	10	15
Ala Val Gln Val Asp Leu Val Glu Lys Asp Leu Leu Pro Ala Ser Leu			
20	25	30	
Thr Ile Trp Phe Pro Leu Phe Gln Ala Asn Thr Pro Pro Ala Val Leu			
35	40	45	
Leu Asp Gln Leu Lys Thr Leu Thr Ile Thr Thr Leu Tyr Ala Ala Ser			
50	55	60	
Gln Asn Gly Pro Ile Leu Lys Val Asn Ala Ser Ala Gln Gly Ala Ala			
65	70	75	80
Met Ser Val Leu Pro Lys Lys Phe Glu Val Asn Ala Thr Val Ala Leu			
85	90	95	
Asp Glu Tyr Ser Lys Leu Asp Phe Asp Lys Leu Thr Val Cys Asp Val			
100	105	110	
Lys Thr Val Tyr Leu Thr Thr Met Lys Pro Tyr Gly Met Val Ser Lys			
115	120	125	
Phe Val Ser Ser Ala Lys Ser Val Gly Lys Lys Thr His Asp Leu Ile			
130	135	140	
Ala Leu Cys Asp Phe Met Asp Leu Glu Lys Asn Ile Pro Val Thr Ile			
145	150	155	160
Pro Ala Phe Ile Lys Ser Val Ser Ile Lys Glu Ser Ala Thr			
165	170	175	
Val Glu Ala Ala Ile Ser Ser Glu Ala Asp Gln Ala Leu Thr Gln Ala			
180	185	190	
Lys Ile Ala Pro Tyr Ala Gly Leu Ile Met Ile Met Thr Met Asn Asn			
195	200	205	
Pro Lys Gly Ile Phe Lys Lys Leu Gly Ala Gly Thr Gln Val Ile Val			
210	215	220	
Glu Leu Gly Ala Tyr Val Gln Ala Glu Ser Ile Ser Arg Ile Cys Lys			
225	230	235	240
Ser Trp Ser His Gln Gly Thr Arg Tyr Val Leu Lys Ser Arg			

245

250

<210> 65
<211> 254
<212> PRT
<213> human Metapneumo virus

<400> 65
Met Glu Ser Tyr Leu Val Asp Thr Tyr Gln Gly Ile Pro Tyr Thr Ala
1 5 10 15
Ala Val Gln Val Asp Leu Val Glu Lys Asp Leu Leu Pro Ala Ser Leu
20 25 30
Thr Ile Trp Phe Pro Leu Phe Gln Ala Asn Thr Pro Pro Ala Val Leu
35 40 45
Leu Asp Gln Leu Lys Thr Leu Thr Ile Thr Leu Tyr Ala Ala Ser
50 55 60
Gln Asn Gly Pro Ile Leu Lys Val Asn Ala Ser Ala Gln Gly Ala Ala
65 70 75 80
Met Ser Val Leu Pro Lys Phe Glu Val Asn Ala Thr Val Ala Leu
85 90 95
Asp Glu Tyr Ser Lys Leu Asp Phe Asp Lys Leu Thr Val Cys Asp Val
100 105 110
Lys Thr Val Tyr Leu Thr Thr Met Lys Pro Tyr Gly Met Val Ser Lys
115 120 125
Phe Val Ser Ser Ala Lys Ser Val Gly Lys Lys Thr His Asp Leu Ile
130 135 140
Ala Leu Cys Asp Phe Met Asp Leu Glu Lys Asn Ile Pro Val Thr Ile
145 150 155 160
Pro Ala Phe Ile Lys Ser Val Ser Ile Lys Glu Ser Glu Ser Ala Thr
165 170 175
Val Glu Ala Ala Ile Ser Ser Glu Ala Asp Gln Ala Leu Thr Gln Ala
180 185 190
Lys Ile Ala Pro Tyr Ala Gly Leu Ile Met Ile Met Thr Met Asn Asn
195 200 205
Pro Lys Gly Ile Phe Lys Lys Leu Gly Ala Gly Thr Gln Val Ile Val
210 215 220
Glu Leu Gly Ala Tyr Val Gln Ala Glu Ser Ile Ser Arg Ile Cys Lys
225 230 235 240
Ser Trp Ser His Gln Gly Thr Arg Tyr Val Leu Lys Ser Arg
245 250

<210> 66
<211> 765
<212> DNA
<213> human Metapneumo virus

<400> 66
atggagtcct acctagtata caccttatcaa ggcattcctt acacagcagc tgttcaagtt 60
gatctaatacg aaaaggaccc ttacactgca agcctaaca tatggttccc ttgtttcag 120
gcacacacac caccagcagt gctgctcgat cagctaaaaa ccctgacaat aaccactctg 180
tatgctgcat cacaaaatgg tccaaatactc aaagtgaatg catagcccc aggtgcagca 240
atgtctgtac ttcccaaaaa atttgaagtc aatgcgactg tagcactcga tgaatatacg 300
aaactggaat ttgacaaact cacagtctgt gaagtaaaaa cagtttactt aacaaccatg 360
aaaccatacg ggatggtatac aaaatttgtg agctcagcca aatcagttgg caaaaaaaca 420
catgatctaa tcgcactatg tgatttatg gatctagaaa agaacacacc tgttacaata 480
ccagcattca tcaaatacg ttcataatcaa gagagtgagt cagctactgt tgaagctgct 540
ataagcgttg aagcagacca agctctaaca caggccaaaa ttgcacccat tgcgggattt 600
attatgatca tgactatgaa caatcccaa ggcatttca aaaagcttgg agctgggact 660
caagtcatacg tagaacttagg agcatatgtc caggctgaaa gcataagcaa aatatgcaag 720
acttggagcc atcaaggac aagatatgtc ttgaagtcca gataa 765

<210> 67
<211> 765
<212> DNA
<213> human Metapneumo virus

<400> 67
atggagtccct atctggtaga cacttatcaa ggcattccctt acacagcagc tttcaagtt 60
gatcttagtag aaaaggacct gttacctgca agcctaaca tatggttccc cttgtttcag 120
gccaatacac caccagcagt tctgcttgat cagctaaaga ctctgactat aactactcg 180
tatgctgcat cacaaagtgg tccaaatacta aaagtgaatg catcagcccc gggtcagca 240
atgtctgtac ttcccaaaaa gttgaagtc aatgcgactg tagcacttga cgaatatacg 300
aaatttagaat ttgacaaact tacagtctgt gaagtaaaaa cagtttactt aacaaccatg 360
aaaccatatg ggatggtatac aaagtttgc agctcgccca aatcagttgg caaaaaaaca 420
catgatctaa tcgcattatg tgatTTTATG gatctagaaa agaacacacc agttacaata 480
ccagcattta tcaaattcgt ttctatcaag gagagtgaat cagccactgt tgaagctgca 540
ataaggcagtg aaggcagacca agctctaaca caagccaaaa ttgcacccca tgcgggactg 600
atcatgatta tgaccatgaa caatccaaa ggcattattca agaagcttgg agctgggacc 660
caagttatag tagaacttagg agcatatgtc caggctgaaa gcataagtaa aatatgcaag 720
acttggagcc atcaagaac aagatatgtg ctgaagtcca gttaa 765

<210> 68
<211> 765
<212> DNA
<213> human Metapneumo virus

<400> 68
atggagtccct atcttagtaga cacttatcaa ggcattccat atacagctgc tttcaagtt 60
gaccctggtag aaaaagattt actgccagca agtttgcacaa tatggttcc tttatttcag 120
gccaacacac caccagcagt tctgcttgat cagctaaaaa ctttgcacaaat aacaactctg 180
tatgctgcat cacagaatgg tccaaatactc aaggtaatg catctgcccc aggtgcgtcc 240
atgtctgtac ttcccaaaaa attcgaggta aatgcactg tagcacttga tgaatacagt 300
aaacttgatt ttgacaaagct gacggctctgc gatgttaaaa cagtttattt gacaactatg 360
aaaccgtacg ggatgggtc aaaaatttgc agttcagccaa aatcagttgg caaaaaagaca 420
catgatctaa ttgcactatg tgacttcatg gacctagaga aaaaatatacc tgtgacaata 480
ccagcattca taaagtcaatgttcaatccaa gagagtgaat cagccactgt tgaagctgca 540
ataaggcagcg aaggccagacca agccttgaca caagccaaaa ttgcacccca tgcaggacta 600
attatgatca tgaccatgaa caatccaaaa ggtatattca agaaaacttagg ggctggaaaca 660
caagtgatag tagagctggg ggcattatgtt caggctgaga gcatcagtag gatctgcaag 720
agctggagtc accaaggaac aagatacgtt cttttttttt gataa 765

<210> 69
<211> 765
<212> DNA
<213> human Metapneumo virus

<400> 69
atggagtccct atcttagtggc cacttatcaa ggcattccctt acacagctgc tttcaagtt 60
gatctggtag aaaaagactt actaccagca agtttgcacaa tatggttcc tctattccaa 120
gccaacacac caccagcggt ttgcctcgat cagctaaaaa ctttgcactat aacaactctg 180
tatgctgcat cacagaatgg tccaaatactc aaggtaatg catcagctca gggtcgtct 240
atgtctgtac ttcccaaaaa attcgaggta aatgcactg tggcacttga tgaatacagc 300
aaacttgact ttgacaaagtt aacggtttgc gatgttaaaa cagtttattt gacaaccatg 360
aaggccatatg ggatgggtc aaaaatttgc agttcagccaa aatcagttgg caaaaaagaca 420
catgatctaa ttgcactgtg tgacttcatg gacctagaga aaaaatatacc tgtgacaata 480
ccagcattca taaagtcaatgttcaatccaa gagagtggat cagccactgt tgaagctgca 540
ataaggcagtg aggccgacca agcattaaca caagccaaaa ttgcacccca tgcaggacta 600
atcatgatca tgaccatgaa caatccaaaa ggtatattca agaaaacttagg agctggaaaca 660
caagtgatag tagagctggg ggcattatgtt caagccgaga gcatcagtag gatctgcaag 720
agctggagtc accaaggaac aagatatgtt cttttttttt gataa 765

<210> 70
<211> 394

<212> PRT

<213> human Metapneumo virus

<400> 70

Met Ser Leu Gln Gly Ile His Leu Ser Asp Leu Ser Tyr Lys His Ala
 1 5 10 15
 Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr
 20 25 30
 Thr Ala Val Thr Pro Ser Ser Leu Gln Gln Glu Ile Thr Leu Leu Cys
 35 40 45
 Gly Glu Ile Leu Tyr Ala Lys His Ala Asp Tyr Lys Tyr Ala Ala Glu
 50 55 60
 Ile Gly Ile Gln Tyr Ile Ser Thr Ala Leu Gly Ser Glu Arg Val Gln
 65 70 75 80
 Gln Ile Leu Arg Asn Ser Gly Ser Glu Val Gln Val Val Leu Thr Arg
 85 90 95
 Thr Tyr Ser Leu Gly Lys Ile Lys Asn Asn Lys Gly Glu Asp Leu Gln
 100 105 110
 Met Leu Asp Ile His Gly Val Glu Lys Ser Trp Val Glu Glu Ile Asp
 115 120 125
 Lys Glu Ala Arg Lys Thr Met Ala Thr Leu Leu Lys Glu Ser Ser Gly
 130 135 140
 Asn Ile Pro Gln Asn Gln Arg Pro Ser Ala Pro Asp Thr Pro Ile Ile
 145 150 155 160
 Leu Leu Cys Val Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Ile
 165 170 175
 Glu Val Gly Leu Glu Thr Thr Val Arg Arg Ala Asn Arg Val Leu Ser
 180 185 190
 Asp Ala Leu Lys Arg Tyr Pro Arg Met Asp Ile Pro Lys Ile Ala Arg
 195 200 205
 Ser Phe Tyr Asp Leu Phe Glu Gln Lys Val Tyr His Arg Ser Leu Phe
 210 215 220
 Ile Glu Tyr Gly Lys Ala Leu Gly Ser Ser Ser Thr Gly Ser Lys Ala
 225 230 235 240
 Glu Ser Leu Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln
 245 250 255
 Thr Met Leu Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Asn Ile Met
 260 265 270
 Leu Gly His Val Ser Val Gln Ala Glu Leu Lys Gln Val Thr Glu Val
 275 280 285
 Tyr Asp Leu Val Arg Glu Met Gly Pro Glu Ser Gly Leu Leu His Leu
 290 295 300
 Arg Gln Ser Pro Lys Ala Gly Leu Leu Ser Leu Ala Asn Cys Pro Asn
 305 310 315 320
 Phe Ala Ser Val Val Leu Gly Asn Ala Ser Gly Leu Gly Ile Ile Gly
 325 330 335
 Met Tyr Arg Gly Arg Val Pro Asn Thr Glu Leu Phe Ser Ala Ala Glu
 340 345 350
 Ser Tyr Ala Lys Ser Leu Lys Glu Ser Asn Lys Ile Asn Phe Ser Ser
 355 360 365
 Leu Gly Leu Thr Asp Glu Glu Lys Glu Ala Ala Glu His Phe Leu Asn
 370 375 380
 Val Ser Asp Asp Ser Gln Asn Asp Tyr Glu
 385 390

<210> 71

<211> 394

<212> PRT

<213> human Metapneumo virus

<400> 71

Met Ser Leu Gln Gly Ile His Leu Ser Asp Leu Ser Tyr Lys His Ala
 1 5 10 15
 Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr
 20 25 30
 Thr Ala Val Thr Pro Ser Ser Leu Gln Gln Glu Ile Thr Leu Leu Cys
 35 40 45
 Gly Glu Ile Leu Tyr Ala Lys His Ala Asp Tyr Lys Tyr Ala Ala Glu
 50 55 60
 Ile Gly Ile Gln Tyr Ile Ser Thr Ala Leu Gly Ser Glu Arg Val Gln
 65 70 75 80
 Gln Ile Leu Arg Asn Ser Gly Ser Glu Val Gln Val Val Leu Thr Arg
 85 90 95
 Thr Tyr Ser Leu Gly Lys Val Lys Asn Asn Lys Gly Glu Asp Leu Gln
 100 105 110
 Met Leu Asp Ile His Gly Val Glu Lys Ser Trp Val Glu Glu Ile Asp
 115 120 125
 Lys Glu Ala Arg Lys Thr Met Ala Thr Leu Leu Lys Glu Ser Ser Gly
 130 135 140
 Asn Ile Pro Gln Asn Gln Arg Pro Ser Ala Pro Asp Thr Pro Ile Ile
 145 150 155 160
 Leu Leu Cys Val Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Ile
 165 170 175
 Glu Val Gly Leu Glu Thr Thr Val Arg Arg Ala Asn Arg Val Leu Ser
 180 185 190
 Asp Ala Leu Lys Arg Tyr Pro Arg Met Asp Ile Pro Lys Ile Ala Arg
 195 200 205
 Ser Phe Tyr Asp Leu Phe Glu Gln Lys Val Tyr Tyr Arg Ser Leu Phe
 210 215 220
 Ile Glu Tyr Gly Lys Ala Leu Gly Ser Ser Thr Gly Ser Lys Ala
 225 230 235 240
 Glu Ser Leu Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln
 245 250 255
 Thr Met Leu Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Asn Ile Met
 260 265 270
 Leu Gly His Val Ser Val Gln Ala Glu Leu Lys Gln Val Thr Glu Val
 275 280 285
 Tyr Asp Leu Val Arg Glu Met Gly Pro Glu Ser Gly Leu Leu His Leu
 290 295 300
 Arg Gln Ser Pro Lys Ala Gly Leu Leu Ser Leu Ala Asn Cys Pro Asn
 305 310 315 320
 Phe Ala Ser Val Val Leu Gly Asn Ala Ser Gly Leu Gly Ile Ile Gly
 325 330 335
 Met Tyr Arg Gly Arg Val Pro Asn Thr Glu Leu Phe Ser Ala Ala Glu
 340 345 350
 Ser Tyr Ala Lys Ser Leu Lys Glu Ser Asn Lys Ile Asn Phe Ser Ser
 355 360 365
 Leu Gly Leu Thr Asp Glu Glu Lys Glu Ala Ala Glu His Phe Leu Asn
 370 375 380
 Val Ser Asp Asp Ser Gln Asn Asp Tyr Glu
 385 390

<210> 72
 <211> 394
 <212> PRT
 <213> human Metapneumo virus

<400> 72
 Met Ser Leu Gln Gly Ile His Leu Ser Asp Leu Ser Tyr Lys His Ala
 1 5 10 15
 Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr
 20 25 30

Thr Ala Val Thr Pro Ser Ser Leu Gln Gln Glu Ile Thr Leu Leu Cys
 35 40 45
 Gly Glu Ile Leu Tyr Thr Lys His Thr Asp Tyr Lys Tyr Ala Ala Glu
 50 55 60
 Ile Gly Ile Gln Tyr Ile Cys Thr Ala Leu Gly Ser Glu Arg Val Gln
 65 70 75 80

 Gln Ile Leu Arg Asn Ser Gly Ser Glu Val Gln Val Val Leu Thr Lys
 85 90 95
 Thr Tyr Ser Leu Gly Lys Gly Lys Asn Ser Lys Gly Glu Glu Leu Gln
 100 105 110
 Met Leu Asp Ile His Gly Val Glu Lys Ser Trp Ile Glu Glu Ile Asp
 115 120 125
 Lys Glu Ala Arg Lys Thr Met Val Thr Leu Leu Lys Glu Ser Ser Gly
 130 135 140
 Asn Ile Pro Gln Asn Gln Arg Pro Ser Ala Pro Asp Thr Pro Ile Ile
 145 150 155 160
 Leu Leu Cys Val Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Ile
 165 170 175
 Glu Val Gly Leu Glu Thr Thr Val Arg Arg Ala Asn Arg Val Leu Ser
 180 185 190
 Asp Ala Leu Lys Arg Tyr Pro Arg Ile Asp Ile Pro Lys Ile Ala Arg
 195 200 205
 Ser Phe Tyr Glu Leu Phe Glu Gln Lys Val Tyr Tyr Arg Ser Leu Phe
 210 215 220
 Ile Glu Tyr Gly Lys Ala Leu Gly Ser Ser Ser Thr Gly Ser Lys Ala
 225 230 235 240
 Glu Ser Leu Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln
 245 250 255
 Thr Leu Leu Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Asn Ile Met
 260 265 270
 Leu Gly His Val Ser Val Gln Ser Glu Leu Lys Gln Val Thr Glu Val
 275 280 285
 Tyr Asp Leu Val Arg Glu Met Gly Pro Glu Ser Gly Leu Leu His Leu
 290 295 300
 Arg Gln Ser Pro Lys Ala Gly Leu Leu Ser Leu Ala Asn Cys Pro Asn
 305 310 315 320
 Phe Ala Ser Val Val Leu Gly Asn Ala Ser Gly Leu Gly Ile Ile Gly
 325 330 335
 Met Tyr Arg Gly Arg Val Pro Asn Thr Glu Leu Phe Ser Ala Ala Glu
 340 345 350
 Ser Tyr Ala Arg Ser Leu Lys Glu Ser Asn Lys Ile Asn Phe Ser Ser
 355 360 365
 Leu Gly Leu Thr Asp Glu Glu Lys Glu Ala Ala Glu His Phe Leu Asn
 370 375 380
 Met Ser Gly Asp Asn Gln Asn Asp Tyr Glu
 385 390

<210> 73
 <211> 394
 <212> PRT
 <213> human Metapneumo virus

<400> 73
 Met Ser Leu Gln Gly Ile His Leu Ser Asp Leu Ser Tyr Lys His Ala
 1 5 10 15
 Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr
 20 25 30
 Thr Ala Val Thr Pro Ser Ser Leu Gln Gln Glu Ile Thr Leu Leu Cys
 35 40 45
 Gly Glu Ile Leu Tyr Thr Lys His Thr Asp Tyr Lys Tyr Ala Ala Glu

50	55	60													
Ile	Gly	Ile	Gln	Tyr	Ile	Cys	Thr	Ala	Leu	Gly	Ser	Glu	Arg	Val	Gln
65					70				75					80	
Gln	Ile	Leu	Arg	Asn	Ser	Gly	Ser	Glu	Val	Gln	Val	Val	Leu	Thr	Lys
					85				90					95	
Thr	Tyr	Ser	Leu	Gly	Lys	Gly	Lys	Asn	Ser	Lys	Gly	Glu	Glu	Leu	Gln
					100				105					110	
Met	Leu	Asp	Ile	His	Gly	Val	Glu	Lys	Ser	Trp	Val	Glu	Glu	Ile	Asp
					115				120					125	
Lys	Glu	Ala	Arg	Lys	Thr	Met	Val	Thr	Leu	Leu	Lys	Glu	Ser	Ser	Gly
					130				135					140	
Asn	Ile	Pro	Gln	Asn	Gln	Arg	Pro	Ser	Ala	Pro	Asp	Thr	Pro	Ile	Ile
					145				150					160	
Leu	Leu	Cys	Val	Gly	Ala	Leu	Ile	Phe	Thr	Lys	Leu	Ala	Ser	Thr	Ile
					165				170					175	
Glu	Val	Gly	Leu	Glu	Thr	Thr	Val	Arg	Arg	Ala	Asn	Arg	Val	Leu	Ser
					180				185					190	
Asp	Ala	Leu	Lys	Arg	Tyr	Pro	Arg	Val	Asp	Ile	Pro	Lys	Ile	Ala	Arg
					195				200					205	
Ser	Phe	Tyr	Glu	Leu	Phe	Glu	Gln	Lys	Val	Tyr	Tyr	Arg	Ser	Leu	Phe
					210				215					220	
Ile	Glu	Tyr	Gly	Lys	Ala	Leu	Gly	Ser	Ser	Ser	Thr	Gly	Ser	Lys	Ala
					225				230					240	
Glu	Ser	Leu	Phe	Val	Asn	Ile	Phe	Met	Gln	Ala	Tyr	Gly	Ala	Gly	Gln
					245				250					255	
Thr	Met	Leu	Arg	Trp	Gly	Val	Ile	Ala	Arg	Ser	Ser	Asn	Asn	Ile	Met
					260				265					270	
Leu	Gly	His	Val	Ser	Val	Gln	Ala	Glu	Leu	Lys	Gln	Val	Thr	Glu	Val
					275				280					285	
Tyr	Asp	Leu	Val	Arg	Glu	Met	Gly	Pro	Glu	Ser	Gly	Leu	Leu	His	Leu
					290				295					300	
Arg	Gln	Ser	Pro	Lys	Ala	Gly	Leu	Leu	Ser	Leu	Ala	Asn	Cys	Pro	Asn
					305				310					320	
Phe	Ala	Ser	Val	Val	Leu	Gly	Asn	Ala	Ser	Gly	Leu	Gly	Ile	Ile	Gly
					325				330					335	
Met	Tyr	Arg	Gly	Arg	Val	Pro	Asn	Thr	Glu	Leu	Phe	Ser	Ala	Ala	Glu
					340				345					350	
Ser	Tyr	Ala	Arg	Ser	Leu	Lys	Glu	Ser	Asn	Lys	Ile	Asn	Phe	Ser	Ser
					355				360					365	
Leu	Gly	Leu	Thr	Asp	Glu	Glu	Lys	Glu	Ala	Ala	Glu	His	Phe	Leu	Asn
					370				375					380	
Met	Ser	Asp	Asp	Asn	Gln	Asp	Asp	Tyr	Glu						
					385				390						

<210> 74
 <211> 1185
 <212> DNA
 <213> human Metapneumo virus

<400> 74
 atgtctttc aagggattca cctgagtgtat ttatcataca agcatgctat attaaaagag 60
 tctcagtaca caataaaaag agatgtgggt acaaacaactg cagtgcacacc ctcatcattg 120
 caacaagaaa taacactgtt gtgtggagaa attctgtatg ctaaacatgc tgactacaaa 180
 tatgctgcag aaataggaat acaatatatt agcacagctt taggatcaga gagagtgcag 240
 cagattctga ggaactcagg cagtgaagtc caagtggct taaccagaac gtactctctg 300
 gggaaaatta aaaacaataa aggagaagat ttacagatgt tagacataca cggggtagag 360
 aagagctggg tagaagagat agacaaagaaa gcaagaaaa caatggcaac cttgcctaag 420
 gaatcatcag gtaatatccc acaaataatcg aggccctcag caccagacac acccataatc 480
 ttattatgtg taggtgcctt aatattcact aaactagcat caaccataga agtgggacta 540
 gagaccacag tcagaaggc taaccgtgt acaagtgtat cactcaagag ataccctaga 600
 atggacatac caaagattgc cagatccttc tatgacttat ttaacaaa agtgtatcac 660

agaagtttgt tcatttagtga tggcaaaggca ttaggctcat catctacagg cagcaaaggca 720
 gaaagtctat ttgttaatat attcatgcaa gcttatgggg ccggtc当地 aatgctaagg 780
 tgggggtca ttgccaggtc atccaacaat ataatgttag gacatgtatc cgtccaaact 840
 gagttaaaac aggtcacaga agtctatgac ttggtgcgag aaatggggccc tgaatctgga 900
 ctctacatt taaggcaaaag cccaaaagct ggactgttat cactagccaa ctgtccaaac 960
 tttgcagtg ttgttctcgaaatgcctca ggcttaggca taatcggtat gtatcgaggg 1020
 agagtaccaa acacagaatt atttcagca gctgaaagtt atgccaagg tttgaaagaa 1080
 agcaataaaa taaatttctc ttcatcattaa cttacagatg aagagaaaaga ggctgcagaa 1140
 catttcttaa atgtgagtga cgacagtcaa aatgattatg agtaa 1185

<210> 75

<211> 1185

<212> DNA

<213> human Metapneumo virus

<400> 75

atgtctcttc aagggattca cctgagtgtat cttatcatata agcatgctat attaaaaagag 60
 tctcagtata caataaaagag agatgttaggc acaacaaccg cagtgc当地 ctc当地 catttgc 120
 caacaagaaa taacactatt gtgtggagaa attctatag ctaagcatgc tgattacaaa 180
 tatgctgc当地 aaataggaat acaatataatt agc当地 ctc当地 taggatc当地 gagagtacag 240
 cagattctaa gaaactcagg tagtgaagtc caagtgggtaaaccacac gtactcctt 300
 gggaaaggta aaaacaacaa aggagaagat ttacagatgt tagacatata cggagtagag 360
 aaaagctggg tggagagat agacaaaagaa gcaagaaaaaa caatggcaac ttgc当地 420
 gaatcatcag gcaatattcc acaaaaatcag aggcccttc当地 caccagacac acccataatc 480
 ttattatgtg tagtgc当地 aatatttacc aactagcat caactataga agtgggatta 540
 gagaccacag tcagaagagc taaccgtgtat ctaagtgtat cactcaaaag ataccctagg 600
 atggacatac caaaaatcgc tagatcttc tatgacttat ttgaacaaaag agtgtattac 660
 agaagtttgt tcatttagtga tggcaaaggca ttaggctcat cctctacagg cagcaaaggca 720
 gaaagtttat tcgttaatat attcatgcaa gcttacgggtc ctgtccaaac aatgctgagg 780
 tgggggtca ttgccaggtc atctaacaat ataatgttag gacatgtatc tttcaagct 840
 gagttaaaac aagtccacaga agtctatgac ctggtgcgag aaatggggccc tgaatctgga 900
 ctctacatt taaggcaaaag cccaaaagct ggactgttat cactagccaa ttgc当地 960
 ttgc当地 tagtgc当地 aatgcctca ggcttaggca taataggtat gtatcgaggg 1020
 agagtccaa acacagaact atttcagca gcagaaagct atgccaagg tttgaaagaa 1080
 agcaataaaa ttaactttc ttcatcattaa cttacagatg aagaaaaaga ggctgcagaa 1140
 cacttc当地 aatgtgagtga cgacagtcaa aatgattatg agtaa 1185

<210> 76

<211> 1185

<212> DNA

<213> human Metapneumo virus

<400> 76

atgtctcttc aagggattca cctaaagtgtat cttatcatata aacatgctat attaaaaagag 60
 tctcaatata caataaaaag agatgttaggc accacaactg cagtgc当地 ttcatcatttgc 120
 caacaagaaa taacactttt gtgtggggaa atacttata ctaaacacac tgattacaaa 180
 tatgctgc当地 agataggaat acaatataatt tgc当地 ctc当地 taggatc当地 aagagtacaa 240
 cagattttga gaaactcagg tagtgaagtt cagggtggc当地 taaccacac atactcctt 300
 gggaaaggca aaaacagtaa aggggaagag ctgc当地 tagatataca tggagtgaa 360
 aagagttgga tagaagaaaat agacaaaagag gcaagaaaaaa caatggtaac ttgc当地 420
 gaatcatcag gtaacatccc acaaaaaccag agaccccttc当地 caccagacac accaataatt 480
 ttattatgtg tagtgc当地 aatatttact aactagcat caacaataga agttggatta 540
 gagactacag tttagaagagc taataggtg ctaagtgtat cactcaaaag ataccacagg 600
 atagatatac caaagattgc tagatctttt tatgaactat ttgaacaaaag agtgtactac 660
 agaagtttat tcatttagtga cggaaaagct ttaggctcat cttcaacagg aagcaaaggca 720
 gaaagtttgt ttgttaatat attatgcaat gcttacgggtc ctggccaaact actgctaagg 780
 tgggggtca ttgccagatc atccaacaac ataatgttag ggc当地 tttcaatct 840
 gaattgtacgc aagtttacaga ggtttatgac ttggtgagag aaatggggccc tgaatctgga 900
 cttttacatc taagacaaaag tccaaaggca gggctgttat ctttgc当地 ttgc当地 960
 ttgc当地 tagtgc当地 aatgcctca ggtctaggca taatcggaat gtacagaggg 1020
 agagtaccaa acacagatgcttgc当地 gcaagaaagtt atgccaagg cttaaaagaa 1080
 agcaataaaa tcaacttctc ttgc当地 taggg cttacagatg aagaaaaaga agctgcagaa 1140

cacttcttaa acatgagtgg tgacaatcaa aatgattatg agtaa

1185

<210> 77
<211> 1185
<212> DNA
<213> human Metapneumo virus

<400> 77
atgtctcttc aaggattca cctaagtat ctgtcatata aacatgctat attaaaagag 60
tctcaataca caataaaaag agatgttaggc accacaactg cagtgcacacc ttcatcattg 120
cagcaagaga taacactttt gtgtggagag attcttaca ctaaacatac tgattacaaa 180
tatgctgcag agatagggat acaatatatt tgcacagctc taggatcaga aagagtacaa 240
cagatttaa gaaattcagg tagtgagggtt caggtggttc taaccaagac atactctta 300
ggaaaaggta aaaatagtaa aggggaagag ttgcaaatgt tagatataca tggagtggaa 360
aagagttggg tagaagaaat agacaaagag gcaagaaaaa caatggtgac tttgctaaag 420
gaatcatcag gcaacatccc acaaaaccag aggcccttcag caccagacac accaataatt 480
ttattgtgt taggtgtttt aatattcact aaactagcat caacaataga agttggacta 540
gagactacag tttagaaggc taacagagtg ttaagtgtat cgctcaaaag ataccctagg 600
gtagatatac caaagattgc tagatctttt tatgaactat ttgagcagaa agtgttattac 660
aggagtctat tcattgagta tggaaagct ttaggctcat cttcaacagg aagcaaagca 720
gaaagtttggttgtttaatattatgc gcttatggag ccggtcagac aatgctaagg 780
tggggtgtca ttgccagatc atctaacaac ataatgtcg ggcatgtatc tgcataatc 840
gaattgaaac aagttacaga gtttatgtat ttgtaagag aaatgggtcc tgaatctggg 900
cttttacate taagacaaag tccaaaggca ggactgttat cttggctaa ttgccccat 960
tttgcttagt ttgttcttgg taatgctca ggtctaggtt taatcggaaat gtacagggaa 1020
agagtgcacacacagacttatttctgc gcaagaaatgtt atgcccagaag cttaaaagaa 1080
agcaacaaaaa tcaacttctc ctcatttaggg ctcacagacg aagaaaaaga agctgcagaa 1140
cacttcttaa acatgagtga tgacaatcaa gatgattatg agtaa 1185

<210> 78
<211> 294
<212> PRT
<213> human Metapneumo virus

<400> 78
Met Ser Phe Pro Glu Gly Lys Asp Ile Leu Phe Met Gly Asn Glu Ala
1 5 10 15
Ala Lys Leu Ala Glu Ala Phe Gln Lys Ser Leu Arg Lys Pro Gly His
20 25 30
Lys Arg Ser Gln Ser Ile Ile Gly Glu Lys Val Asn Thr Val Ser Glu
35 40 45
Thr Leu Glu Leu Pro Thr Ile Ser Arg Pro Ala Lys Pro Thr Ile Pro
50 55 60
Ser Glu Pro Lys Leu Ala Trp Thr Asp Lys Gly Gly Ala Thr Lys Thr
65 70 75 80
Glu Ile Lys Gln Ala Ile Lys Val Met Asp Pro Ile Glu Glu Glu
85 90 95
Ser Thr Glu Lys Val Leu Pro Ser Ser Asp Gly Lys Thr Pro Ala
100 105 110
Glu Lys Lys Leu Lys Pro Ser Thr Asn Thr Lys Lys Val Ser Phe
115 120 125
Thr Pro Asn Glu Pro Gly Lys Tyr Thr Lys Leu Glu Lys Asp Ala Leu
130 135 140
Asp Leu Leu Ser Asp Asn Glu Glu Asp Ala Glu Ser Ser Ile Leu
145 150 155 160
Thr Phe Glu Glu Arg Asp Thr Ser Ser Leu Ser Ile Glu Ala Arg Leu
165 170 175
Glu Ser Ile Glu Glu Lys Leu Ser Met Ile Leu Gly Leu Leu Arg Thr
180 185 190
Leu Asn Ile Ala Thr Ala Gly Pro Thr Ala Ala Arg Asp Gly Ile Arg
195 200 205
Asp Ala Met Ile Gly Val Arg Glu Glu Leu Ile Ala Asp Ile Ile Lys

210	215	220
Glu Ala Lys Gly Lys Ala Ala Glu Met Met Glu Glu Glu Met Ser Gln		
225	230	235
Arg Ser Lys Ile Gly Asn Gly Ser Val Lys Leu Thr Glu Lys Ala Lys		240
245	250	255
Glu Leu Asn Lys Ile Val Glu Asp Glu Ser Thr Ser Gly Glu Ser Glu		
260	265	270
Glu Glu Glu Pro Lys Asp Thr Gln Asp Asn Ser Gln Glu Asp Asp		
275	280	285
Ile Tyr Gln Leu Ile Met		
290		

<210> 79
<211> 294
<212> PRT
<213> human Metapneumo virus

<400> 79		
Met Ser Phe Pro Glu Gly Lys Asp Ile Leu Phe Met Gly Asn Glu Ala		
1	5	10
Ala Lys Leu Ala Glu Ala Phe Gln Lys Ser Leu Arg Lys Pro Asn His		15
20	25	30
Lys Arg Ser Gln Ser Ile Ile Gly Glu Lys Val Asn Thr Val Ser Glu		
35	40	45
Thr Leu Glu Leu Pro Thr Ile Ser Arg Pro Thr Lys Pro Thr Ile Leu		
50	55	60
Ser Glu Pro Lys Leu Ala Trp Thr Asp Lys Gly Gly Ala Ile Lys Thr		
65	70	75
80		
Glu Ala Lys Gln Thr Ile Lys Val Met Asp Pro Ile Glu Glu Glu		
85	90	95
Phe Thr Glu Lys Arg Val Leu Pro Ser Ser Asp Gly Lys Thr Pro Ala		
100	105	110
Glu Lys Lys Leu Lys Pro Ser Thr Asn Thr Lys Lys Lys Val Ser Phe		
115	120	125
Thr Pro Asn Glu Pro Gly Lys Tyr Thr Lys Leu Glu Lys Asp Ala Leu		
130	135	140
Asp Leu Leu Ser Asp Asn Glu Glu Glu Asp Ala Glu Ser Ser Ile Leu		
145	150	155
160		
Thr Phe Glu Glu Arg Asp Thr Ser Ser Leu Ser Ile Glu Ala Arg Leu		
165	170	175
Glu Ser Ile Glu Glu Lys Leu Ser Met Ile Leu Gly Leu Leu Arg Thr		
180	185	190
Leu Asn Ile Ala Thr Ala Gly Pro Thr Ala Ala Arg Asp Gly Ile Arg		
195	200	205
Asp Ala Met Ile Gly Ile Arg Glu Glu Leu Ile Ala Asp Ile Ile Lys		
210	215	220
Glu Ala Lys Gly Lys Ala Ala Glu Met Met Glu Glu Glu Met Asn Gln		
225	230	235
240		
Arg Thr Lys Ile Gly Asn Gly Ser Val Lys Leu Thr Glu Lys Ala Lys		
245	250	255
Glu Leu Asn Lys Ile Val Glu Asp Glu Ser Thr Ser Gly Glu Ser Glu		
260	265	270
Glu Glu Glu Pro Lys Asp Thr Gln Glu Asn Asn Gln Glu Asp Asp		
275	280	285
Ile Tyr Gln Leu Ile Met		
290		

<210> 80
<211> 294
<212> PRT

<213> human Metapneumo virus

<400> 80

Met Ser Phe Pro Glu Gly Lys Asp Ile Leu Phe Met Gly Asn Glu Ala			
1	5	10	15
Ala Lys Ile Ala Glu Ala Phe Gln Lys Ser Leu Lys Lys Ser Gly His			
20	25	30	
Lys Arg Thr Gln Ser Ile Val Gly Glu Lys Val Asn Thr Ile Ser Glu			
35	40	45	
Thr Leu Glu Leu Pro Thr Ile Ser Lys Pro Ala Arg Ser Ser Thr Leu			
50	55	60	
Leu Glu Pro Lys Leu Ala Trp Ala Asp Asn Ser Gly Ile Thr Lys Ile			
65	70	75	80
Thr Glu Lys Pro Ala Thr Lys Thr Asp Pro Val Glu Glu Glu			
85	90	95	
Phe Asn Glu Lys Lys Val Leu Pro Ser Ser Asp Gly Lys Thr Pro Ala			
100	105	110	
Glu Lys Lys Ser Lys Phe Ser Thr Ser Val Lys Lys Lys Val Ser Phe			
115	120	125	
Thr Ser Asn Glu Pro Gly Lys Tyr Thr Lys Leu Glu Lys Asp Ala Leu			
130	135	140	
Asp Leu Leu Ser Asp Asn Glu Glu Asp Ala Glu Ser Ser Ile Leu			
145	150	155	160
Thr Phe Glu Glu Lys Asp Thr Ser Ser Leu Ser Ile Glu Ala Arg Leu			
165	170	175	
Glu Ser Ile Glu Lys Leu Ser Met Ile Leu Gly Leu Leu Arg Thr			
180	185	190	
Leu Asn Ile Ala Thr Ala Gly Pro Thr Ala Ala Arg Asp Gly Ile Arg			
195	200	205	
Asp Ala Met Ile Gly Ile Arg Glu Glu Leu Ile Ala Glu Ile Ile Lys			
210	215	220	
Glu Ala Lys Gly Lys Ala Ala Glu Met Met Glu Glu Glu Met Asn Gln			
225	230	235	240
Arg Ser Lys Ile Gly Asn Gly Ser Val Lys Leu Thr Glu Lys Ala Lys			
245	250	255	
Glu Leu Asn Lys Ile Val Glu Asp Glu Ser Thr Ser Gly Glu Ser Glu			
260	265	270	
Glu Glu Glu Pro Lys Glu Thr Gln Asp Asn Asn Gln Gly Glu Asp			
275	280	285	
Ile Tyr Gln Leu Ile Met			
290			

<210> 81

<211> 294

<212> PRT

<213> human Metapneumo virus

<400> 81

Met Ser Phe Pro Glu Gly Lys Asp Ile Leu Phe Met Gly Asn Glu Ala			
1	5	10	15
Ala Lys Ile Ala Glu Ala Phe Gln Lys Ser Leu Lys Arg Ser Gly His			
20	25	30	
Lys Arg Thr Gln Ser Ile Val Gly Glu Lys Val Asn Thr Ile Ser Glu			
35	40	45	
Thr Leu Glu Leu Pro Thr Ile Ser Lys Pro Ala Arg Ser Ser Thr Leu			
50	55	60	
Leu Glu Pro Lys Leu Ala Trp Ala Asp Ser Ser Gly Ala Thr Lys Thr			
65	70	75	80
Thr Glu Lys Gln Thr Lys Thr Asp Pro Val Glu Glu Glu			
85	90	95	
Leu Asn Glu Lys Lys Val Ser Pro Ser Ser Asp Gly Lys Thr Pro Ala			

100	105	110
Glu Lys Lys Ser Lys Ser Pro Thr Asn Val Lys Lys Val Ser Phe		
115	120	125
Thr Ser Asn Glu Pro Gly Lys Tyr Thr Lys Leu Glu Lys Asp Ala Leu		
130	135	140
Asp Leu Leu Ser Asp Asn Glu Glu Asp Ala Glu Ser Ser Ile Leu		
145	150	155
Thr Phe Glu Glu Arg Asp Thr Ser Ser Leu Ser Ile Glu Ala Arg Leu		
165	170	175
Glu Ser Ile Glu Glu Lys Leu Ser Met Ile Leu Gly Leu Leu Arg Thr		
180	185	190
Leu Asn Ile Ala Thr Ala Gly Pro Thr Ala Ala Arg Asp Gly Ile Arg		
195	200	205
Asp Ala Met Ile Gly Ile Arg Glu Glu Leu Ile Ala Glu Ile Ile Lys		
210	215	220
Glu Ala Lys Gly Lys Ala Ala Glu Met Met Glu Glu Glu Met Asn Gln		
225	230	235
Arg Ser Lys Ile Gly Asn Gly Ser Val Lys Leu Thr Glu Lys Ala Lys		
245	250	255
Glu Leu Asn Lys Ile Val Glu Asp Glu Ser Thr Ser Gly Glu Ser Glu		
260	265	270
Glu Glu Glu Pro Lys Glu Thr Gln Asp Asn Asn Gln Gly Glu Asp		
275	280	285
Ile Tyr Gln Leu Ile Met		
290		

<210> 82

<211> 885

<212> DNA

<213> human Metapneumo virus

<400> 82

atgtcattcc ctgaaggaaa agatattctt ttcatggta atgaagcagc aaaatttagca 60
gaagctttcc agaaatcatt aagaaaaacca ggtcataaaaa gatctcaatc tattatagga 120
gaaaaagtga atactgtatc agaaacattg gaattaccta ctatcagtag acctgcaaaa 180
ccaaaccatac cgtcagaacc aaagttagca tggacagata aaggtggggc aacccaaaact 240
gaaataaagc aagcaatcaa agtcatggat cccattgaag aagaagagtc taccgagaag 300
aaggtgtcac cctccagtgta tggaaaaacc cctgcagaaa agaaactgaa accatcaact 360
aacacccaaa agaagggttc atttacacca aatgaaccag ggaatataac aaagttggaa 420
aaagatgctc tagatttgc ctcagataat gaagaagaag atgcagaatc ttcaatctt 480
acctttgaag aaagagatac ttcatcatta agcattggagg ccagattgga atcaatagag 540
gagaaaaattaa gcatgatatt agggctatta agaacactca acattgtcac agcaggaccc 600
acagcagcaa gagatgggat cagagatgca atgattggcg taagagagga attaatagca 660
gacataataa aggaagctaa agggaaagca gcagaaatga tggaaagagga aatgagtc 720
cgatcaaaaa taggaaatgg tagtgtaaaa ttaacagaaa aagcaaaaaga gctcaacaaa 780
attgttgaag atgaaaagcac aagtggagaa tccgaagaag aagaagaacc aaaagacaca 840
caagacaata gtcaagaaga tgacatttac cagttaatta tgttag 885

<210> 83

<211> 885

<212> DNA

<213> human Metapneumo virus

<400> 83

atgtcattcc ctgaaggaaa agatattctt ttcatggta atgaagcagc aaaattggca 60
gaagctttcc aaaaatcatt aagaaaaaccc aatcataaaaa gatctcaatc tattatagga 120
gaaaaagtga acactgtatc tggaaacattg gaattaccta ctatcagtag acctacccaaa 180
ccgaccatat tggcagagcc gaagttagca tggacagaca aaggtggggc aatcaaaaact 240
gaagcaaaagc aaacaatcaa agtattggat cctattgaag aagaagagtt tactgagaaa 300
aggggtgtc cctccagtgta tggaaaaact cctgcagaaa agaagttgaa accatcaacc 360
aacactaaaa agaagggtc atttacacca aatgaaccag gaaaatacac aaagttggag 420

aaagatgctc tagacttgct ttcagacaat gaagaagaag atgcagaatc ctcaatctta 480
 acttcgaag aaagagatac ttcatcatta agcatttgaag ccagactaga atcgatttag 540
 gagaaattaa gcatgtatt agggcttta agaacactca acattgctac agcaggaccc 600
 acagcagcaa gagatggat cagagatgca atgattggca taagggagga actaatagca 660
 gacataataa aagaagccaa gggaaaagca gcagaatga tggagaaga aatgaaccag 720
 cgacaaaaaa taggaaacgg tagtgtaaaa ttaactgaaa aggcaaagga gctcaacaaa 780
 attgttgaag acgaaagcac aagtggtcaa tcagaagaag aagaagaacc aaaagacaca 840
 cagggaaaata atcaagaaga tgacattac cagttatca tgttag 885

<210> 84

<211> 885

<212> DNA

<213> human Metapneumo virus

<400> 84

atgtcattcc ctgaaggaaa ggatattctg ttcatggta atgaagcagc aaaaatagcc 60
 gaagcttcc agaaatcaact gaaaaatca ggtcacaaaga gaactcaatc tattgttaggg 120
 gaaaaagtttta acactatatac agaaaactcta gaactaccta ccatcagcaa acctgcacga 180
 tcacatcacac tgctggacc accaattggca tggcagaca acagcggat caccaaaatc 240
 acagaaaaac cagcaaccaa aacaacagat cctgttgaag aagaggaatt caatgaaaag 300
 aaagtgttac cttccagtga tggaaagact cctgcagaga aaaaatcaaa gtttcaacc 360
 agtgtaaaaa agaaagtttc cttcacatca aatgaaccag gggaaatacac caaacttagag 420
 aaagatgccc tagattgtct tcagacaaat gggaaagaag acgcagaatc ctcaatccta 480
 acctttgagg agaaagatac atcatcaacta agcatttgaag ctagactaga atctatagaa 540
 gagaagttga gcatgtatt aggactgctt cgtacactta acattgcaac agcaggacca 600
 acagctgcac gagatggat tagggatgca atgattggta taagagaaga gctaatacg 660
 gagataatta aggaagccaa gggaaaagca gctgaaatga tggagaaga gatgaatcaa 720
 agatcaaaaa taggaaatgg cagtgtaaaa ctaaccgaga aggcaaaaga gctcaacaaa 780
 attgttgaag acgagagcac aagcgggtgaa tcagaagaag aagaagaacc aaaagaaaact 840
 caggataaca atcaaggaga agatatttat cagttatca tgttag 885

<210> 85

<211> 885

<212> DNA

<213> human Metapneumo virus

<400> 85

atgtcattcc ctgaaggaaa agatatcctg ttcatggta atgaagcagc aaaaatagca 60
 gaagcttcc agaaatcaact aaaaagatca ggtcacaaaa gaacccagtc tattgttaggg 120
 gaaaaagttaa acactatatac agaaaactcta gagctaccta ccatcagcaa acctgcacga 180
 tcacatcacac tgcttagagcc accaattggca tggcagaca gcagcggagc caccaaaacc 240
 acagaaaaac aacaaccaa aacaacagat cctgttgaag aagaggaact caatgaaaag 300
 aaggatcac cttccagtga tggaaagact cctgcagaga aaaaatcaaa atctccaacc 360
 aatgtaaaaa agaaagtttc cttcacatca aatgaaccag gggaaatacac taaacttagaa 420
 aaagatgccc tagattgtct tcagacaaat gggaaagaag acgcagagtc ctcaatccta 480
 acctttgagg agagagacac atcatcaacta agcatttggg ctagactaga atcaatagaa 540
 gagaagctaa gcatgtatt aggactgctt cgtacactta acattgcaac agcaggacca 600
 acggctgcaa gggatggat cagagatgca atgattggta taagagaaga actaatagca 660
 gaaataataa aagaagccaa gggaaaagca gccgaaatga tggaaagagga aatgaatcaa 720
 aggtcaaaaa taggaaatgg cagtgtaaaa ctaaccgaga aggcaaaaga acttaataaa 780
 attgttgaag acgagagcac aagtggtcaa tcagaagaag aagaagaacc aaaagaaaact 840
 caggataaca atcaaggaga agatatctac cagttatca tgttag 885

<210> 86

<211> 183

<212> PRT

<213> human Metapneumo virus

<400> 86

Met	Ile	Thr	Leu	Asp	Val	Ile	Lys	Ser	Asp	Gly	Ser	Ser	Lys	Thr	Cys
1														15	
Thr	His	Leu	Lys	Lys	Ile	Ile	Lys	Asp	His	Ser	Gly	Lys	Val	Leu	Ile

20	25	30
Val Leu Lys Leu Ile Leu Ala Leu Leu Thr Phe Leu Thr Val Thr Ile		
35	40	45
Thr Ile Asn Tyr Ile Lys Val Glu Asn Asn Leu Gln Ile Cys Gln Ser		
50	55	60
Lys Thr Glu Ser Asp Lys Lys Asp Ser Ser Ser Asn Thr Thr Ser Val		
65	70	75
Thr Thr Lys Thr Thr Leu Asn His Asp Ile Thr Gln Tyr Phe Lys Ser		
85	90	95
Leu Ile Gln Arg Tyr Thr Asn Ser Ala Ile Asn Ser Asp Thr Cys Trp		
100	105	110
Lys Ile Asn Arg Asn Gln Cys Thr Asn Ile Thr Thr Tyr Lys Phe Leu		
115	120	125
Cys Phe Lys Ser Glu Asp Thr Lys Thr Asn Asn Cys Asp Lys Leu Thr		
130	135	140
Asp Leu Cys Arg Asn Lys Pro Lys Pro Ala Val Gly Val Tyr His Ile		
145	150	155
Val Glu Cys His Cys Ile Tyr Thr Val Lys Trp Lys Cys Tyr His Tyr		
165	170	175
Pro Thr Asp Glu Thr Gln Ser		
180		

<210> 87

<211> 179

<212> PRT

<213> human Metapneumo virus

<400> 87

1	5	10	15
Met Ile Thr Leu Asp Val Ile Lys Ser Asp Gly Ser Ser Lys Thr Cys			
20	25	30	
Thr His Leu Lys Lys Ile Ile Lys Asp His Ser Gly Lys Val Leu Ile			
35	40	45	
Ala Leu Lys Leu Ile Leu Ala Leu Leu Thr Phe Phe Thr Ile Thr Ile			
50	55	60	
Thr Ile Asn Tyr Ile Lys Val Glu Asn Asn Leu Gln Ile Cys Gln Ser			
65	70	75	80
Lys Thr Glu Ser Asp Lys Glu Asp Ser Pro Ser Asn Thr Thr Ser Val			
85	90	95	
Leu Ile Gln Arg Tyr Thr Asp Ser Val Ile Asn Lys Asp Thr Cys Trp			
100	105	110	
Lys Ile Ser Arg Asn Gln Cys Thr Asn Ile Thr Thr Tyr Lys Phe Leu			
115	120	125	
Cys Phe Lys Pro Glu Asp Ser Lys Ile Asn Ser Cys Asp Arg Leu Thr			
130	135	140	
Asp Leu Cys Arg Asn Lys Ser Lys Ser Ala Ala Glu Ala Tyr His Thr			
145	150	155	160
Val Glu Cys His Cys Ile Tyr Thr Ile Glu Trp Lys Cys Tyr His His			
165	170	175	
Pro Ile Asp			

<210> 88

<211> 177

<212> PRT

<213> human Metapneumo virus

<400> 88

Met Lys Thr Leu Asp Val Ile Lys Ser Asp Gly Ser Ser Glu Thr Cys

1	5	10	15
Asn Gln Leu Lys Lys Ile Ile Lys Lys His Ser Gly Lys Val Leu Ile			
20	25	30	
Ala Leu Lys Leu Ile Leu Ala Leu Leu Thr Phe Phe Thr Ala Thr Ile			
35	40	45	
Thr Val Asn Tyr Ile Lys Val Glu Asn Asn Leu Gln Ala Cys Gln Pro			
50	55	60	
Lys Asn Glu Ser Asp Lys Lys Val Thr Lys Pro Asn Thr Thr Ser Thr			
65	70	75	80
Thr Ile Arg Pro Thr Pro Asp Pro Thr Val Val His His Leu Lys Arg			
85	90	95	
Leu Ile Gln Arg His Thr Asn Ser Val Thr Lys Asp Ser Asp Thr Cys			
100	105	110	
Trp Arg Ile His Lys Asn Gln Arg Thr Asn Ile Lys Ile Tyr Lys Phe			
115	120	125	
Leu Cys Ser Gly Phe Thr Asn Ser Lys Gly Thr Asp Cys Glu Glu Pro			
130	135	140	
Thr Ala Leu Cys Asp Lys Lys Leu Lys Thr Ile Val Glu Lys His Arg			
145	150	155	160
Lys Ala Glu Cys His Cys Leu His Thr Thr Glu Trp Gly Cys Leu His			
165	170	175	
Pro			

<210> 89
<211> 177
<212> PRT
<213> human Metapneumo virus

<400> 89			
Met Lys Thr Leu Asp Val Ile Lys Ser Asp Gly Ser Ser Glu Thr Cys			
1	5	10	15
Asn Gln Leu Lys Lys Ile Ile Lys Lys His Ser Gly Lys Leu Leu Ile			
20	25	30	
Ala Leu Lys Leu Ile Leu Ala Leu Leu Thr Phe Phe Thr Val Thr Ile			
35	40	45	
Thr Val Asn Tyr Ile Lys Val Glu Asn Asn Leu Gln Ala Cys Gln Leu			
50	55	60	
Lys Asn Glu Ser Asp Lys Lys Asp Thr Lys Leu Asn Thr Thr Ser Thr			
65	70	75	80
Thr Ile Arg Pro Ile Pro Asp Leu Asn Ala Val Gln Tyr Leu Lys Arg			
85	90	95	
Leu Ile Gln Lys His Thr Asn Phe Val Ile Lys Asp Arg Asp Thr Cys			
100	105	110	
Trp Arg Ile His Thr Asn Gln Cys Thr Asn Ile Lys Ile Tyr Lys Phe			
115	120	125	
Leu Cys Phe Gly Phe Met Asn Ser Thr Asn Thr Asp Cys Glu Glu Leu			
130	135	140	
Thr Val Leu Cys Asp Lys Lys Ser Lys Thr Met Thr Glu Lys His Arg			
145	150	155	160
Lys Ala Glu Cys His Cys Leu His Thr Thr Glu Trp Trp Cys Tyr Tyr			
165	170	175	
Leu			

<210> 90
<211> 552
<212> DNA
<213> human Metapneumo virus

<400> 90
atgataacat tagatgtcat taaaagtcat gggcttcaa aaacatgtac tcacacctaaa 60
aaaataattaa aagaccactc tggtaaagtgc ttattgtac ttaagttaat attagcttta 120
ctaacatttc tcacagtaac aatcaccatc aattatataa aagtggaaaa caatctgca 180
atatgccagt caaaaactga atcagacaaa aaggactcat catcaaatac cacatcagtc 240
acaaccaaga ctactctaaa tcatacgatc acacagtatt taaaagttt gattcaagg 300
tatacaacta ctgcaataaa cagtgacaca tgctggaaaa taaacagaaa tcaatgcaca 360
aatataacaa catacaattt ttatgtttt aaatctgaag acacaaaaac caacaattgt 420
gataaactga cagattttatc cagaaaacaaa cccaaaccag cagttggagt gtatcacata 480
gtagaatgcc attgtatata cacagttaaa tggaaagtgc atcattaccc aaccgatgaa 540
acccaatcct aa 552

<210> 91
<211> 540
<212> DNA
<213> human Metapneumo virus

<400> 91
atgataacat tagatgtcat taaaagtcat gggcttcaa aaacatgtac tcacacctaaa 60
aaaataatca aagaccatttc tggtaaagtgc ttattgtac ttaagttaat attagcttta 120
ctaacatttt tcacaataac aatcactata aattacataa aagtggaaaa caatctacaa 180
atatgccagt caaaaactga atcagacaaa gaagactcat catcaaatac cacatccgtc 240
acaaccaaga ctactctaga ccatgtatc acacagtatt taaaagttt aattcaagg 300
tatagacatt ctgtgataaa caaggacaca tgctggaaaa taagcagaaa tcaatgcaca 360
aatataacaa cataataattt ttatgtttt aaacctgagg actcaaaaat caacagtgt 420
gatagactga cagatctatc cagaaaacaaa tcaaaaatcag cagtgaaagc atatcataca 480
gtagaatgcc attgtatata cacaattttag tggaaagtgc atcaccaccc aatagattaa 540

<210> 92
<211> 534
<212> DNA
<213> human Metapneumo virus

<400> 92
atgaaaacat tagatgtcat aaaaagtcat ggatcctcag aaacgtgtaa tcaactcaaa 60
aaaataataa aaaaacactc aggttaaagtgc ttattgtac taaaactgtat attggcccta 120
ctgacatttt tcacagcaac aatcactgtc aactatataa aagtggaaaa caatttgcag 180
gcatgtcaac caaaaaatga atcagacaaa aaggtcacaa agccaaatac cacatcaaca 240
acaatcagac ccacaccgca tccaaactgtc gtacatcatt tgaaaaggct gattcagaga 300
cacaccaact ctgtcataaa agacagcgat acttgttggaa gaatacacaat gaatcaacgt 360
acaaatataa aaatatacaa gttcttatgc tctgggttca caaatttcaaa aggtacagat 420
tgtgagaaac caacagccct atgcacaaa aagttaaaaa ccatgtatc aaaaacataga 480
aaagcagaat gtcactgtct acatacaacc gagtgggggt gccttcattt ctaa 534

<210> 93
<211> 534
<212> DNA
<213> human Metapneumo virus

<400> 93
atgaaaacat tagatgtcat aaaaagtcat ggatcctcag aaacatgtaa tcaactcaaa 60
aaaataataa aaaaacactc aggttaaatttgc ttattgtcat taaaactgtat attggcccta 120
ttgacgttt tcacagtaac aattactgtt aactatataa aagtggaaaa caatttgcag 180
gcatgtcaat taaaaaatga atcagacaaa aaggacacaa agctaaatac cacatcaaca 240
acaatcagac ccattccttca tctaaatgtc gtacagtact tgaaaaggct gattcagaaa 300
cacaccaact ttgtcataaa agacagagat accttgttggaa gaatacacaat gaatcaatgc 360
acaaatataa aaatataaa gttcttatgt ttcgggttca tgaattcaac aaatacagac 420
tgtgagaaac taacagttt atgtgataaa aagtcaaaaa ccatgtacaa aaaaacatagg 480
aaagcagagt gtcactgtct acatacaacc gagtgggtt gttattatct ttaa 534

<210> 94
<211> 13294
<212> DNA
<213> human metapneumo virus

<220>
<221> misc_feature
<222> (0)...(0)
<223> human MPV protein

<400> 94
acgcgaaaaa aacgcgtata aattaaattc caaacaaaac gggacaataaaaatgtctc 60
ttcaaggat tcacctaagt gatctatcat ataaacatgc tatattaaaa gagtctcaat 120
acacaataaa aagagatgt a ggcaccacaa ctgcagtgc accttcata ttacaacaag 180
aaataactt tttgtgtggg gaaataactt acactaaaca cactgattac aaatatgctg 240
ctgagatagg aatacaaatat atttgacacag ctctaggatc agaaagagta caacagattt 300
tgagaaactc aggttagtga gttcaggtgg ttctaacca aacatactcc tttagggaaag 360
gcaaaaacag taaagggaa gagctgcaga tgttagatat acatggatg gaaaagagtt 420
ggatagaaga aatagacaaa gaggcaagaa agacaatggt aactttgtt aagaatcat 480
caggtAACAT CCCACAAAAC CAGAGACCTT CAGCACCAGA CACACCAATA ATTATTATT 540
gtgttaggtgc cctaatattc actaaactag catcaacaat agaagttgga ttagagacta 600
cagttagaag agctaata g tgctaaatg atgcactcaa aagataccca aggatagata 660
taccaaaatg tgcttagatct tttttaga ac tatttgaaca aaaagtgtac tacagaagtt 720
tattcattga gtacggaaaa gctttaggtt catcttcaac aggaagcaaa gcagaaagtt 780
tgtttgtaaa tatattttagt caagctttagt gagctggcca aacactgcta aggtgggtg 840
tcattggccag atcatccaaac aacataatgc tagggcatgt atctgtgca tctgaattga 900
agcaagttac agaggtttat gacttggta gagaatggg tcctgaatct gggctttac 960
atctaagaca aagtccaaag gcagggtgtt tatttgc aatttgc aatttgcata 1020
gtgttggctt tggcaatgt tcaggtctag gcataatcg aatgtacaga gggagagtt 1080
caaacacaga gctatcccgc gcaagcagaaa gttatggccag aagcttaaa gaaagcaata 1140
aaatcaactt ctcttcgttta gggcttacag atgaagaaaa agaagctgca gaacactct 1200
taaacatgag tggtagacaat caagatgattt atgatattt aaaaactgg gacaagtcaa 1260
aatgtcttc cctgaaggaa aggtatctt gttcatgggt aatagacggc aaaaatagc 1320
cgaagcttc cagaatcac tggaaaaatc aggtcacaag agaactcaat ctattgttagg 1380
ggaaaaagtt aacactatata cagaaactct agaactacct accatcagca aacctgcacg 1440
atcatctaca ctgctggaaac caaaattggc atgggcagac aacagcgaa tcacccaaat 1500
cacagaaaaa ccagcaacca aaacaacaga tcctgtttaga gaagagggaa tcaatggaaa 1560
gaaagtgtt ccttccagtg atgggaagac tcctgcagag aacatcgaa aacttgcac 1620
cagttaaaaa aagaaagttt ccttacatc aaatgaacca gggaaataca ccaaactaga 1680
gaaagatgcc ctagatttgc tctcagacaa tgaggaagaa gacgcagaat cctcaatct 1740
aacttttagg gagaagata catcatact aagcattgaa gctagactag aatctataga 1800
agagaagttt agcatgatata taggactgt tcgtacactt aacattgca cagcaggacc 1860
aacagctgca cgagatggaa ttagggatgc aatgatggg ataagagaag agctaata 1920
agagataatt aaggaagcca agggaaaagc agctgaaatg atggaagaag agatgaatca 1980
aagatcaaaa ataggaaatg gcagtgtaaa actaaccgag aaggcaaaag agctcaacaa 2040
aattgttggaa gacgagagca caagcggta atcagaagaa gaagaagaac caaaagaaaac 2100
tcaggataac aatcaaggag aagatattt tcagttatc atgttagtta ataaaaataaa 2160
acaatggac aagtcaagat ggagtccat ctagtagaca cttatcaagg cattccat 2220
acagctctg ttcaagtgtt cctggtagaa aaagatttac tgccagcaag tttgacaata 2280
tggttccctt tatttccaggc caacacacca ccagcagttc tgcttgatca gctaaaaacc 2340
ctgacaataa ccactctgtt tgctgcata cagaatgggtt caatactca ggtttatgtca 2400
tctgccaag gtgctgcatc gtctgtactt cccaaaaat tcgaggtaaa tgcaactgt 2460
gcacttgcatg aatacagttaa acttgatttt gacaagctga cggctctgcga tggaaaaaca 2520
gttttattgtt caactatgaa accgtacggg atgggtgtca aatttgcag ttcagccaaa 2580
tcagttggca aaaagacaca tgatctattt gcaactatgtt acttcatgga ccttagagaaa 2640
aatataactg tgacaatacc agcattcata aagttagttt caatcaaaaga gagtgaatca 2700
gccacttgtt aagctgcaat aagcagcga gcccaccaag ctttgacaca agccaagatt 2760
gccccctatg caggactaat tatgatcatg accatgaaca atccaaaagg tatattcaag 2820
aaacttagggg ctggaacaca agttagatgt gagctggggg catatgtca ggctgagagc 2880
atcagtagga tctgcaagag ctggagtcac caaggaacaa gatacgtact aaaatccaga 2940
taaaaataac tgccttaatc aataattgtt tatataactc tagagattaa taagcttatt 3000
attataqttt tataaaaata aattagaatt agaagggcat caatagaag cggacaaat 3060

aaaaatgtct tggaaagtga tgatcatcat ttgcgttactc ataaacacccc agcacgggct 3120
aaaggagagt tatttggaaag aatcatgttag tactataact gagggatacc tcagtgtttt 3180
aagaacaggc tggcacacta atgtcttcac attagaagtt ggtatgttg aaaatcttac 3240
atgtactgtat ggaccttagt taatcaaaaac agaactttagt ctaacaaaaaa gtgccttaag 3300
ggaactcaaa acagtctctg ctgatcagtt ggcgagagag gagaaatttg aaaaatcccg 3360
acaatcaaga tttgtcttag gtgcgatagc tctcgagtt gctacagcag cagcagtcac 3420
agcaggcatt gcaatagcca aaaccataag gcttgagagt gaggtaatg caattaaagg 3480
tgctctcaa ccaaactaatg aagcagtatc cacattaggg aatgggtgtc gggtcctagc 3540
caactgcagt agagagctaa aagaattttgt gagaaaaaac ctgactatgt caatcaacag 3600
gaacaaatgt gacattgtg atctgaagat ggctgtcagc ttcaacttcaat tcaacagaag 3660
atttctaaat gttgtcgccg agttttcaga caatgcaggg ataaacaccag caatatcatt 3720
ggacctgtatg actgtatgtc agttggccag agctgtatca tacatgccaa catctgcagg 3780
gcagataaaa ctgatgttgg agaaccgcgc aatggtaagg agaaaaggat ttggaaatct 3840
gataggggtc tacggaagct ctgtgattta catggttcaa ttggcgatct ttgggtgtcat 3900
agatacacct tggatca tcaaggcagc tccctcttc tcagaaaaaa acgggaatta 3960
tgcttcgcctc ctaagagagg atcaagggtg gtattgtaaa aatgcaggat ctactgttta 4020
ctacccaaat gaaaagact gcgaaaacaag aggtgatcat gtttttgc agacagcagc 4080
aggatcaat gttgctgagc aatcaagaga atgcaacatc aacatatcta ctaccaacta 4140
ccccatgcaaa gtcagcacag gaagacaccc tataaggcatg gttgactat cacctctcgg 4200
tgcttgggtg gcttgctata aaggggtaag ctgctcgatt ggcagcaatt ggggttggaaat 4260
catcaaacaa ttacccaaag gctgctcata c'ataaccaac caggatgcag acactgtAAC 4320
aattgacaat accgtgtatc aactaagcaa agttgaaggt gaacagcatg taataaaagg 4380
gagaccagg tcaagcagtt ttgatccaat caagtttct gaggatcagt tcaatgttgc 4440
gcttgatcaa gtcttcgaaa gcattgagaa ctagtcaggca ctatggacc agtcaaacaa 4500
aattctaaac agtgcagaaa aagaaacac tggtttcatt atcgtatcaa ttgggttgc 4560
tgttcttggt ctaaccatga tttcgttgcg catcatcatc ataatcaaga aaacaagaa 4620
gcccacagga gcacctccag agctgaatgg tgcaccaac ggccgttca taccacatag 4680
ttagtttaatt aaaaaatggg acaaataatc atgtctcgta aggctccatg caaatatgaa 4740
gtgcggggca aatgcacac agggagtgtat tgcaaaatca atcacaatattt ctggagttgg 4800
cctgatagat atttattgtt aagatcaat tatctcttaa atcagctttt aagaaacaca 4860
gataaggctg atggtttgc aataatatca ggagcaggtt gagaagatag aactcaagac 4920
tttgccttg gttctactaa tgggttcaaa gggtacattt atgacaacca aggaataacc 4980
aaggctgcag cttgctatag tctacacaac ataatcaagc aactacaaga aacagaagta 5040
agacaggcta gagacaacaa gctttctgtat agcaaacatg tggcgctcca caacttgata 5100
ttatcctata tggagatgag caaaactcct gcatctctaa tcaacaaacctt aaagaaacta 5160
ccaaggaaaa aactgaagaa attagcaaga ttaataattt attatcagc aggaactgac 5220
aatgactctt catatgcctt gcaagacagt gaaagacta atcaagtgc gtaaaacatgg 5280
tcccaaatttccatttccatg aggcatgtatc tatgatattt actcacaatgg aattaaaaga 5340
aacactgtct gatggatag taaaatcata caccatattt tatagtgtt acttagaaaa 5400
tatagaataatataatgtt aacttactt aagttagtaa aaaaataaaaa tagaatggaa 5460
taatgacaa tgaaaacattt agatgtatc aaaaatgtatg gatcttcaga aacgtgtat 5520
caactcaaaa aaataataaa aaaacactca ggttaatgtc ttattgcact aaaactgata 5580
ttggccttac tgacattttt cacagcaaca atcactgtca actatataaa agtagaaaac 5640
aatttgcagg catgtcaacc aaaaatgaa tcagacaaaa aggtcacaaa gccaaatacc 5700
acatcaacaa caatcagacc cacacccgtt ccaactgtatc tacatcattt gaaaaggctg 5760
attcagagac acaccaactc tgtcacaaaaa gacagcgata ctgttggag aatacacaag 5820
aatcaacgtt caaatataaa aatatacaag ttctttagtgc ctgggttccatc aaattcaaaa 5880
ggtacagatt gtgaggaacc aacagcccta tgcacaaaa agttaaaaac catagtagaa 5940
aaacatagaa aagcagaatg tcaactgtcta catacaaccc agtgggggtg cttcatccc 6000
taaaaataaca cggctttcaa cattaaaatc agaacaacctt ccacccaggat ctatcaatac 6060
agtggtttag ccattttaaa accaatattt atcttaggtt cagcacactt tgcaataata 6120
tgcaatagtc aatagttaaa ccactgttgc aaactcatcc ataataatataat cactgagtaa 6180
tacaaaatca agaaaatggg acaagtggct atggaagttt gagttggagaa cattcgagcg 6240
atagacatgt tcaaaagcaaa gataaaaaac cgtataagaa gcagcaggat ttagtgcattt 6300
gctacactga tccttattgg actaacagcg ttaagcatgg cacttaatattt ttcctgtatc 6360
atcgatcatg caacattaag aaacatgtatc aaaacagaaa actgtgtcaat catgccgtcg 6420
gcagaaccaa gcaaaaagac cccaaatgacc tccacagcag gcccaaacac caaaccataat 6480
ccacagcaag caacacagtg gaccacagag aactcaacat cccactgtgc aaccccaagag 6540
ggccatccat acacaggagc aactcaaaaca tcagacacaa cagtcctccca gcaaaaccaca 6600
gacaacaca cagcaccgct aaaatcaacc aatgaacaga tcacccagac aaccacagag 6660
aaaaagacaa tcagagcaac aacccaaaaa agggaaaaag gaaaagaaaa cacaacccaa 6720
accacaagca cagctgcaac ccaaaacaacc aacaccacca accaaatcatc aaatgcaagt 6780

aaatttccaa gaccttggaga gaaaaatcat ggaacaatat gaaaatagta ggagtgcacat 10560
ctcctgttat tgtagcatgt atggatgtt tttatgcac tagtttcatt taaaaggaa 10620
taattattga aaaattcgat actgacaaga ccacaagagg tcagagggg cccaaaagcc 10680
cctgggttagg atcaaggact caagagaaaa aattggttcc ttttataat agacaattc 10740
tttcaaaaaca aaaaaaagag caacttggaa caataggaa aatgagggtt gtgtacaaag 10800
gaactccagg gctaagaaga ttgctcaaca agatttgcatt aggaagctt ggtttagct 10860
ataaatgtgt gaaaccttta ttaccatgt tcatgagtgt aaacttctt cataggtt 10920
ctgttagtag tagaccatg gaattcccag ctctgttcc agttacagg acaacaaatt 10980
accattttga cactagtcca atcaaccaag cattaagtga gaggttcggg aacgaagaca 11040
ttaattttgt gttccaaaat gcaatcagct gcggatttag tataatgagt gtgttagaac 11100
agttactgg tagaagccca aaacaattag tccaatccc tcaattagaa gagatagata 11160
ttatgcctcc ttctgttattt caagaaaaat tcaattataa actagtgtt aagataacct 11220
ccgatcaaca catcttcagt cctgacaaaa tagacattt aacacttaggg aagatgttca 11280
tgcctaccat aaaaggtcaa aaaactgtac agttcttaaa taagagagaa aactattttc 11340
atggaaataa tttaattgaa ttcttactgt cagactgtc atgcccactgg tttgggat 11400
taacagaaca gtgcataagaa aacaatatct tttagggaaat ttgggtat gggttcatct 11460
cagatcatgc ttcatgttgc ttcaaggtt ttctatgtt attttaaaacc aacttttat 11520
gtatgtggg attcgaaggaa aagaatgtaa aagatgaaga tataatagat gaatccattt 11580
acaaattttt aagaatttgac aacacccccc ggagaatgtt cagcaaaatc atgtttgaat 11640
caaaagtcaa aaaaagaata atgttatatg atgtaaaattt cttatcatttta gtaggttata 11700
taggatttaa aaactggttt atagaacagt taagagtggt agaatttgcattt gaggtaacctt 11760
ggattgtcaa tgtaggaagga gagttgtt aattttaaatc aatcaaaattt tatctgcagt 11820
taatagaaca aagtctatct ttgagaataa ctgtattgtt ttatacagac atggcacatg 11880
ctcttacacg attaatttagg aaaaaattgtt tgtagtataa tgcactctt aatccaagtt 11940
catcaccaat gttaatctt actcaggta ttgatcccc aacacaacta gactattttc 12000
ctaggataat atttgagagg tttaaaatgtt atgataccat ttcagactac aacaaaggaa 12060
agttacaagaa gaatttacatg acattttac catggcaaca cgtaaacagg tacaattttt 12120
tcttagttc tacaggttgtt aaagtcagett tgaagacatg catcgggaaa ttgataaagg 12180
atttaaatcc taaagttctt tactttattt gagaaggagg aggttaactgg atggcaagaa 12240
cagcatgtga atatcctgtat ataaaatttgc tatataaggat tttaaaggat gacccctgtatc 12300
accatttaccc attagaatat caaagggtaa taggtgtatct aatagggtt atagatagt 12360
gtgaaggatt atcaatggaa accacagatg caactcaaaa aactcattttt gacttgcatac 12420
acagaataag taaagatgtt ttattgtataa cattgtgtga tgcagaattt aaaaacagaa 12480
atgattttttt taagatgtt atcttttggaa gaaaacatgtt attttatgtt agaatttgcata 12540
cagctttaggg aacagatctt tacttttttggaa gaaaacatgtt tgcgggtggac tgcataatata 12600
aatttaccatt tttttagaa tctgttagctt ctttttttattt gcaaggaaagc aaatttacatg 12660
ggtcagaatgtt acatactttt ttaacattttt gtcatcacaa taatcttaccc tgcataatgg 12720
aaataaaaaaa ttccaaaatgtt agaatacgat ttttttttttgc ttttttttttgc tccaaagaaac 12780
tggacaacaa atcaatttgaa gcaaaactgc aatcttttttgc ttttttttttgc tccaaagaaac 12840
taaacaaaaaa ggagttaat agacaaaaga aatttttttttgc ttttttttttgc tccaaagaaac 12900
ctatagcaac agttggccgc agtaagatgtt tagaattccaa atggttaaatg aataaaagca 12960
gtacaataat tgatgttgc gacatattttt ttttttttttgc ttttttttttgc tccaaagaaac 13020
atttcttgc agcatttagat aacacatacc ccaatatgtt ttttttttttgc ttttttttttgc tccaaagaaac 13080
gaaatgcaga aataaaagaa ctaatcaagg ttttttttttgc ttttttttttgc tccaaagaaac 13140
aataataatg ataatgttgc accataatctt cacacaactg agaaaataat cgtctaaacag 13200
ttttagttgtt catttttttttgc ttttttttttgc ttttttttttgc tccaaagaaac 13260
aatttgaaattt ttccaaaatgtt agaatacgat ttttttttttgc ttttttttttgc tccaaagaaac 13294

<210> 95
<211> 13350
<212> DNA
<213> human metapneumo virus

```
<400> 95
gtataaaatta gattccaaaa aaatatggga caagtaaaaa tgtctcttca agggatttcac 60
ctgagtgtatt tatacatacaa gcatgctata taaaagagt ctcagttacac aataaaaaga 120
gatgtgggta caacaactgc agtgacacccc tcatacattgc aacaagaaaa aacactgttg 180
tgtggagaaaa ttctgttatgc taaacatgtc gactacaaat atgctgcaga aataggaata 240
caatatatta gcacagctt aggatcagag agagtgcagc agattcttag gaactcaggc 300
agtgaagtcc aagtggtctt aaccagaacg tactctctgg ggaaaattaa aaacaataaa 360
```

ggagaagatt tacagatgtt agacatacac gggtagaga agagctgggt agaagagata 420
 gacaagaag caaggaaaac aatggcaacc ttgcttaagg aatcatcagg taatatccca 480
 caaatcaga ggcctcagc accagacaca cccataatct tattatgtt aggtgccta 540
 atattcaact aactagcatc aaccatagaa gtgggactag agaccacagt cagaaggct 600
 aaccgtgtac taagtatgc actcaagaga taccctagaa tggacatacc aaagattgcc 660
 agatccttct atgacttatt tgaacaaaaa gtgtatcaca gaagttgtt cattgagtt 720
 gcaaagcat taggctcatc atctacaggc agcaaagcag aaagtcttatt tgtaatata 780
 ttcatgcaag cttatgggc cggtcaaaaca atgctaaggt ggggggtcat tgccaggtca 840
 tccaacaata taatgttagg acatgtatcc gtccaaagctg agttaaaaaca ggtcacagaa 900
 gtctatgact tggtcgaga aatggccct gaatctggac ttctacattt aaggcaaaagc 960
 ccaaaagctg gactgttac actagccaac tgcccaact ttgcaagtgt tggtctcgga 1020
 aatgcctcag gcttaggcat aatcggtatg tatkagggg gagtacaaa cacagaatta 1080
 tttcagcag ctgaaagttt tgccaaaagt ttgaaagaaa gcaataaaaat aaatttctct 1140
 tcattaggac ttacagatga agagaaagag gctgcagaac atttcttaaa tgtgagtgac 1200
 gacagtcaaa atgattatga gtaattaaaaa aagtgggaca agtcaaaatg tcattccctg 1260
 aaggaaaaaga tattctttc atggtaatg aagcagaaaa attagcagaa gcttccaga 1320
 aatcattaag aaaaccaggc cataaaaagat ctcaatctat tataggagaa aaagtgaata 1380
 ctgtatcaga aacattggaa ttacctacta tcagtagacc tgccaaacca accataccgt 1440
 cagaaccaaa gtttagatgg acagataaaag gtggggcaac caaaactgaa ataaagcaag 1500
 caatcaaagt catggatccc attgaagaag aagagtctac cgagaagaag gtgctaccct 1560
 ccagtgtatgg gaaaaccctt gcagaaaaaga aactgaaacc atcaactaac accaaaaaaga 1620
 agtttatt tacaccaaat gaaccaggaa aatataaaaaa gttggaaaaa gatgctctag 1680
 attgctctc agataatgaa gaagaagatg cagaatcttcc aatcttaacc tttgaagaaa 1740
 gagataacttc atcattaaagc attggggca gattggatc aatagaggag aaattaagca 1800
 ttagatagg gcttattaaagc acatcaaca ttgctacagc agacccaca gcagcaagag 1860
 atgggatcag agatgcaatg attggcgtaa gagaggaatt aatagcagac ataataaagg 1920
 aagctaaagg gaaagcagca gaaatgttgg aagaggaat gagtcaacga tcaaaaatag 1980
 gaaatggtag tgtaaaaaatc acagaaaaaa caaaagagct caacaaaattt gttgaagatg 2040
 aaagcacaag tggagaatcc gaagaagaag aagaacccaaa agacacacaa gacaatagtc 2100
 aagaagatga catttaccat ttaattatgt agttaataaa aaataaaacaa tgggacaagt 2160
 aaaaatggag tcctacctg tagacaccta tcaaggcatt ctttacacag cagctgttca 2220
 agttgatcta atagaaaaagg acctgttacc tgcaagccta acaatatggt tccctttgtt 2280
 tcaggccaaac acaccaccag cagtgtgct cgatcgta aaaaccctga caataaccac 2340
 tctgtatgct gcatcacaaa atggccaat actcaaagtg aatgcacatc cccaaagggtgc 2400
 agcaatgtct gtacttcccc aaaaatttga agtcaatgctg actgttagcac tcgatgaata 2460
 tagcaaactg gaatttgaca aactcacaatg ctgtgaagta aaaacagttt acttaacaac 2520
 catgaaacca tacggatgg tatcaaaattt tgtagctca gccaaatcag ttggaaaaaa 2580
 aacacatgtt ctaatcgac tatgtgattt tatggatcta gaaaagaaca cacctgttac 2640
 aataccagca ttcatcaaat cagttcaat caaagagatg gatcagcta ctgttgaagc 2700
 tgctataagc agtgaagcag accaagctt aacacaggcc aaaatttgcac cttatgcggg 2760
 attaattatg atcatgacta tgaacaatcc caaaggcata ttcaaaaacgg ttggagctgg 2820
 gactcaagt atagtagaaac taggacatc tgccaggct gaaagcataa gcaaaaatatg 2880
 caagacttgg agccatcaag ggacaagata tgcttgaag tccagatc aaccaagcac 2940
 cttggccaaag agtactaacc cctatctcat agatcaatggc gtcaccatc tagttatata 3000
 aaaaatcaagt tagaacaaga attaaatcaa tcaagaacgg gacaaataaa aatgtcttgg 3060
 aaagtggtaga tcatttttc attgttataa acacctcaac acggctttaa agagagctac 3120
 ttagaagatg catgtacac tataactgaa ggatatctca gtgttcttag gacaggttgg 3180
 tacaccaatg ttttacact ggaggttaggc gatgttagaga accttacatg tgccgatgga 3240
 cccagctttaa taaaacaga attagacctg accaaaatgt cactaagaga gctcagaaca 3300
 gttctgctg atcaacttggc aagagaggag caaattgaaa atcccgacaa atcttagattc 3360
 gttcttaggag caatagcact cggtgttgc actgcacgtc cagttacaggc aggtgttgc 3420
 attgccaaaaa ccatccggct tggaaatgtt gtaacacgaa ttaagaatgc cctcaaaaag 3480
 accaatgaag cagtatctac attggggat ggagttctg tggatggcaac tgcagtgaga 3540
 gagctgaaag attttgttag caagaatcta acacgtcata tcaacaaaaaa caagtgcac 3600
 attgctgacc tggaaatggc cgttagcttca agtcaattca acagaaggat ccttaatgtt 3660
 gtgcggcaat tttcagacaa cgctggataa acaccacaa tatctttggc cttatgaca 3720
 gatgctgaac tagccagac tggatccaaat gtcacatc ctgcaggaca aataaaaactg 3780
 atgttggaga accgtgcaat ggttggaaaga aaagggttcg gattcctgtt aggagttac 3840
 ggaagctccg taatttacat ggttggactg ccaatcttgc ggtttagata cacgccttgc 3900
 tggatgtttaa aagcagcccc ttcttggca gggaaaaagg gaaactatgc ttgccttta 3960
 agagaagacc aaggatggta ttgtcaatggc gcaagggtca ctgttacta cccaaatgaa 4020
 aaagactgtg aaacaagagg agaccatgtc ttttgcgaca cagcagcagg aatcaatgtt 4080

gctgagcagt caaaggagtg caacataaac atatctacta ctaattaccc atgcaaagtt 4140
 agcacagaa gacatccat cagtatgggt gcactatctc ctcttgggc tttgggtgct 4200
 tgctacaagg gagtgagctg ttccattggc agcaacagag tagggatcat caagcaactg 4260
 aacaaggct gctcttata aaccaacca gacgcagaca cagtgacaat agacaacact 4320
 gtataccgc taagcaaagt tgaaggcgaa cagcatgta taaaaggaag gccagtgtca 4380
 agcagcttg acccagtcg gttccatgaa gatcaatc atttgcact tgaccaagtt 4440
 ttccagagca ttgagaacag tcaggcctg gtggatcaat caaacaagat cctaaggcgt 4500
 gcagagaaag gaaacactgg cttccatcatt gtaataattc taattgtctgt cttggctct 4560
 accatgatcc tagtgagttt tttatcata ataaagaaaa caaagaaacc cacaggagca 4620
 cttccagagc tgagtgggtg cacaacaaat ggcttcatac cacaatatta gttataaa 4680
 aataaaagtaa attaaaataa attaaaatta aaaataaaaaa ttggggacaa atcataatgt 4740
 ctcgcaaggc tccgtcaaa tatgaagtgc ggggcaaatg caatagagga agtgagtgca 4800
 agttaacca caattactgg agttggccag atagataactt attaataaga tcaaattatt 4860
 tattaaatca acttttaagg aacactgata gagctgatgg cttatcaata atatcaggag 4920
 caggcagaga agataggaca caagatttg tccttaggttc cacaatgtg gttcaagggt 4980
 atattgtga taaccaaagc ataacaaaag ctgcagcctg ttacagtcta cataatataa 5040
 tcaaacaact acaagaagtt gaagtttaggc aggctagaga taacaaacta tctgacagca 5100
 aacatgtac acttcacaaat ttagtccat cttatatgg gatgagcaaa actcctgcat 5160
 cttaatcaa caatctcaag agactgccg gagagaaact gaaaaaattt gcaaagctca 5220
 taattgactt atcagcaggc gctgaaaatg actcttcata tgccttgc当地 gacagtggaa 5280
 gcaactaatca agtgcagtg gcatggccat gtttcattt ctatagaggt tgatgacatg 5340
 atatggactc acaaggactt aaaagaagct ttatctgtat ggatagtggaa gtctcataact 5400
 aacattaca attgttattt agaaaaacata gaaattatatt atgtcaaggc ttacttaagt 5460
 tagtaaaaac acatcaggt gggataaaatg acaatgataa cattagatgt cattaaaagt 5520
 gatgggtctt caaaaaaaaatg tactccatc aaaaaaaaaa ttaaagccca ctctggtaaa 5580
 gtgttattt tacttaagtt aatattagct ttactacat ttctcacatg aacaatcacc 5640
 atcaattata taaaagttgg aaacaatctg caaatatgcc agtcaaaaaac tgaatcagac 5700
 aaaaaggact catcatcaaa taccacatca gtcacacca agactactt aaatcatgat 5760
 atcacacagt attttaaaag ttgattcaaa aggtatacaa actctgcaat aaacagtgac 5820
 acatgctgaa aaataaacag aaatcaatgc acaaataataa caacatacaa atttttatgt 5880
 tttaaatctg aagacacaaa aaccaacaaat tggataaaat tgacagattt atgcagaaac 5940
 aaacccaaaac cagcagttgg agtgtatcac atagtagaaat gcccattgtat atacacagtt 6000
 aaatggaaagt gctatcatta cccaaaccat gaaacccat cctaaatgtt aacaccagat 6060
 taggatccat ccaagtctgt tagtcaaca atttagttt ttaaaaatatt ttgaaaaca 6120
 agtaagtttca tatgataactt cataataataa agtataatt aattgcttaa tcatacatcac 6180
 aacattattc gaaaccataa ctattcaatt taaaagtaa aaaacaataa catgggacaa 6240
 gttagttatgg aggtgaaagt ggagaacatt cgaacaatag atatgctca agcaagagta 6300
 aaaaatcggt tggcacgcag caaatgcttt aaaaatgcct ctttggctct cataggaata 6360
 actacattga gtattgcctt caatatctat ctgatcataa actataaaaat gaaaaaaaaac 6420
 acatctgaat cagaacatca caccagctca tcacccatgg aatccagcag agaaactcca 6480
 acggccccca cagacaactc agacaccaac tcaagccac agatccaaat tcaacagtcc 6540
 acagaaggct ccacactctt cttgcagcc tcagcaagct caccagagac agaaccaaca 6600
 tcaacccagg atacaacaaa cccggccccc ttctgcaca cacaacaaac accaccaagg 6660
 gcaagcagaa caaagacaag tccggcagtc cacacaaaaa acaacccaaag gacaagctt 6720
 agaacacatt ctccaccacg ggcaacgcaca aggacggcac gcagaaccac cactctccgc 6780
 acaagcagca caagaaagag accgtccaca gcatcagttc aacctgacat cagcgcacaca 6840
 acccacaaaaa acgaagaagc aagtccagcg agcccacaaa catctgcaag cacaacaaga 6900
 atacaagga aagcgttgg ggcacacaca tcaacacat acaaccaac tagttaacaa 6960
 aaaatacaaa ataactctaa gataaaccat gcagacacca acaatggaga agccaaaaga 7020
 caattcacaat tctcccaaaa aaggcaacaa caccatatta gctctgccc aatctccctg 7080
 gaaaaaaacac tgcctccat tccaaaataa ccacaaccac cccaaagaaaa aaactggca 7140
 aaacaacacc caagagacaa ataaacatgg atccctctaa tgaatccact gttatgtct 7200
 atttccctga ctcatatctt aaggagtga ttcccttag tgagactaat gcaattgggt 7260
 catgtctctt aaaaagaccc tacctaaaaa atgacaacac tgcaaaagtt gccatagaga 7320
 atccgtttat cgagcatgtt agactaaaaa atgcagttca ttctaaatgtt aaaaatatcg 7380
 attacaagat agtagagcca gtaaacatgc aacatgaaat tatgaagaat gtacacagtt 7440
 gtgagctcac attattaaa cagttttaa caaggagtaa aaatattagc actctcaat 7500
 taaatatgt atgtgatgg ctgcagttaa agtctacatc agatgatacc tcaatcctaa 7560
 gttttataga tggataaattt ataccttagt gggtaagcaa ttgttttagt aattggtaca 7620
 atctcaacaa gttgattctg gaattcagga aagaagaat aataagaact gttcaatct 7680
 tgttaggtc attgggtaaa ttgtttttt ttgtatcatc atatggatgt atagtcaaga 7740
 gcaacaaaag caaaagagtg agttcttca catacaatca actgttaaca tggaaagatg 7800

ttagttaag tagattcaat gcaaattttt gtatatgggt aagcaacagt ctgaatgaaa 7860
 atcaagaagg gctagggttg agaagtaatc tgcaaggcat attaactaat aagcttatg 7920
 aactgtaga ttatatgctt agtttatgtt gcaatgaagg ttctcaactt gtgaaagagt 7980
 tcgaaggctt tattatgagt gaaattctta ggattactga acatgctaa ttcagtacta 8040
 gatttagaaa tactttatta aatggattaa ctgatcaattt aacaaaattt aaaaataaaa 8100
 acagactcg agttcatggt accgtgttag aaaataatga ttatccaatg tacgaagttg 8160
 tacttaagtt attaggagat actttgagat gtattaaattt attaataat aaaaacttag 8220
 agaatgctgc tgaattatac tatataattt gaatattcgg tcacccaaatg gtagatgaaa 8280
 gagatgcaat ggatgctgtc aaattaaaca atgaaatcac aaaaatccctt aggtgggaga 8340
 gcttgcacaga actaagaggg gcattcatat taaggattat caaaggattt gtagacac 8400
 aacaaaagatg gcccaaattt aaaaactttaa aagtgcctt tagagagatgg actatgtact 8460
 tcaaagcaaa aagttcccc agtcaacttg aattaagcga acaagattt ttagagctt 8520
 ctgcaataca gttgaacaa gagtttctg tccctgaaaaa aaccaacccctt gagatggat 8580
 taaatgataa agctatatca cctcctaaaaa gattaatatg gtctgtgtat ccaaaaaattt 8640
 acttacctga gaaaataaaaaa aatcgatatac tagaagagac ttcaatgca agtgatagtc 8700
 tcaaaacaag aagagtacta gagtactatt taaaagataa taaattcgac caaaaagaac 8760
 taaaatgta tgggtttaaa caagaatattt taaatgataa ggatcatattt gtctcgctaa 8820
 ctggaaaaga aagagaattt agtgttaggtt gaaatgttgc tatgcaacca gaaaaacagc 8880
 gacaaataca aatattggct gaaaaattttt tagctgataa tattgtacct ttttcccag 8940
 aaacctaacc aagatgtt gatcttagatc ttcagagaat aatggaaatc aaatcgaaac 9000
 tttcttctat taaaactaga agaaatgata gttataataa ttacattgca agagcatcca 9060
 tagtaacaga tttaaatgtaa ttcaaccaag cctttaggtt gaaaactaca gcgatctgt 9120
 cgatgttagc agatgaacta catggAACAC aaagcttattt ctgttgggtt catcttatcg 9180
 tccctatgac aacaatgata tggcctata gacatgcacc accagaaaca aaaggttaat 9240
 atgatataga taagatagaa gagcaaagt gtttattatg atatcatatg ggtggattt 9300
 aaggatgggt tccaaaactc tggacaatggt aagcttatc tctttagat gttgtatctg 9360
 taaaacacag atgtcaatgtt acatctttt taaacgggtt gaaatggata atagatgtaa 9420
 gtaaaccaggtaa tttttttttttagt gaaatgtt gacatggattt agcttggctg 9480
 taaaatgta aaaaagaaata agagatgcat acagaaatattt agggcataaa cttaaagaag 9540
 gggaaacata tataatcaaga gatcttcattt ttataatgaa ggtgatttcaaa tctgaaggag 9600
 taatgcattcc taccctata aaaaagatctt taagagtggg accatggata aacacaatattt 9660
 tagatgacat taaaaccaggtaa gcaatgttcaatggatctt atgtcaggaa tttagaattt 9720
 gggggaaag cataatagtt agtctgatattt taaggaattt ttggctgtat aatttataca 9780
 tgcataatc aaagcaacac ccccttagcgg ggaagcattt attcaaaacaa ctaaaataaa 9840
 cattaacatc agtgcagaga ttttttggaa taaaaaagggaa aatgaagta gtagatctat 9900
 gatgaacat accaatgcgg tttggaggag gagatccatg agtcttctat agatcttct 9960
 atagaaggac ccctgatattt ttaactgaaatg caatcgtca tggatattt ctgtttaagaa 10020
 tatcagccaa cataagaaat gaaatggggaaa taagtttctt caaaggcttca ctgtcaatag 10080
 aaaaaaaatgta acgtgctaca ctgacaacac taatgagaga tccctcaatg gttggcttag 10140
 agcgacaacg aaaaatgttca agtgcataatc atagaacacg agttaccacg atcttgc 10200
 tttctccaaa tcaacttttcc agcgatagttt ctatcacta cttttttttttaatggatattt 10260
 tcgaaatcat tgcgttccaaatcataatc tttatcctca tggactgaga gttttgtatg 10320
 aatcattacc ttttcataaaa gctggaaaaatg ttttggatattt gatatcgagaa acgaaatcca 10380
 taaccaactt attacagaga acatctgttca ttaatgggtt gatatttggatattt gatatttggatattt 10440
 ccatgatgtt gggatggatattt ctatcacta cttttttttttaatggatattt gatatttggatattt 10500
 tagaaatttcc aaccaatctt aatggtaggc ttttggatattt gatatttggatattt gatatttggatattt 10560
 gggatggatattt atggaaatattt ttttggatattt gatatttggatattt gatatttggatattt 10620
 gcatggatgtt ctatcatatcacta ttttggatattt gatatttggatattt gatatttggatattt 10680
 gcaatgttcaatggatattt gatatttggatattt gatatttggatattt gatatttggatattt 10740
 ctcaagagaa aaaaatttttttcc acatggatattt gatatttggatattt gatatttggatattt 10800
 aacagcttca agcaatttggatattt gatatttggatattt gatatttggatattt gatatttggatattt 10860
 gattactcaa taagatttttcc ttttggatattt gatatttggatattt gatatttggatattt 10920
 tattaccttttttcc gtttggatattt gatatttggatattt gatatttggatattt gatatttggatattt 10980
 tggaaatccccc agcatcgatcc ttttggatattt gatatttggatattt gatatttggatattt 11040
 ctatcatatcacta ttttggatattt gatatttggatattt gatatttggatattt gatatttggatattt 11100
 atgcaatcgatcc ttttggatattt gatatttggatattt gatatttggatattt gatatttggatattt 11160
 caaaaatgtt gtttggatattt gatatttggatattt gatatttggatattt gatatttggatattt 11220
 ttcaagggaa attcaatttttttcc aatggatattt gatatttggatattt gatatttggatattt 11280
 gtcccgatccaa aatggatattt gatatttggatattt gatatttggatattt gatatttggatattt 11340
 agaaaacaga ttttggatattt gatatttggatattt gatatttggatattt gatatttggatattt 11400
 agtcttgc ttttggatattt gatatttggatattt gatatttggatattt gatatttggatattt 11460
 aaaataatattt ttttggatattt gatatttggatattt gatatttggatattt gatatttggatattt 11520

acttcaaaat attccttatgt gtctttaaa ctaaactttt atgtagttgg gggtcccaag 11580
 ggaaaaacat taaagatcaa gatatagtag atgaatcaat agataaactg ttaaggattg 11640
 ataatactt ttggagaatg ttcagcaagg ttatgttga atcaaagggt aagaaaagga 11700
 taatgttata tgatgtaaaa ttcttatcat tagtaggtt tatagggtt aagaatttgt 11760
 ttatagaaca gttgagatca gctgagttgc atgaggtacc ttggattgtc aatgccaaag 11820
 gtgatctggt tgagatcaag tcaattaaaa tctatttgc actgatagag caaagttat 11880
 ttttaagaat aactgtttt aactatacag atatggcaca tgctctaca agattaatca 11940
 gaaagaagtt gatgtgtat aatgcactat taactccgt tccatcccc atggtaatt 12000
 taactcaagt tattgtatct acagaacaat tagtttattt ccctaagata acatttgaaa 12060
 ggctaaaaaa ttatgacact agtcaaatt atgctaaagg aaagctaaca aggaattaca 12120
 tgatactgtt gccatggcaa catgttataa gatataactt tgtcttagt tctactggat 12180
 gtaaagttag tctaaaaaca tgcattggaa aactttagaa agatctaaac cctaaagttc 12240
 tgtactttat tggagaaggg gcaggaaatt ggatggccag aacagcatgt gaatatcctg 12300
 acatcaaatt tgtatacaga agttaaaag atgacatttgc tcatttgc acttggat 12360
 accagagagt tataggagaa ttaagcagga taatagatag cggtgaaggg ctttcaatgg 12420
 aaacaacaga tgcaactcaa aaaactcatt gggatttgc acacagagta agcaaagatg 12480
 cttaattat aactttatgt gatgcagaat ttaaggacag agatgatttt ttaagatgg 12540
 taattctatg gaggaaacat gtattatcat gcagaatttgc cactacttgc 12600
 tctatttattt cgcaaagtat catgctaaag actgcaatgt aaaatttacat tttttgtga 12660
 gatcagttagc caccttattt atgcaaggtt gtaaactgtc aggctcagaa tgctacatac 12720
 tcttaaactt aggeccaccac aacaatttac cctgcattgg agaaatacaa aattctaaga 12780
 tgaaaatagc agtgtgtat gattttatgc ctgaaaaaaaaa acttgacaaat aatctattt 12840
 aagccaactg taaatcattt ttatcaggc taagaatacc gataaaaatgg aaagaattaa 12900
 atagacagag aaggatttta acactacaaa gcaaccattt ttctgttagca acagttggag 12960
 gtagcaaggt catagagttt aatggttaa caaaacaaggc aaacacaata attgatttgt 13020
 tagaacatattt ttaaatttgc cccaaagggtt aattaaatattt tgattttttt gaagcatttt 13080
 aaaataactt ccctaataatg attaaactt tagataatct aggaatgc gagataaaaaa 13140
 aactgatcaa agtaacttgc tatattgttgc taagttaaaaa atgaaaaatg ataaaaatga 13200
 taaaataggt gacaacttca tactatttca aagtaatcat ttgattatgc aattatgtaa 13260
 tagttatattt aaaaactaaaaa atcaaaagggtt agaaactaac aactgtcatt aagtttattt 13320
 aaaataagaa attataatttgc gatgtatacg 13350

<210> 96

<211> 13215

<212> DNA

<213> human metapneumo virus

<400> 96

acgcggaaaaa aacgcgtata aattaagttt caaaaaaaaacca tgggacaagt gaaaatgtct 60
 cttaaggga ttcaccttgc tgatctatca tacaaggatc tstatattaaa agagtctcag 120
 tataataaa agagatgtt aggccacaaca accgcagtga caccctcatc attgcaacaa 180
 gaaataacac tattgtgtgg agaaattctt tatgctaagc atgctgatta caaatatgtct 240
 gcagaaatag gaatacaata tattagcaca gctctaggat cagagaggtt acagcagatt 300
 ctaagaaact caggtatgtt agtccaaatgt gttttacca gaacgtactc cttggggaaa 360
 gttttttttt acaaaaggaga agatttacag atgttagaca tacacggagt agagaaaaagc 420
 tgggtggaaag agatagacaa agaagcaaga aaaacaatgg caactttgtt taaagaatca 480
 tcaggcaata ttccacaaaaa tcagaggcct tcagcaccatg acacacccat aatcttattt 540
 tggtaggtt ccttaatattt taccaaaacta gcatcaacta tagaagtggg attagagacc 600
 acagtcgaaa gagctaaatgt tggactaattt gatgcactca aaagataccc taggatggac 660
 ataccaaaaaa tgccttagatc ttcttatgtac ttatttgcac aaaaatgttca ttacagaatgt 720
 ttgttcattt agtatggcaaa agcatttaggc tcatttcata caggcagcaaa agcagaaaaatgt 780
 ttatttcgtt atatatttcat gcaagtttac ggtgctggc aaacaatgtt gagggtgggaaa 840
 gtcattgcca ggtcatctaa caatataatgt ttaggacatg tattttttca agctgagttt 900
 aaacaagtca cagaagtctt tgacctgggtt cgagaaaatgg gcccgttcaatc tgggctcccta 960
 catttaaggc aaagcccaaaa agctggactt ttatcactatg ccaattgtcc caactttgtct 1020
 agtgttgc tcggcaatgc ctcaggcttta ggcataatag gtatgtatgc cggggagatgt 1080
 ccaaacacag aactattttc agcagcagaa agctatgttca agatgtttgaa agaaagcaat 1140
 aaaattaact ttcttcattt aggactcaca gatgaagaaa aagaggctgc agaacaacttc 1200
 ctaaatgtga gtgacgacag tcaaaatgtt tatgatgtttaat taaaatgggaaatgc ggacaagtca 1260
 aaatgtcattt ccctgaagggaa aagatatttgc ttcatgggtaatc gcaaaaatttgg 1320

cagaagactt taaaaatca ttaagaaaac ctaatcataa aagatctcaa tctattatag 1380
gagaaaaagt gaacactgta tctgaaacat tggaattacc tactatcagt agacctacca 1440
aaccgaccat atgtcagag ccgaagttag catggacaga caaagggtgg gcaatcaaa 1500
ctgaagcaaa gcaacaatc aaagttatgg atcctattga agaagaagag ttactgaga 1560
aaagggtgct gcctccagt gatggaaaa ctctgcaga aaagaaggtaa aaaccatcaa 1620
ccaacactaa aaagaaggtc tcattcac caaatgaacc agaaaaatac acaaagttgg 1680
agaaagatgc tctagacttg cttcagaca atgaagaaga agatgcagaa tcctcaatct 1740
taaccttcga agaaagagat acttcatcat taagcattga agccagacta gaatcgattg 1800
aggagaaaatt aagcatgata ttagggctat taagaacact caacattgt acagcaggac 1860
ccacagcgc aagagatggg atcagagat caatgattgg cataaggag gaactaatag 1920
cagacataat aaaagaagcc aagggaaaag cagcagaaat gatggaagaa gaaatgaacc 1980
agcggacaaa aataggaaac ggtagtgtaa aattaactga aaaggcaag gagctcaaca 2040
aaatttgtga agacgaaagc acaagtggt aatccgaaga agaagaagaa caaaagaca 2100
cacagggaaa taatcaagaa gatgacattt accagttat tatgtagttt aataaaaata 2160
aaaatgggac aagtggaaaat ggagtcctat ctgttagaca cttatcaagg catcccttac 2220
acagcagctg ttcaagttga tctagtagaa aaggacctgt tacctgcag cctaacaata 2280
tggttccccct tggcaggc caatacacca ccagcagttc tgcttgcata gcttaagact 2340
ctgactataa ctactctgtg tgctgcata caaagtggtc caatactaaa agtgaatgca 2400
tcagccagg gtgcagcaat gtctgtactt cccaaaaagt ttgaagtcaa tgcfactgt 2460
gcacttgacg aatatagcaa attagaattt gacaaactt cagtcgtgaa agtggaaaaca 2520
gtttacttaa caaccatgaa accatatggg atgttatcaa agttgtgag ctccggccaa 2580
tcagttggca aaaaaacaca tgatctaattt gcattatgtg attttatgaa tctagggaaaag 2640
aacacaccag ttacaatacc agcatttttca aatcagttt cttatcaagga gagtgaatca 2700
gccactgtt aagtcgaat aagcagttaa gcagaccaag ctctaaacaca agccaaaatt 2760
gcacccctt cggactgt catgattatg accatgaaca atcccaagg catattcaag 2820
aagcttggag ctgggaccca agttatgaa gaactaggag catatcaaga ggatgttca 2880
ataagtaaaa tatcgaagac ttggagccat caaggaacaa gatatgtct gaagtcctgt 2940
taacagccaa gcaacctggc caagaactac caactctatt ctatcaacaca agccaaaatt 3000
attttagtta tataaaaatc aagtttagaa aagaattaaa tcaatcaaga acgggacaaa 3060
taaaaatgtc ttgaaagtg gtgatcatt tttcattgtc aataacacca caacacggc 3120
ttaaagagag ctacctagaa gaatcatgtc gcactataac tgagggatat cttagtgc 3180
tgaggacagg ttgttatacc aacgttttta cattagaggt ggggtatgt aaaaaccta 3240
catgttctga ttgaccttagc ctaataaaaa cagaattaga tctgacccaaa agtgcactaa 3300
gagagctcaa aacagtctct gctgaccaat tggcaagaga ggaacaaattt gagaatccc 3360
gacaatctag gttgttcta ggagcaatag cactcgggtg tgcaacacgca gctgcagtca 3420
cagcagggtg tgaatttgc aaaaccatcc ggcttggag gtaagtccaa gcaattaaga 3480
atgccctcaa aacgaccaat gaagcagttt ctacattggg gaatggagtt cgagtgttgg 3540
caactgcagt gagagagcta aaagacttt tgaccaagaat ttaaactctgt gcaatcaaca 3600
aaaacaagtg cgacattgtat gacctaaaaa tggctgttag cttcagtc aaataacacca 3660
ggtttctaaa tggcggcgg gtaaaaagcag ccccttcttg aataacacca gcaatatctt 3720
tggacttaat gacagatgtc gaactagcca gggccgttca taacatgccc acatctgcag 3780
gacaaataaa attgtatgtt gagaaccgtg cgatgggtcg tccgttaattt acacgggtc 3840
tgatagggtt ctacgggagc tccgttaattt acacgggtc tagacacgca ttgctggata 3900
tagacacgca ttgctggata gtaaaaagcag ccccttcttg atgcttgcctt cttaagagaa 3960
actacccaa tgagaaaagac gaccaagggtt ggtattgtca tccgttgc gacacagcag 4020
caggaattaa tggcggcgg gtaaaaagcag ccccttcttg aataacacca gcaatatctt 4080
accatcgaa agtcagcaca ggaagacatc ctatcgtat caacatcc actacaaaatt 4140
gggctctgg tggacttgcata aaaggagttt gctgttccat ggttgcactg tctccttgc 4200
tctatcaagca gctgaacaaa cttatcgtat gggcggcgg gacacagcag 4260
caatcgaa gctgaacaaa cactgtatata caatcgtat ggttgcactg tctccttgc 4320
caatcgaa gctgaacaaa cactgtatata caatcgtat ggttgcactg tctccttgc 4380
ggagaccagt gtcaggcgc tttgatccaa tcaagtttcc aacatcgaa gacacagcag 4440
cacttgacca agttttttagt aacatttttca acagccaggc tggcggcgg gacacagcag 4500
gaatccaaag cagtgcagag aaaggaaata ctggcttata ttagtagat caatcaaaca 4560
ctgtccttgg ctctagcat atccttagtga gcatcttcat tataatcaag aaaaacaaaga 4620
aaccacccgg agcacctcca gagctgatgt gtgtcacaaa caatggcttc ataccacaca 4680
gttagttat taaaataaa ataaaatttgg gacaaatca taatgtctcg caaggctcca 4740
tgcaaatatg aagtgcgggg caaatgcaac agaggaagtg agtgtaaatgtaa accacacaat 4800
tactggagtt ggccagatag atacttatta ataagatcaa actatctatt aaatcagctt 4860
ttaaggaaca ctgatagagc tgatggcttca tcaataatata gagggtatata tgatgataac 4920
agaacgcaag attttgttctt aggttccacc aatgtggttc aacataatca gcaactacaa 4980
caaaacataaa caaaaqctqc aqccctqctac agtctacaca

aaaggtaaag ttaggcaggc tagagatagc aaacttatctg acagcaagca tggggactc 5100
cataacttaa tcttatctta catggagatg agcaaaaactc ccgcatttt aatcaacaat 5160
cttaaaagac tgccgagaga aaaactgaaa aaattagcaa agctgataat tgacttatca 5220
gcaggcgctg acaatgactc ttcatatgcc ctgcaagaca gtaaagcac taatcaagtg 5280
cagtgagcat ggtctgttt tcattactat agaggttgat gaaatgatat ggactaaaa 5340
agaattaaaa gaagctttgt ccgatggat agtgaagtct cacaccaaca tttacaattg 5400
ttattnagaa aacatagaaa ttatataatgt caaggcttac ttaagttgt aaaaacacac 5460
atcagagtgg gataagtgac aatgataaca ttagatgtca taaaagtga tgggtcttc 5520
aaaacatgt a ctcacccaa aaaataatc aaagaccatt ctggtaaagt gcttattgca 5580
cttaagttaa tattagctt actaacattt ttccacaataa caatcactat aaattacata 5640
aaagtagaaa acaatctaca aatatgccag tcaaaaactg aatcagacaa agaagactca 5700
ccatcaaata ccacatccgt cacaaccaag actactctag accatgat aacacagtat 5760
tttaaaagat taattcaag gtatacagat tctgtgataa acaaggacac atgtggaaa 5820
ataagcagaa atcaatgcac aaatataaca acatataaat tttatgtt aacactgttag 5880
gactcaaaaa tcaacagtt tgatagactg acagatctat gcagaaacaa atcaaaatcat 5940
gcagctgaag catatcatac agtagaatgc catgcatat acacaattga gtgaagtgc 6000
tacaccacc caatagatta aacccattt tgaatgtt aactagacta ggatccgtct 6060
aagactatca gttcaatagt ttagttt aaaaatattt gagaacaggt aagttctat 6120
ggcacttcat agcaataggt aataattaac agcttaatta taattaaaac attatttaaa 6180
accgtacta tttaatttac aaagtaaaaa caaaaatatg ggacaagtag ttatggaggt 6240
gaaagttagag aacatccgag caatagacat gctcaagac agagtggaaa atcgtgtggc 6300
acgttagaaaa tgctttaaaa atgcttctt aatcctcata ggaataacta cactgagtat 6360
agctctcaat atctatctga tcataaaacta cacaatacaa aaaaccacat ccgaatcaga 6420
acaccacacc agtcaccac ccacagaacc caacaaggaa gcttcaacaa tctccacaga 6480
caacccagac atcaatccaa gtcacacagca tccaaactcaa cagtcacacag aaaaacccac 6540
actcaacccc gcagcatcag cgagccatc agaaacagaa ccaagtcacatc caccagacac 6600
aacaacccgc ctgtccctccg tagacaggtc cacagcacaat gcaatccatc gcaatcccc 6660
gacaaaacccg acagtccaca caatcaacaa cccaaacaca gcttccagta cacaatcccc 6720
accacggaca acaacgaagg caatcccgag agccaccact ttccgcatga gcagcacagg 6780
aaaaagagcca accacaaatc tagtccagtc cgacagcagc accacaaccc aaaaatcatga 6840
agaaacaggt tcagcgaacc cacaggcgte tgcagcacaat atgcaaaact agcacaccaa 6900
taatataaaa ccaaattagt taacaaaaaa tgccgatag tagtccaaatc aacatgttag 6960
gtaccaacaa tcaagaaacc aaaagacaac tcacaatctc cttttttttt cttttttttt 7020
atgtcagtt tgcattcaaa tcttgggg aaaccttctac ccacatacta aacacatcac 7080
aaccatctca agaaaaagaaa ctggccaaaa cagcatccaa gagacaaata gcaatggatc 7140
ctcttaatga atccactgtt aatgtcttccatccatc gtagtccatc gtagtccatc 7200
cttttagtga aactaatgca atgggtcat gtctttttt aagaccttac taaaaaaatg 7260
acaacactgc aaaagtgtcc atagagaatc ctgttattga gcatgtgaga ctcaaaaatg 7320
cagtcaattc taaaatgaaa atatcagatt acaaggttgtt agagccagta aacatgcaac 7380
atgaaataat gaagaatgtc cacagtgtg agtcacactt atgaaacacag ttttttacaa 7440
ggagtaaaaa cattagact ctcaaaattaa atatgatatg tgattggctg caattaaagt 7500
ctacatcaga tgatccatca atcctaagtt tcataatgtt agaattata cctagttggg 7560
taagcaactg gtttagtaat tggtacaatc tcaataatgtt aattttggaa ttccagaagag 7620
aggaagtaat aagaaccggc tcaatcttgc aggtttttt gggtaaatta gtttttattt 7680
tatcatcata cggatgtatc gtcaagagca aaaaaagcaa aagagtggc ttcttcacat 7740
acaatcaact gttAACATGGG aaagatgtga tggtaatgtt attaatgcg aattttgtt 7800
tatggtaag caatagtctg aatgaaaatc aggaagggtt agggtaaaga agtaatctac 7860
aaggtagttt aactataaaa ctatatgaaa ctgttagatta tatgcttaagt ttatgttgca 7920
atgaaggttt ctcaacttgc aaagaggctg aagggtttttt tatgagtgaa atccttagga 7980
ttactgaaca tgctcaattc agtactatgtt ttagaaatata tttttaatat ggattaacag 8040
atcaattaaac aaaattaaaaa aataaaaaaca gactcagagt tcatggtacc gtattagaaa 8100
ataatgatta tccatgtat gaagttgtac tttttttttt aggagataact ttgagatgtt 8160
tcaattattt aactataaaa aacttagaga atgctgcaga attataatcat atttttttttt 8220
tttttggtca tccaatggta gatggaaagag atgcaatggaa tgctgtcaaa tttttttttt 8280
aaatcacaacaa aatcctaagg ttggagagct tgacagaact aagaggagca ttcatattaa 8340
ggattatcaa aggattttgtg gacaacaaaca aaaggtggcc caaaaataaa aattttatag 8400
tgcttagcaa aagatggact atgtacttca aagctaaaaa ttatcccaagt caactcgaat 8460
taagtgaaca agactttcta gagcttgcg caatacaatt tgaacaagag ttttctgttc 8520
ctgaaaaaac caatcttgcg atggtattaa atgacaaagc catatcacct cctaaaagat 8580
taatattgtc tggttatcca aagaattact tacctgagac gataaaaaat cgatatttag 8640
aagaaacttt caatgcgagc gatagtctca aaacaagaag agtactagag tactattttt 8700
aagacaataa atttgcataa aaggaactt aagttatgtt agttagacaa gaatattttt 8760

tgataaaggagc acatggtc tcattaactg gaaaagaaag agaattaagt gtaggtgaa 8820
tggctat gcaaccagga aaacagcgac aaatacaaatttggcagaaa aaattgttag 8880
ctgataacat tgtacccccc ttccccggaaa ccttaacaaa gtatggtgat ctagatcc 8940
agagaataat ggaaatcaaa tcagaacttt ctcttatcaa aaccagaaga aatgacagtt 9000
ataataatta cattgcaaga gcatccatag taacagattt gagaaggttc aacaaggcct 9060
ttagatatga aactacagcg atctgtgcgg atgtagcaga cgaattacat ggaacacaaa 9120
gcttattctg ttgttacat cttatcgcc ctatgactac aatgataatgt gcctatagac 9180
atgcaccacc agaaacaaaa ggtgaatatg atatagataa gatagaagag caaagtggc 9240
tatatagata tcacatgggc ggtattgaag gatgggtgtca aaaactctgg acaatggaa 9300
ctatatctt attggatgtt gtatctgtaa agacacgggt tcaaattgaca tctttattaa 9360
acggtgataa ccaatcaata gatgtaaatg aaccagtcaa gttatctgaa gggttagatg 9420
aagtgaaggc agattatcgcc ttagcaataa aaatgctaaa agaaataaga gatgcataca 9480
gaaatataagg ccataaactt aaagaagggg aaacatataat atcaagggtt cttcaattta 9540
taagcaaggt gattcaatct gaaggagtg tgcattctac ccctataaaa aaggtcttga 9600
gagtaggacc atgataaac acaatattag atgacattaa aactagtgt gagtcaatag 9660
ggagtctatg tcaagaatataa gaatttaggg gagaagcat aatagttagt ctgatattaa 9720
gaaacttctg gctgtataac ttatacatgc atgaaatcaaa gcaacatctt ttgcagggg 9780
aacagttatt caaacaacta aataaaacat taacatcagt gcagagattt tttgaaat 9840
aaaaggaaaa tgaggtagta gatctatgg tgaacatacc aatgcaattt ggaggaggag 9900
atccagtagt cttctataga tctttatataa gaaggacccc tgatttttt actggggca 9960
tcagccatgt agatattctg taaaaatataat cagtaacat aaaaatgaa acggaaatgaa 10020
gtttcttcaa agcctacta tcaatagaaa aaaaatgaaacg tgctacactg acaacgctaa 10080
tgagagatcc tcaatgtttt ggatcagaac gacaagcaaa ttaagtctt ccccaatca aatcttctgt gatagtgtca 10200
gaacagcagt taccatgtc tacactatag cagaaatgaa gaagaagtgg gaatcattgc agaaaacata aacacgtt 10260
atcctcatgg gctgagagta taaacatgt atcaggggaca aatctataa ccaacttatt tcacaaaagct gaaaaagttt 10320
atggtgaaga tattgacagg gatgtatcta tgatgttggaa aatcttagg tccgcttata 10380
gaatattgtc agtagttgtt gatgtatag aatattccaat caaatctaataat ggtaggctgaa 10500
tatgttgtca aatctctagg actttaagag agacatcatg ttatataatg cattgccc 10560
gagtaacatc tcctagcatc actacatgta tggatgtcat aatgcaact agttctt 10620
tgaagggat aattatagaa aagttcagca ctgacagaac tggcagcat tactcaacaa 10680
caaaaagccc ttgggttaggg tcgagttactc aagagaaaaaa aaccccttataatgatgtt 10740
gacaaattct ttcaaaaacaa caaagagaac agctagaagc ttgcagcat tactcaacaa 10800
tgtataaagg gacaccaggc aagttcagca ctgacagaac aaccccttataatgatgtt 10860
gcattagttt caaatgtgtt agacctatgg aattcccagc ttgcagcat tactcaacaa 10920
ataggttattc tgtcagtagt caacaaatttccatgacttataatgatgtt 10980
caatgacat tatgccacca actagtctta ttaatcaagc ttgcagcat tactcaacaa 11040
agataacttc tgatcaacat ttccaaaatg cgatcagctg agaagccaa aacagttatg ttaatacc 11100
aatgctcat gcttactata aagttcagca ctgacagaac ccagtgttca aagggaaatttcaatgacat 11160
attatttcca tgggaacaat tggatgttca aaccccttataatgatgtt 11220
gtgggatatt aacagaacaa tggatgttca aaccccttataatgatgtt 11280
ggtttatatc agatcatgtt aatcttctgttccatgacttataatgatgtt 11340
aactttatg tagttggggaa atcaataga taaattgttca aatcttctgttccatgacttataatgatgtt 11400
aatcaataga taaattgttca tggatgttca aaccccttataatgatgtt 11460
tgtttgaaacc aaaagtttaag tagctcacat aggtttca aatcttctgttccatgacttataatgatgtt 11520
aaatacccatg gattgtcaacttgc tctcacacga tggatgttca aaccccttataatgatgtt 11580
atttgcaact gatagaacaa ccccaatccatgacttataatgatgtt 11640
tggcacatgc tctcacacga attcttccatgacttataatgatgtt 11700
ccccaaatccatgacttataatgatgtt 11760
attacttccc caagataaca tggatgttcaacttgc tctcacacga tggatgttca aaccccttataatgatgtt 11820
ctaaagaaaa gctaaacaaga aatccatgacttataatgatgtt 11880
ataactttgtt ctttagttct tggatgttca aaccccttataatgatgtt 11940
ttatgaaaga cttaaatccatgacttataatgatgtt 12000
tggccagaac agcatgtgaa tggatgttcaacttgc tctcacacga tggatgttca aaccccttataatgatgtt 12060
accttgcata tcattatccatgacttataatgatgtt 12120
tagatagtgg tgaaggactt tggatgttcaacttgc tctcacacga tggatgttca aaccccttataatgatgtt 12180
attqataca cagggttaagc aatccatgacttataatgatgtt 12240
ttatgatgttcaacttgc tctcacacga tggatgttca aaccccttataatgatgtt 12300
ttatgatgttcaacttgc tctcacacga tggatgttca aaccccttataatgatgtt 12360
ttatgatgttcaacttgc tctcacacga tggatgttca aaccccttataatgatgtt 12420
ttatgatgttcaacttgc tctcacacga tggatgttca aaccccttataatgatgtt 12480

aggacagaga tgatTTTTT aagatggtaa ttcttatggag aaaacatgt a ttatcatgca 12540
 gaatttgcac tacttatggg acggacctc atttattcgc aaagtatcat gctaaagact 12600
 gcaatgtaaa attacCTTT tttgtgagat cagttgctac tttcattatg cagggttagta 12660
 agctgtcagg ttcaaatgc tacatactct taacactagg ccaccacaac agtttaccc 12720
 gccatggaga aataaaaaat tctaagatga aaatagcagt gtgtaatgtat ttttatgtcg 12780
 caaaaaaaaaa cgacaataaa tcaatttgaag ctaattgtaa atcacttttgc tcagggctaa 12840
 gaataccat aaataagaag gaactagata gacagagaag attattaaca ctacaaagca 12900
 atcatttttc tggcaaca gttggcggtt gcaagatcat aggtctaaa tggttaacaa 12960
 acaaagcaag tacaataattt gatttttttag aacatattttt aaattctcca aagggcgaat 13020
 taaattatga ttttttttga gcattggaga acacttaccc taatatgatt aaactaatag 13080
 ataacttagg gaatgcagag attaaaaaaac ttatcaaagt aacaggatac atgcttgtaa 13140
 gtaaaaaatg aaaaatgtat aagatgacaa aatagatgac aacttcatac tattctaaat 13200
 taatttatttgc attat 13215

<210> 97
 <211> 13135
 <212> DNA
 <213> human metapneumo virus

<400> 97
 acgcggaaaa aacgcgtata aattaaattc caaacaaaaac gggacaaata aaaaatgtctc 60
 ttcaagggtt tcacctaagt gatctgtcat ataaacatgc tatattaaaaa gagtctcaat 120
 acacaataaa aagagatgtt ggcaccacaa ctgcagtgtac accttcatca ttgcagcaag 180
 agataacact tttgtgtgga gagattctttt actactaaaca tactgattac aataatgtcg 240
 cagagatagg gatacaatattt atttgcacag ctctaggatc agaaagagta caacagattt 300
 taagaaatttcc aggttagttag gttcaggtgg ttctaaccaa gacatactct ttagggaaag 360
 gtaaaaaatag taaaggggaa gagttgcaaa tgtagatatacatggatg gaaaaagagtt 420
 gggtagaaga aatagacaaa gaggtcaagaa aaacaatgtt gactttgtca aaggaatcat 480
 caggcaacat cccacaaaaac cagaggcctt cagcaccaga cacaccaata attttattgt 540
 gtgttaggtgc tttatatttcc actaaaacttag catcaacaat agaagttgga ctagagacta 600
 cagttagaag ggctaacaga gtgttagtgc atgcgctaa aagataaccctt agggtagata 660
 taccaaagat tgcttagatct ttttatgtac tatttgagca gaaagtgtat tacaggagtc 720
 tattcattgtt gtagggaaa gctttaggtt catcttcaac aggaagcaaa gcagaaagtt 780
 tgtaggtaaa tatattttatg caagctttagt gaggccgtca gacaatgtca aggtgggtg 840
 tcattgccag atcatctaaac aacataatgc tagggcatgt atctgtgca gctgaattga 900
 aacaagttac agaggttttt gattttgtt gagaatggg tcctgaatctt gggcttttac 960
 atctaaagaca aagtccaaag gcaggactgt ttcgttgc taatttgc aattttgtca 1020
 gtgtgtttct tggtaatgtt tcaggcttagt gtataatcg aatgtacagg ggaagagtgc 1080
 caaacacaga gctattttctt gcagcggaaa gttatgcgc aagttaaaaa gaaagcaaca 1140
 aaatcaactt ctccttcattt gggctcagc acgaagaaaaa agaagctcga gaacacttct 1200
 taaacatgtt gtagtacaaat caagatgtt atgatgtt aaaaaaaaaactgg gacaagtcac 1260
 aatgttcattt cctgtttttttt aagatatccctt gttcatgggtt aatgtacagg caaaaatagc 1320
 agaagcttcc cggaaatcac taaaaagatc aggtcacaaaaa agaaccctgtt ctattgttagg 1380
 gggaaaaatgtt aacactatat cggaaactctt agagcttaccc accatcagca aacctgcac 1440
 atcatctaca ctgttagtgc caaaatttgc atggccagac agcagcggag ccaccaaaac 1500
 cacagaaaaaa caaacaaacca aaacaacaga tcctgttggaa gaagaggaac tcaatgaaaa 1560
 gaaggatata ccttccaggatg atggaaagac tcctgcagag aaaaaatcaa aatctccaaac 1620
 caatgtaaaaa aagaaaatgtt ccttcacatc aatgtacccca gggaaaatata ctaaactatgaa 1680
 aaaagatgtcc cttagatttgc tcttcagacaa tgaggtttttt gacgcagatgtt cctcaatcc 1740
 aaccccccgtt gggaaaaatgtt aatgtacccca aatgtacccca aatgtacccca 1800
 agagaagctt aatgtacccca aatgtacccca aatgtacccca aatgtacccca 1860
 aacggctgc aatgtacccca aatgtacccca aatgtacccca aatgtacccca 1920
 agaaaataata aatgtacccca aatgtacccca aatgtacccca aatgtacccca 1980
 aagggtttttttt aatgtacccca aatgtacccca aatgtacccca aatgtacccca 2040
 aattttttttttt aatgtacccca aatgtacccca aatgtacccca aatgtacccca 2100
 tcaggataac aatgtacccca aatgtacccca aatgtacccca aatgtacccca 2160
 acaatggggac aatgtacccca aatgtacccca aatgtacccca aatgtacccca 2220
 acagctgtcg ttcaggatgtt aatgtacccca aatgtacccca aatgtacccca 2280
 tggttttttttt aatgtacccca aatgtacccca aatgtacccca aatgtacccca 2340
 ttgtactataa caactctgtt aatgtacccca aatgtacccca aatgtacccca 2400

tatgcaataa tcaatggtca aaccactgtt gcaaactcac ccataatata atcaactgagt 6180
 aatacaaaaac aagaaaaatgg gacaagtggc catggaaagta agagtggaga acattcgccc 6240
 aatagacatg ttcaaagcaa aaatgaaaaa ccgtataaga agtagcaagt gctatagaaa 6300
 tgctacactg atccttattg gattaacagc attaagtatg gcacttaata ttttttaat 6360
 cattgattat gcaatgtta aaaacatgc caaagtggaa cactgtgtta atatgccccc 6420
 ggtagaacca agcaagaaga ccccaatgac ctctgcagta gacttaaaca ccaaacccaa 6480
 tccacagcg gcaacacagt tggccgcaga ggattcaaca tctctagcag caacccctaga 6540
 ggaccatcta cacacaggg caactccaac accagatgca acagtcttc agcaaaccac 6600
 agacgagtc acaacatgc tgagatcaac caacagacag accacccaaa caaccacaga 6660
 gaaaaagcca accggagcaa caacccaaaaa agaaaaccaca actcgaacta caagcacagc 6720
 tgcaacccaa acactcaaca ctaccaacca aactagctat gtgagagagg caaccacaac 6780
 atccgcccaga tccagaaca gtgcacaaac tcaaagcagc gaccaaacaa cccaggcagc 6840
 agacccaagc tccccaccac accatacaca gaaaagcaca acaacaacat acaacacaga 6900
 cacatcctct ccaagtagtt aacaaaaaaaaa ctataaaata atcatgaaaaa ccgaaaaact 6960
 agaaaaagtta atttgaactc agaaaaagaac acaaacacta tatgaattgt ttgagcgtat 7020
 atactaatga aatagcatct gtttgtcat caataatacc atcattattt aagaataaag 7080
 aagaagctaa aattcaaggg acaaataaca atggatccat tttgtgaatc cactgtcaat 7140
 gtttatcttc ctgactcata tctcaaagga gtaatatctt tcagtgaaac caatgcaatt 7200
 ggctcatgcc ttttggaaaag accctatcta aaaaaagata acatgctaa agttgctgta 7260
 gaaaaccctg ttgttgaaca tgtcaggctt agaaatgcag tcatgaccaa aatgaagata 7320
 tcagattata aagtgggtga accaattaat atgcaggcatc aaataatgaa aatatatacac 7380
 agttgtgagc tcacattattt aaaaacattc ttaaagaaaa gtaaaaaacat tagctctta 7440
 aaattaatgtatgatgtt ttgtttagac tttaaattcc cctcagataa cacatcaatt 7500
 cttaaatttt tagatgttga gtttatacct gtttgggtga gcaattgggt tagtaactgg 7560
 tataatctca ataaaattat cttagagttt agaagagagg aagtaataag aactggtca 7620
 attttatgtt gatcactagg caagttgtt ttcatgttat catcttatgg gtgtgttagt 7680
 aaaagcaaca aaagaaaaag agtaagttt ttcacatata accaactgtt aacatggaaa 7740
 gatgtgatgt taagtaggtt caatgcaaac ttttgatata gggtaagtaa caacctgaac 7800
 aaaaatcaag aaggactagg atttagaagt aatctgcaag gtatgttaac caataaaatta 7860
 tatgaaactg ttgattatata gttaaatgtca ttttagtaatg aagggttctc actagtgaaa 7920
 gagttcgaag gctttattat gaggaaatt cttaaaatattt ctgagcatgc tcaattcagt 7980
 actaggttt ggaataactt attaaatggg ttgactgaac aattatcaat gttgaaagct 8040
 aaaaacagat ctagagttt tggactata tttagaaaca atgattaccc catgtatgaa 8100
 gtagtactt aattattagg ggacactttt aaaaagtataa aattattaat taacaagaat 8160
 ttagaaaaatg ctgcagaatt atattatata tttagaaattt ttggacaccc tatggtagat 8220
 gagagggaaag caatggatgc tggtaaattt aataatgaga ttcaaaaaat tcttaaactg 8280
 gagagcttaa cagaactaag aggagcattt atactaagaaa tttaaaaagg gtttggat 8340
 aataaaaaaa gatggcttaa aattaagaat ttaaaagtgc tcagtaaaaat atgggttatg 8400
 tatttcaag cccaaatgtt cccttagccaa ctttgagctaa gtgtacaaga ttttttagaa 8460
 cttgctcgag tacaatgttca agacggattt tctgtccctg aaaaaaccaa ecttgagat 8520
 gtattaaatg ataaagcaat atcccttcca aaaaagttaa tatggcggtt atatccaaaa 8580
 aattatctac ctgaaattat aaaaatcaa tatttagaaag aggtcttcaa tgcaagtgc 8640
 agtcaaagaa cgaggagagt ctttagaaatt tacttaaaag atgcaaaatt tgatcaaaaa 8700
 gaccttaaac gttatgtact taaaacaagag tatctaaatg acaaagacca cattgtctca 8760
 ttaactggga agggaaagaga attaagtgtt ggcaggatgt ttgcaatgca accaggcaaa 8820
 caaagacaaa tacagatact agctgagaaa cttctagctg ataataattgt acccttttc 8880
 ccagaaacctt taacaaagta tggacttg gatctccaa gaattatgaa aatgaaatca 8940
 gaactttctt ccattaaaac taggaagaat gatagttaca acaattatat tgcaagagcc 9000
 tccatagtaa cagacctaag taaaattcaat caagcctta gatagaaac cacagctatc 9060
 tgtcagatg tagcagatga gttacatgtt acgcaagct tattttgtt gttacatctt 9120
 attgttccca tgaccacaat gatatgtgca tacagacatg caccaccaga aacaaagggg 9180
 gagatgaca tagacaaaat agaagagcaa agtgggctat acagatatca tatgggaggg 9240
 attgaagggt ggtgtcagaa gttatggaca atggaagcga tatttttgtt agatgttagt 9300
 tctgttaaga ctcgttgcata gatgacctct ctattaaacg gagacaatca atcaatagat 9360
 gtcagtaaac cagtaaaatt gtcgtaaaggat atagatgaaag taaaagcaga ttatagctt 9420
 gcaattaaaa tgcttaaaga gataagagat gcctataaaa acattggcca taaactcaaa 9480
 gaaggtgaaa catatatatac aagagatctc caatttataa gtaaggtgat tcaatctgag 9540
 ggggtcatgc atccctacccc cataaaaaaaat attaaagg tagtccctg gataaataca 9600
 atactagatg acattaaaaac cagtgcagaa tcaataggga gtctgtgtca agaactagag 9660
 ttcagaggag aaagtatgtt agttagctt atattaagga atttctggct gtataactta 9720
 tacatgcattt agtcaaaaaca gcatccgtt gctggaaaac aactgtttaa gcaattgaac 9780
 aaaacactaa catctgtgca aagattttt gagctgaaga aagaaaaatga tttgggttac 9840

ctatggatga atataccaaat gcagtttggaa gggggagacc cagtagttt ttacagatct 9900
 ttttacagaa ggactcctga ttccctgact gaagcaatca gccatgtggaa ttactgtta 9960
 aaagtttgcg acaatattaa aatgagact aagatacgat tctttaaagc ottattatct 10020
 atagaaaaga atgaacgtgc aacattaaca acactaatga gagaccccca ggcggttagga 10080
 tcggaaagac aagctaaggat aacaagtgtat ataataatgaa cagcagttac tagcatactg 10140
 agtctatctc cgaatcagct ctttgtat agtgctatac actatagcag aaatgaagaa 10200
 gaagtccggaa tcattgcaga caacataaca cctgtttatc ctcacggatt gagagtgctc 10260
 tatgaatcac tacctttca taaggctgaa aagggtgtca atatgatatac aggtacaaag 10320
 tctataacta acctattgca gagaacatct gctatcaatg gtgaagatata tgatagagca 10380
 gtgtctatga tgtagagaa cttagggtt ttatcttagga tattgtcagt aataattaat 10440
 agtatagaaa taccattaa gtccaatggc agattgatata gctgtcaaata ttctaaagact 10500
 ttgagagaaaa aatcatggaa caatatggaa atagtaggag tgacatctcc aagtattgt 10560
 acatgtatgg atgttgtgtt tcaactagt tctcattaa aaggaataat tattgaaaaaa 10620
 ttcagttactg acaagaccac aagaggtcag aggggaccaa aaagccctg ggtaggatca 10680
 agcactcaag agaaaaaaatt agttcctgtt tataatagac aaattcttc aaaacaacaa 10740
 aaggagcaac tggaaacaat agaaaaaaatg aggtgggtgt ataaaggaaac tccagggct 10800
 agaagattgc tcaataagat ttgcatacgaa agtttaggtt ttagctataa atgtgtaaaa 10860
 cctctattac caagattcat gagtgtaaac ttcttacata gtttatctgt tagtagcaga 10920
 cccatggaaat tcccagottc tggccagct tataggacaa caaattacca ctttgacact 10980
 agtccaatca accaaggcatt aagtggagg ttcgggaaacg aagacattaa tctagtgtt 11040
 caaaatgcgaa tcagctgcgg aattagtata atgagtgtt tagaacaggta aactggtaga 11100
 agcccaaaac aattagtctt aatcccccaa tttagaagaga tagatattat gcttcctcct 11160
 gtatttcaag gaaaatcaa ttataaacta gttgataaaaa taacctctga tcaacacatc 11220
 ttcagtcctg aaaaaataga catattaaaca cttagggaga tgcttatgcc tactataaaa 11280
 ggtcaaaaaaa ctgatcagg tctttaataag agagaaaaact attccatgg aaataattta 11340
 attgaatctt tatctgcagc acttgcattgc cactgggtgtt gaatattaaac agaacatgt 11400
 gtagaaaaaca atatcttag gaaagactgg ggtgatgggt tcatatcaga tcatgcctc 11460
 atggatttca agatattct atgtgtattt aaaaccaaac ttttatgttag ttggggatcc 11520
 caagggaaaa atgtaaaaga tgaagatata atagatgaat ccattgacaa attattaaga 11580
 attgacaaca cttttggag aatgttcagc aaagtcatgt ttagatcaaa ggtcaaaaaaa 11640
 agaataatgt tatatgatgt aaaattccta tcattagtag gtttatatagg attaaaaaaac 11700
 tggtttatag agcagttaaag agtagtagaa ttgcattgaag tggccctggat tgtcaatgt 11760
 gaaggggagc tagttgaaat taaaccatac aaaattttt tgcagttat agaacaagg 11820
 ctatcttaa gaataactgt ttgaattat acagacatgg cacatgtct tacacgatta 11880
 attaggaaga aattgtatgt tgataatgca ctcttcaatc caagttcatc accaatgtt 11940
 agtctaactc aagttatcga tcctacaaca cagctagact attttcctaa ggtgatattt 12000
 gaaaggtaa aaagttatga taccaggta gactacaaca aagggaaaggta aacaagaaat 12060
 tacatgacat tattaccatg gcagcacgta aacaggatata attttgtctt tagttcaaca 12120
 ggtgtaaaaa tcagctgaa gacatgcata gggaaattga taaaggactt aaaccctaag 12180
 gttctttact ttattggaga aggaggcaggta aactggatgg caagaacacg atgtgagtt 12240
 cctgacataa aattttatgata taggatgtt aaggatgatc ttgatcatca ttaccattta 12300
 gaatatcaaa ggttaatagg tgatttaat agggttaatg atgggtgggtga aggactatca 12360
 atggagacca cagatgcac tcaaaagact cattggact taatacacag aataagtaaa 12420
 gatgctttat tgataacattt gttgtatgca gaattcaaaa acagagatga tttctttaaa 12480
 atggttaattt ttggagaaa acatgttata tcatgttagaa tctgtacagc ttatggaaaca 12540
 gatctttact tatttgcaaa gtagatgcgc acggactgca atataaaaattt accatttttt 12600
 gtaagggtctg tagctacttt tattatgca ggaagcaat tgcaggatc agaatgttac 12660
 atacttttaa cattaggtca tcacaataat ctgcattgcc atggagaaaat acaaaaattcc 12720
 aaaatgagaa tagcagttgt taatgatttc catgcctcaa aaaaactaga caacaaatca 12780
 atgaagcta actgtaaaatc tcttctatca ggattaagaa taccataaaa caaaaaagag 12840
 ttaaatagac aaaagaaaact gttAACACTA caaagcaatc attcttccat agcaacagtt 12900
 ggcggcagta agattataga atccaaatgg ttaaagaata aagcaagtac aataattgt 12960
 tggttagagc atatcttggaa ttctccaaaaa ggtgaattaa actatgattt ctgttggaaaca 13020
 ttagagaaca catacccaa tatgtatcaag cttatagata acctggggaaa tgcagagata 13080
 aaaaaactaa tcaaagttcc tgggtatatac tttgtgagta agaagtaata ataat 13135

<210> 98

<211> 907

<212> DNA

<213> Human metapneumo virus

<400> 98

atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtaaaaaat 60
 cgtgtggcac gcagcaaatg cttaaaaat gccttttg tcctcatagg aataactaca 120
 tttagtattg ccctcaatat ctatctgatc ataaactata aaatgcaaaa aaacacatct 180
 gaatcagaac atcacaccag ctcacccatc atggaatcca gcagagaaac tccaaacggtc 240
 cccacagaca actcagacac caactcaagc ccacagcatc caactcaaca gtccacagaa 300
 ggctccacac tctactttgc agcctcagca agtcaccag agacagaacc aacatcaaca 360
 ccagatacaa caaacccccc gcccctcggtc gacacacaca caacaccacc aagcgcaagc 420
 agaacaaga caagtccggc agtccacaca aaaaacaacc caaggacaag ctctagaaca 480
 cattctccac cacggggcaac gacaaggacg gcacgcagaa ccaccactct ccgcacaagc 540
 agcacaagaa agagaccgtc cacagcatca gtccaaacctg acatcagcgc aacaacccac 600
 aaaaacgaag aagcaagtcc agcgagccca caaatctg caagcacaac aagaatacaa 660
 aggaaaagcg tggaggccaa cacatcaaca acataacaacc aaactagtt aaaaaaaaaata 720
 caaaaataact ctaagataaa ccatgcagac accaacaatg gagaagccaa aagacaattc 780
 acaatctccc caaaaaggca acaacaccat attagctctg cccaaatctc cctggaaaaa 840
 acactcgccc atataccaaa aataccacaa ccaccccaag aaaaaaactg ggcaaaacaa 900
 caccCAA 907

<210> 99
 <211> 908
 <212> DNA
 <213> Human metapneumo virus

<400> 99
 atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag tgtaaaaaat 60
 cgtgtggcac gcagcaaatg cttaaaaat gccttttg tcctcatagg aataactaca 120
 tttagtattg ccctcaatat ctatctgatc ataaactata aaatgcaaaa aaacacatct 180
 gaatcagaac atcacaccag ctcacccatc atggaatcca gcagagaaac tccaaacggtc 240
 cccacagaca actcagacac caactcaagc ccacagcatc caactcaaca gtccacagaa 300
 ggctccacac tctactttgc agcctcagca agtcaccag agacagaacc aacatcaaca 360
 ccagatacaa caaacccccc gcccctcggtc gacacacaca caacaccacc aagcgcaagc 420
 agaacaaga caagtccggc agtccacaca aaaaacaacc caaggacaag ctctagaaca 480
 cattctccac cacggggcaac gacaaggacg gcacgcagga accaccactc tccgcacaag 540
 cagcacaaga aagagaccgt ccacagcatc agtccaaacct gacatcagcg caacaaccc 600
 caaaaacgaa gaagcaagtc cagcgagccca acaaacatct gcaagcaca caagaataca 660
 aaggaaaagc gtggaggccaa acacatcaac aacatacaac caaactagtt aaaaaaaaaat 720
 acaaaaataac tctaagataa accatgcaga caccacaaat ggagaagccaa aagacaatt 780
 cacaatctcc ccaaaaaggc aacaacacca tattagctct gccaaatct ccctggaaaa 840
 aacactcgcc catataccaa aataccacaa accacccca gaaaaaaaaact gggcaaaaca 900
 acacccaa 908

<210> 100
 <211> 907
 <212> DNA
 <213> Human metapneumo virus

<400> 100
 atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtaaaaaat 60
 cgtgtggcac gcagcaaatg cttaaaaat gccttttg tcctcatagg aataactaca 120
 cttagtattg ccctcaatat ctatctgatc ataaactata aaatgcaaaa aaacacatct 180
 gaatcagaac atcacaccag ctcacccatc atggaatcca gcagagaaac tccaaacggtc 240
 cccacagata attcagacac caactcaagc ccacaacatc caactcaaca gtccacagaa 300
 ggctccacac tctactttgc agcctcagca aactcaccag agacagaacc aacatcaaca 360
 ccagacacaa caaacccccc gcccctcggtc gacacacaca caacaccacc aagcgcaagc 420
 agaacaaga caagtccggc agtccacaca aaaaacaacc caaggataag ctccagaaca 480
 cactctccac catggggcaac gacaaggacg gcacgcagaa ccaccactct ccgcacaagc 540
 agcacaagaa agagaccgtc cacagcatca gccccacccg acatcagcgc aacaacccac 600
 aaaaacgaag aagcaagtcc agcgagccca caaatctg caagcacaac aagaacacaa 660
 aggaaaagcg tggaggccaa cacatcaaca acataacaacc aaactagtt aaaaaaaaaata 720
 caaaaataact ctaagataaa ccatgcagac accaacaatg gagaagtc aagacaattc 780
 acaatctccc caaaaaggca acaacaccat attagctctg cccaaatctc cctggaaaaa 840
 acactcgccc atataccaaa aataccacaa ccaccccaag aaaaaaactg ggcaaaacaa 900
 caccCAA 907

<210> 101
<211> 907
<212> DNA
<213> Human metapneumo virus

<400> 101
atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtaaaaaat 60
cgtgtggcac gcagcaaatg cttaaaaat gcctcttgg tcctcatagg aataactaca 120
tttagtattt ccctcaatat ctatctgatc ataaaactata aaatgaaaaa aaacacatct 180
gaatcagaac atcacaccag ctcatcacc c atgaaatcca gcagagaaac tccaaacggtc 240
cccacagata attcagacac caactcaagc ccacaacatc caactcaaca gtccacagaa 300
ggctccacac tctactttgc aggctcagca aactcaccag agacagaacc aacatcaaca 360
ccagacacaa cagaccgccc gcccttcgtc gacacacaca caacaccacc aagcgcaagc 420
agaacaaaga caagtccggc agtccacaca aaaaacaacc caaggataag ctccagaaca 480
cattctccac catggcaac gacaaggacg gcacgcagaa ccaccactct ccgcacaagc 540
agcacaagaa agagaccgtc cacagcatca gtccaaacccg acatcagcgc aacaacccac 600
aaaaacgaag aagcaagtcc agcgagccca caaacatctg caagcacaac aagaacacaa 660
agaaaaagcg tggaggccaa cacatcaaca acatacaacc aaactagttt aaaaaaaaaata 720
caaataact ctaagataaa ccatgcagac accaacaatg gagaagtcaa aagacaattc 780
acaatctccc caaaaaggca acaacaccat attagctctg cccaaatctc cctggaaaaa 840
acactcgccc atataccaaa aataccacaa ccaccccaag aaaaaaactg ggcaaaacaa 900
ccccca 907

<210> 102
<211> 907
<212> DNA
<213> Human metapneumo virus

<400> 102
atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtaaaaaat 60
cgtgtggcac gcagcaaatg cttaaaaat gcctcttgg tcctcatagg aataactaca 120
tttagtattt ccctcaatat ctatctgatc ataaaactata aaatgaaaaa aaacacatct 180
gaatcagaac atcacaccag ctcatcacc c atgaaatcca gcagagaaac tccaaacggtc 240
cccacagata attcagacac caactcaagc ccacaacatc caactcaaca gtccacagaa 300
ggctccacac tctactttgc aggctcagca agtccaccag agacagaacc aacatcaaca 360
ccagacacaa cagaccgccc gcccttcgtc gacacacaca caacaccacc aagcgcaagc 420
agaacaaaga caagtccggc agtccacaca aaaaacaacc caaggataag ctccagaaca 480
cattctccac catggcaac gacaaggacg gcacgcagaa ccaccactct ccgcacaagc 540
agcacaagaa agagaccgtc cacagcatca gtccaaacccg acatcagcgc aacaacccac 600
aaaaacgaag aagcaagtcc agcgagccca caaacatctg caagcacaac aagaacacaa 660
agaaaaagcg tggaggccaa cacatcaaca acatacaacc aaactagttt aaaaaaaaaata 720
caaataact ctaagataaa ccatgcagac accaacaatg gagaagtcaa aagacaattc 780
acaatctccc caaaaaggca acaacaccat attagctctg cccaaatctc cctggaaaaa 840
acactcgccc atataccaaa aataccacaa ccaccccaag aaaaaaactg ggcaaaacaa 900
ccccca 907

<210> 103
<211> 907
<212> DNA
<213> Human metapneumo virus

<400> 103
atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtggaaaaat 60
cgtgtggcac gcagcaaatg cttaaaaat gcctcttga tcctaataagg aataactaca 120
tttagtatacg ccctcaatat ctatctgatc ataaaactata caatgcaaga aaacacatcc 180
gaatcagaac atcacaccag ctcatcacc c atgaaatcca gcagggaaac tccaaacggtc 240
cccatacgaca actcagacac caatccaggc tcacagtatc caactcaaca gtccacagaa 300
gactccacac tccactctgc agtccagca agtccaccag agacagaacc aacatcaaca 360
ccagacacaa caagccgccc gcccttcgtc gacacacaca caacaccacc aagtgcagc 420
aggacaagga caagtccggc agtccacaca aaaaacaatc caagggttaag ccccgagaaca 480
cattccccac catggcaat gacaaggacg gtccgggaa ccaccactct ccgcacaagc 540
agcacaagaa aaagactgtc tacagcatca gtccaaacccg acagcagcgc aacaacccac 600

aaacacgaag aaacaagccc agtgagcccc caaacatctg caagcacagc aagaccacaa 660
 aggaaggcca tggaggccag cacatcaaca acataacaacc aaactagtta aaaaaaaaata 720
 caaaataact ctaagataaa ccatgttagac accaacaatt gagaagccaa aaggcaattc 780
 acaatctccc aaaaaagcaa caacaccata ttagctccgc ttaaatctcc ctgaaaaaaaa 840
 cactcaccctataccaact ataccacaac catcccaaga aaaaaggctg ggcaaaacaa 900
 cacccaa 907

<210> 104

<211> 908

<212> DNA

<213> Human metapneumo virus

<400> 104

atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtaaaaat 60
 cgtgtggcac gcagcaaatg cttaaaaat gcctttga tcctaataagg aataactaca 120
 ttgagtatag ccctcaatat ctatctgatc ataaactata caatgcaaga aaacacatcc 180
 gaatcagaac atcacaccag ttcatcaccc atggatcca gcagggaaac tccaaacggtc 240
 cctatggaca actcagacac caatccaggc tcacagtatc caactcaaca gtccacagaa 300
 ggctccacac tccactttgc agcctcagca agtcaccag agacagaacc aacatcaaca 360
 ccagacacaa caagccgccc gcccttcgtc gacacacaca caacaccatc aagtgcagc 420
 agaacaaga caagtccggc agtccacaca aaaaacaatc taaggataag ccccgagaaca 480
 cattccccac catggcaat gacaaggacg gtccgtggaa ccaccactt ccgcacaaggc 540
 agcataagaa aaagaccgtc cacagcatc gtccaaacctg acagcagcgc aacaacccac 600
 aaacacgaag aagcaagccc agtgagcccc caagcatctg caagcacagc aagaccacaa 660
 aggaaggcca tggaggccag cacatcaaca acataacaacc aaactagtta aaaaaaaaata 720
 taaaataact ctaagataaa ccatgttagac accaacaatt gagaagccaa aaggcaattc 780
 acaatctccc aaaaaaggca acaacaccat attagctccg cttaaatctc cctggaaaaa 840
 acactcgccc atataccaac tataccacaa ccattccaaag gaaaaagct gggtaaaaca 900
 acacccaa 908

<210> 105

<211> 908

<212> DNA

<213> Human metapneumo virus

<400> 105

atggaggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtaaaaat 60
 cgtgtggcac gcagcaaatg cttaaaaat gcctttga tcctaataagg aataactaca 120
 ttgagtatag ccctcaatat ctatctgatc ataaactata caatgcaaga aaacacatcc 180
 gaatcagaac atcacaccag ctcatcaccc atggatcca gcagagaaac tccaaacggtc 240
 cctatggaca actcagacac caatccaggc tcacagtatc caactcaaca gtccacagaa 300
 ggctccacac tccactttgc agcctcagca agtcaccag agacagaacc aacatcaaca 360
 ccagacacaa caagccgccc gcccttcgtc gacacacaca caacaccatc aagtgcagc 420
 agaataagga caagtccggc agtccacaca aaaaacaatc taaggataag ccccgagaaca 480
 cattccccac catggcaat gacaaggacg gtccgtggaa ccaccactt ccgcacaaggc 540
 agcataagaa aaagaccgtc cacagcatc gtccaaacctg acagcagcgc aacaacccac 600
 aaacacgaag aagcaagccc agtgagcccc caagcatctg caagcacagc aagaccacaa 660
 aggaaggcca tggaggccag cacatcaaca acataacaacc aaactagtta aaaaaaaaata 720
 tacaataact ctaagataaa ccatgttagac accaacaatt gagaagccaa aaggcaattc 780
 acaatctccc aaaaaaggca acaacaccat attagctccg cttaagtctc cctggaaaaa 840
 acactcgccc atataccaac tataccacaa ccattccaaag aaaaaagct gggcaaaaca 900
 acacccaa 908

<210> 106

<211> 888

<212> DNA

<213> Human metapneumo virus

<400> 106

atggaggtga aagttagagaa cattcgagca atagacatgc tcaaagcaag agtaaaaat 60
 cgtgtggcac gtagcaaatg cttaaaaat gcttctttaa tcctcatagg aataactaca 120
 ctgagtatag ctctcaatat ctatctgatc ataaactaca caataaaaaa aaccacatcc 180

gaatcagaac accacaccag ctcaccaccc acagaaccca acaaggaagc ttcaacaatc 240
tccacagaca acccagacat caatccaagc tcacagcatc caactcaaca gtccacagaa 300
aaccacacac tcaacccgc agcatcagcg agcccatcag aaacagaacc agcatcaaca 360
ccagacacaa caaaccgcgt gtcctccgta gacaggcca cagcacaaacc aagtgaaagc 420
agaacaaaga caaaaccgc agtccacaca atcaacaacc caaacacagc ttccagatca 480
caatccccac cacggacaac aacgaaggca atccgcagag ccaccactt ccgcattgagc 540
agcacaggaa aaagaccaac cacaacatta gtccagtcg acagcagcac cacaacccaa 600
aatcatgaag aaacagttc agcgaaccca caggcgctg caagcacaat gcaaaaactag 660
cacaccaata atataaaacc aaattagttt acaaaaaatg cgagatagct ctaaagcaaa 720
acatgttaggt accaacaatc aagaaaccaa aagacaactc acaatctccc taaaacagca 780
acgacaccat gtcagcttg ctcaaatctc tctggagaa acttctaccc acataactaac 840
aacatcacaa ccatctcaag aaaagaaaact gggcaaaaca gcatccaa 888

<210> 107

<211> 888

<212> DNA

<213> Human metapneumo virus

<400> 107

atggaggtga aagtagagaa cattcgagca atagacatgc tcaaagcaag agtaaaaat 60
cgtgtggcac gcagcaaatg cttaaaaat gttctttaa tcctcatagg aataactaca 120
ctgagtatag ccctcaatat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctaccacccc acagaatcca acaaagaaac ttcaacaatc 240
cccatagaca acccagacat caatccaaac tcacagcatc caacccaaaca gtccacagaa 300
agccccacac tcaacccgc agcctcggtg agcccatcag aaacagaacc agcatcaaca 360
ccagacacaa caaaccgcgt gtcctccgta gacagatcca caacacaacc aagtgaaagc 420
agaacaaaga caaaaccacac agtccacaca aaaaacaatc caagtacagt ttccagaaca 480
caatccccac tacggcaac aacgaaggcg gtcctcagag ccaccgctt ccgcacgagc 540
agcacaagaa aaagaccaac cacaacatca gtccagtcg acagcagcac cacaacccaa 600
aatcatgaag aaacaagttc agcgaaccca caggcatctg caagcacaat gcaaaagccag 660
cacaccaaca acataaaacc aaattagttt acaaaaaata cgagatagct ctaaagtaaa 720
acatgttaggt accaacaatc aaggaatcaa aagacaactc acaatctccc taaaacagca 780
acaacatcat gtcagtttg ctcaaatctc cctggagaa acttctgccc acataactaac 840
aacatcacaa ccatctcaag aaaagaaaact gggcaaaaca gcacccaa 888

<210> 108

<211> 888

<212> DNA

<213> Human metapneumo virus

<400> 108

atggaggtga aagtagagaa catccgagca gtagacatgc tcaaagcaag agtcaaaaat 60
cgtgtggcac gcagcaaatg cttaaaaat gcctctttaa tcctcgtagg aataactaca 120
ctgagcatcg ccctcaatat ctatctgatc gtaaactaca caatacaaaa aaccacatcc 180
gaatcagaac accacaccag ctcatccccc acagaatcca acaaaggaac ttcaacaatc 240
cccacagaca acccagacat caatccaaat tcacaacatc caactcaaca gtccacagaa 300
agccccacac tcaacaccgc agcctcggtg agcccatcag aaacagaacc agcatcaaca 360
ccagacacaa caaaccgcgt gtcctccgca gacagatcca caacacaacc aagtgaaagc 420
agaacaaaga caaaagctgac agtccacaca aaaaacaacc taagtacagc ctccagaaca 480
caatcaccac cacggcaac aacgaaggcg gtcctcagag acaccgcctt ccacacgagc 540
agcacaggaa aaagaccaac cacaacatca gtccagtcg gcagcagcac cacaactcaa 600
aatcatgaag aaacaagttc atcgaacccc caggcatctg caagcacaat gcaagaccag 660
gacaccaaca atacaaaaca aaattagttt acaaaaaata caagatagct ctaaagtaaa 720
acatgttaggt accaacagta aagaaatcaa aagacaactc acaatctccc caaaacagca 780
acaacatcat gtcagctcg ctcaaatctc cctggagaa acttctgccc acataactaac 840
aacatcacaa ctatctcaag aaaagaaaact gggcaaaaaa acactcaa 888

<210> 109

<211> 887

<212> DNA

<213> Human metapneumo virus

<400> 109
atggaggtga aagttagagaa catccgagca gtagacatgc tcaaagcaag agttaaaaat 60
cgtgtggcac gcagcaaatg cttaaaaat gccttttaa tcctcgtagg aataactaca 120
ctgagtatag ccctcaatat ctatctgatc gtaaactaca caataaaaaa aaccacatcc 180
gaatcagaac accacactag ctcacccatcc acagaatcca acaaaggAAC ttcaacaatc 240
ccacagacaa cccagacatc aatccaaatt cacaacatcc aactcaacag tccacagaaa 300
gcccccacact caacaccgca gcctcggtga gcccacatcaga aacagaacca gcatcaacac 360
cagacacaac aaaccgcctg tcctccgcag acagatccac aacacaacca agtggaaagca 420
gaacaaagac aaagctgaca gtccacacaa aaaacaacct aagtacagcc tccagaacac 480
aatcaccacc acgggcaaca acgaaggcgg tcctcgagaga caccgcctc cacacgagca 540
gcacaggaaa aagaccaacc acaacatcg tccagtcgg cagcagcacc acaactcaaa 600
atcatgaaga aacaagttca tcgaacccac aggcattctc aagcacaatg caagaccagg 660
acaccaacaa tacaaaacaa aattagttaa caaaaaatac aagatagctc taaagtaaaa 720
catgttagta ccaacagatc aaaaaatcaaa agacaactca taatctcccc aaaacagcaa 780
caacatcatg tcagcttcgc tcaaattctcc ctgggagaaa ctctcgccc catactaaca 840
acatcacaac tatctcaaga aaagaaaactg ggcaaaaaaa cactcaa 887

<210> 110
<211> 888
<212> DNA
<213> Human metapneumo virus

<400> 110
atggaggtga aagttagagaa cattcgagca atagacatgc tcaaagcaag aatgaaaaat 60
cgtgtggcac gcagcaaatg cttaaaaat gccttttaa tcctcgtagg aataactact 120
ctgagtatag ccctcaatat ctatctgatc ataaactaca caataaaaaa aaccacatct 180
gaatcagaac accacactag ctcacccatcc acagaatcca acaaaggAAC ttcaacaatc 240
cctatagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
agcctcacac tcaaccccgcc agcctcggtg agcccatcg aacacgaaacc agcatcaaca 360
ccagacacaa caaaccgcct gtccctcgta gacagatcca caacacaacc aagtggaaagc 420
agaacaaaga caaaaactgac agtccacacaa aaaaacatcc caagtacagt ctctagaaca 480
caatcctcaa tacgggcaac aacgaaggcg gtcctcgag ccaccgcct tcgcacgagc 540
agcacaggag aaagaccaac tacaacatca gtccagtcg acagcagcac cacaacccaa 600
aatcatgaag aaacaggttc agcgaacccca caggcatctg caagcacaat gcaaaaactag 660
cacaccaaca ttgtaaaacc aaattagttaa caaaaaata tgaatagct ctaaagtaaaa 720
acatgttaggt gctaacaatc aaaaaatcaaa aagacatctc ataatctctc caaaacagca 780
acaacatcat gtcaactttg ctcaaattctc cctgggagaa acttcgccc ccataactgac 840
aacatcacaac tcatctcaag aaaagaaaact gggcaaaaca gcaccaaa 888

<210> 111
<211> 888
<212> DNA
<213> Human metapneumo virus

<400> 111
atggaggtga aagttagagaa cattcgagca atagacatgc tcaaagcaag agtggaaaat 60
cgtgtggcac gcagcaaatg cttaaaaat gccttttaa tcctcgtagg aataactact 120
ctgagtatag ccctcaacat ctatctgatc ataaactaca caataaaaaa aaccacatct 180
gaatcagaac accacactag ctcacccatcc acagaatcta acaaaggAAC ttcaacaatc 240
tctatagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
agcctcacac tcagccccc agcctcggtg agcccatcg aacacgaaacc agcatcaaca 360
tcagacacaa caagccgcct gtccctcgta gacagatcca caacacaacc aagtggaaagc 420
agagcaagga caaaaaccgac agtccacacaa aaaaacatcc caagtacagt ttctagaaca 480
caatccccac tacgggcaac aacgaaggcg gtcctcgag ccaccgcct tcgcacgagc 540
agcacaggag agggaccaac cacaacatcg gtccagtcg acagcagcac cacaacccaa 600
aatcatgaag aaacaggttc agcgaacccca caggcatctg caagcacaat gcaaaaactag 660
cacaccaaca ttgtaaaacc aaattagttaa caaaaaata tgaatagtt ctaaagtaaaa 720
acatgttaggt gctaacaatc aaaaaatcaaa aagacacactc ataatctccc taaaacagca 780
acaacatcat gtcaactttg ctcaaattctc cctgggagaa acttcgccc ccataactgac 840
aacatcacaac tcatctcaag aaaagaaaact gggcaaaaca gcaccaaa 888

<210> 112

<211> 888
<212> DNA
<213> Human metapneumo virus

<400> 112
atggaggtga aagttagagaa cattcgagca atagacatgc tcaaagcaag agtaaaaat 60
cgtgtggcac gtagcaaatg cttaaaaat gcttcttaa tcctcatagg aataactaca 120
ctgagttatag ccctcaatat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacaccag ctcaccaccc acagaatcca acaaggaagc ttcaacaatc 240
tccacagaca atccagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
aacccccacac taaacccgc agcatcggtg agctcatcg aaacagaacc agcatcaaca 360
ccagacacaa caaaccgcct gtctccgt aacaggtcca cagcacaacc aagtggaaagc 420
agaacaaaga caaaaccgc acgtccacaca agaaacaacc caagcacagc ttccagcaca 480
caatccccac cacggtaac aacgaaggca atcctcagag ccacccgtt ccgcattgagc 540
agcacaggaa aaagaccgc cacaacatta gtccagtcg acagcagcac cacaacccaa 600
aatcatgaag aaacagggtc agcaaactca cagggcatctg caagcacaat gcaaaactag 660
cactccaaca atataaaacc aaattagttt aaaaaaaaaa cgagatagct ctaaagtaaa 720
acatgttaggc accaacaatc agggaaattaa aagacaactc acaacctccc taaaacagca 780
acgacacccat gtcaactttg ctcaaatctc tctgggagaa acctttgcc acataactaac 840
aacatcacaa tcatctcaag aaaagaaaact gggcaaaaca gcattccaa 888

<210> 113
<211> 888
<212> DNA
<213> Human metapneumo virus

<400> 113
atggaggtga aagttagagaa cattcgagca atagacatgc tcaaagcaag agtaaaaat 60
cgtgtggcac gcagcaaatg cttaaaaat gcttcttaa tcctcatagg aataactact 120
ctgagttatag ccctcaacat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctcaccaccc acagaatcta acaaaagaaac ttcaacaatc 240
ttatagaca actcagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
agcctcacac tcagccccc acgcctcggt agcccatcg aaacagaacc agcatcaaca 360
tcagacacaa caaaccgcct gtctccgt aacagatcca caacacaacc aagtggaaagc 420
agagcaagaa caaaaccgc acgtccacaaag aaaaacatcc caagtacagt ttctagaaca 480
caatccccac tacggcaac aacgaaggcg gtcctcagag ccacccgcct tcgcattgagc 540
agcacaggag agggaccaac cacaacatcg gtccagtcg acagcagcac cacaacccaa 600
aatcatgaag aaacaggctc agcgaacccca cagggcatctg caagcacaat gcaaaaccag 660
cacaccaaca ttgcaaaacc aaattagttt aaaaaaaaaa tgaaatagttt ctaaagtaaa 720
acatgttaggt gccaacaatc aagaaatcaa aagacaactc acaatctccc taaaacagca 780
acaacatcat gccaactttg ctcaaatctc cctgggagaa accctcgccc ccataactgac 840
aacatcacaa tcatctcaag aaaagaaaact gggcaaaaca gcacccaa 888

<210> 114
<211> 888
<212> DNA
<213> Human metapneumo virus

<400> 114
atggaggtga aagttagagaa cattcgagca atagacatgc tcaaagcaag agtaaaaat 60
cgtgtggcac gcagcaaatg cttaaaaat gcttcttaa tcctcatagg aataactact 120
ctgagttatag ccctcaatat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctcaccaccc acagaatcta acaaggaaac ttcaacaatc 240
cctatagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
agcctcacac tctaccaccc atcctcggt agctcatcg aaacagaacc agcatcaaca 360
ccaggcataa caaaccaccc gtccttgc gacagatcca caacacaacc aagtggaaagc 420
agaacaaaga caaaccggac acgtccacaa aaaaacatct caagtacagt ttctagaaca 480
cagtcacccac cacggacaac agcgaaggcg gtcccccagag ccacccgcct tcgcacgagc 540
agcacaggag aaagaccaac cacaacacca gtccagcccg atagcagcac cacaacacaa 600
aatcatgaag aaacaggctc agcgaacccca cagggcatccg caagcacaat gcaaaaccag 660
cacaccaaca ttgcaagacc aaattagttt aaaaaaaaaa tgaaatagct ctaaagtaaa 720
acatgttaggt gccaacaatc aagaaatcaa aagataactc ataatctctc taaaacatca 780

acaacatcat gttaacttg ctcaaattctc tctgggagaa accttcgcc 840
 aacatcacaa tcatctcaag aaaagaaaact gggcaaaaca acacccaa 888

<210> 115
 <211> 888
 <212> DNA
 <213> Human metapneumo virus

<400> 115
 atggaggtga aagttagagaa cattcgagca atagacatgc tcaaagcaag agtaaaaat 60
 cgtgtggcac gcagcaaattt gcttctttaa tcctcatagg aataactact 120
 ctgagtatag ccctcaatat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
 gaatcagaac accacactag ctcaccaccc acagaatcta acaaggaaac ttcaacaatc 240
 cctatagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccgcagaa 300
 agcctcacac tctaccaccc atcctcggtg agctcatcg aaacagaacc agcatcaaca 360
 ccagggataa caaaccacct gtccttgc gacagatcca caacacaacc aagtgaaagc 420
 agaacaaga caaaccggac agtccacaaa aaaaacatct caagtacagt ttctagaaca 480
 cagtcacccac cacggacaaac agcgaaggcg gtccccagag ccaccgcct tcgcacgagc 540
 agcacaggag aaagaccaac cacaacacca gtccagcccg atagcagcac cacaacacaa 600
 aatcatgaag aaacaggctc agcgaacccca caggcatccg caagcacaat gcaaaaccag 660
 cacaccaaca ttgcaagacc aaattagttt aaaaaaaaaa tgaaatagct ctaaagtaaa 720
 acatgttaggt gccaacaatc aagaatcaa aagataactc ataattctctc taaaacatca 780
 acaacatcat gttaacttg ctcaaattctc tctgggagaa accttcgcc 840
 aacatcacaa tcatctcaag aaaagaaaact gggcaaaaca acacccaa 888

<210> 116
 <211> 888
 <212> DNA
 <213> Human metapneumo virus

<400> 116
 atggaggtga aagttagagaa tattcgagca atagacatgc tcaaagcaag agtaaaaat 60
 cgtgtggcac gcagcaaattt gcttctttaa tcctcatagg aataactact 120
 ctgagtatag ccctcaatat ctatctgatc ataaactaca caatacaaaa aaccacatct 180
 gaatcagaac accacactag ctcaccaccc acagaatcta acaaggaaac ttcaacaatc 240
 cctatagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
 agcctcacac tctaccaccc atcctcggtg agctcatcg aaacagaacc agcatcaaca 360
 ccagggataa caaaccacct gtccttgc gacagatcca caacacaacc aagtgaaagc 420
 agaacaaga caaaccggac agtccacaaa aaaaacatct caagtacagt ttctagaaca 480
 cagtcacccac cacggacaaac agcgaaggcg gtccccagag ccaccgcct tcgcacgagc 540
 agcacaggag aaagaccaac cacaacacca gtccagcccg atagcagcac cacaacacaa 600
 aatcatgaag aaacaggctc agcgaacccca caggcatccg caagcacaat gcaaaaccag 660
 cacaccaaca ttgcaagacc aaattagttt aaaaaaaaaa tgaaatagct ctaaagtaaa 720
 acatgttaggt gccaacaatc aagaatcaa aagataactc ataattctctc taaaacatca 780
 acaacatcat gttaacttg ctcaaattctc tctgggagaa accttcgcc 840
 aacatcacaa tcatctcaag aaaagaaaact gggcaaaaca acacccaa 888

<210> 117
 <211> 888
 <212> DNA
 <213> Human metapneumo virus

<400> 117
 atggaggtga aagttagagaa cattcgagca atagacatgc tcaaagcaag agtaaaaat 60
 cgtgtggcac gtagcaaattt gcttctttaa tcctcatagg aataactaca 120
 ctgagcatag ccctcaatat ctatctgatc ataaactaca caatacaaca aaccacatct 180
 gaatcagaac accacaccag ctcaccaccc acagaatcca acaaggaaagc ttcaacaatc 240
 tccacagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
 aaccccccac tcaacccacg agcatcagcg agcccatcg aaacagaatc agcatcaaca 360
 ccagatataaa caaaccgcct gtcctccgt gacaggtcca cggtacaacc aagtgaaaac 420
 agaacaaga caaaaactgac agtccacaca agaaacaacc taagcacagc ctccagtgaca 480
 caatcccccac cacgggcaac aacgaaggca atccgcagag ccaccacccct ccgcacgagc 540

agcacaggaa gaagaccaac cacaacacta gtccagtcg acagcagcac cacaacccaa 600
 aatcatgaag aaacaggctc agcgaaccca cagggatctg caagcacaat gaaaaaccag 660
 cacaccaaca atataaaacc aaatttagtta aaaaaaaaaa ctagatagct cttaaagtaaa 720
 acatgttaggc accaacaatc aagaaaccaa aagataactc acaatccccca caaaacagca 780
 acgacaccat gtcagcttg ctcaaatctc tctggagaa actttgccc acatactaac 840
 aacatcacaa ccatctcaag aaaagaaaact gggcaaaaca gcatccaa 888

<210> 118

<211> 888

<212> DNA

<213> Human metapneumo virus

<400> 118

atggaggtga aagttagagaa cattcgagca atagacatgc tcaaagcaag agtggaaaaat 60
 cgtgtggcac gtagcaaatg cttaaaaaat gcttcttta tcctcatagg aataactaca 120
 ctgagcatag ccctcaatat ctatctgatc ataaaactaca caatacaaaaa aaccacatct 180
 gaatcagaac accacaccag ctcaccaccc acagaatcca acaaggaagc ttcaacaatc 240
 tccacagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
 aaccccacac tcaacccagc agcatcagcg agcccatctag aaacagaatc agcatcaaca 360
 ccagatacaa caaaccgcct gtccctcgta gacaggtcca cggtacaacc aagtggaaaac 420
 agaacaaga caaaaactgac agtcccacaca agaaacaacc taagcacagc ctccagtgaca 480
 caatccccac cacggcaac aacgaaggca atccgcagag ccaccacccct ccgcattgagc 540
 agcacaggaa gaagaccaac cacaacacta gtccagtcg acagcagcac cacaacccaa 600
 aatcatgaag aaacaggctc agcgaacccca cagggatctg caagcacaat gcaaaaaccag 660
 cacaccaaca atataaaacc aaatttagtta aaaaaaaaaa ctagatagct cttaaagtaaa 720
 acatgttaggc accaacaatc aagaaaccaa aagataactc acaatccccca caaaacagca 780
 acgacaccat gtcagcttg ctcaaatctc tctggagaa actttgccc acatactaac 840
 aacatcacaa ccatctcaag aaaagaaaact gggcaaaaca gcatccaa 888

<210> 119

<211> 901

<212> DNA

<213> Human metapneumo virus

<400> 119

atgaaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaac 60
 cgtataagaa gcagcagggtg ctatagaaat gctacactga tccttattgg actaacagcg 120
 ttaagcatgg cacttaatat ttccctgatc atcgatcatg caacattaag aaacatgatc 180
 aaaacagaaa actgtgctaa catgccgtcg gcagaaccaa gcaaaaaagac cccaatgacc 240
 tccacagcac gcccaaacac caaaccctat ccacagcaag caacacagtg gaccacagag 300
 aactcaacat ccccagtagc aaccccccagag ggccatccat acacagggac aactcaaaca 360
 tcagacacaa cagctccca gcaaaccaca gacaaacaca cagcaccgcctt aaaaatcaacc 420
 aatgaacaga tcaccacagac aaccacagag aaaaagacaa tcagagcaac aacccaaaaa 480
 agggaaaaag gaaaagaaaa cacaaccaa accacaagca cagctgcaac cccaaacaacc 540
 aacaccacca accaaatcatc aatgtcaatc gagacaatca caacatccga cagacccaga 600
 actgacacca caacccaaag cagcgaacag acaacccggg caacagaccc aagctccccca 660
 ccacaccatg catagagagg tgcaaaaactc aaatgagcac aacacacaaa catccatcc 720
 aagttagttaa caaaaaacca caaaaataacc ttgaaaacca aaaaaccaaa acataaaccc 780
 agacccagaa aaacatagac accatatgg aaggttctagc atatgcacca atgagatggc 840
 atctgttcat gtagcaatag caccaccatc attcaaggaa taagaagagg cgaaaattta 900
 a 901

<210> 120

<211> 901

<212> DNA

<213> Human metapneumo virus

<400> 120

atgaaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaagaac 60
 cgtataagaa gcagcagggtg ctatagaaat gctacactga tccttattgg actaacagcg 120
 ttaagcatgg cacttaatat ttccctgatc attgatcatg caacattaag aaacatgatc 180
 aaaacagaaa actgtgctaa catgccatcg gcagaaccaa gcaaaaaagac cccaatgacc 240

tccacagcag gcccaggcac cgaacccaat ccacagcaag caacacaatg gaccacagag 300
 aactcaacat ccccaggcgc aacccttagag agccatccat acacaggag aacccaaaca 360
 ccagacataa cagctccccca acaaaccaca gacaaacaca cagcaactgcc aaaatcaacc 420
 aatgaacaga tcacccagac aaccacagag aaaaagacaa ccagagcaac aacccaaaaaa 480
 agggaaaaag aaaaagaaaa cacaaaccaa accacaagca cagctgcaac ccaaacaacc 540
 aacaccacca accaaacccag aaatgcaagt gagacaatca caacatccga cagacccaga 600
 attgacacca caaacccaaag cagcgatcg acaacccggg caacagaccc aagctccccca 660
 ccacaccatg cagcagtgg tgcaaaaaccc aaatgaacac aacacacaaa catctcatcc 720
 aagtagttaa caaaaaatcca caaaaataacc ttgaaaacca aaaaacccaa ccacaaactt 780
 agaccagaa aaacatagac actatatgga aggtttgagc atatgcacca atgaaatgg 840
 atctgttcatttatcaatag cgccaccattttaaggaa taagaagagg caaaaattca 900
 a 901

<210> 121

<211> 860

<212> DNA

<213> Human metapneumo virus

<400> 121

atggaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaac 60
 cgtataagaa gcagcagggtg ctatagaaat gctacactga tccttattgg actaacagcg 120
 ttaagcatgg cacttaatat tttctgtatc atcgatcatg caacattaag aaacatgatc 180
 aaaacagaaa attgtgtcaa catgcccggc gcagaaccaa gcaaaaagac cccaatgacc 240
 tctacagcag gcccaaacac caaacccaa ccacagcaag caacacagtg gaccacggag 300
 aactcaacat tcccaggcgc aacccatcgag ggccatctac acacaggag aactcaaaca 360
 ccagacacaa cagctccatc gcaaaaccaca gacaaacaca cagcaactgcc aaaaatcaacc 420
 aatgaacaaa tcaccccgac aaccacagag aaaaagacaa ccagagcaac aacccaaaga 480
 agggaaaaag gaaaaagaaaa cacaaaccaa accacaagca cagctgtac ccaaacaacc 540
 aacaccacca accaaatcg aaatgcaagc gagacaatca caacatccga cagacccaga 600
 actgactcca caaacccaaag cagcgaacag acaacccggg caacagaccc aagctccccca 660
 ccacatcatg cacagggaaag tgcaaaaaccc aaatgaacac aacacacaaa catccatcc 720
 aagtagttaa caaaaaatca gaccagaaa aacatagaca ctatatggaa ggtccgagca 780
 tatgcaccga tgaaaatggca tttgttcatttatcaatag gccaccattttaaggaa 840
 aagaagaggc aaaaattca 860

<210> 122

<211> 861

<212> DNA

<213> Human metapneumo virus

<400> 122

atggaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaac 60
 cgtataagaa gcagcagggtg ctatagaaat gctacactga tccttattgg actaacagcg 120
 ttaagcatgg cacttaatat tttctgtatc atcgatcatg caacattaag aaacatgatc 180
 aaaacagaaa attgtgtcaa catgcccggc gcagaaccaa gcaaaaagac cccaatgacc 240
 tccacagcag gcccaaacac caaacccaa ccacagcaag caacacagtg gaccacggag 300
 aactcaacat ccccgaggc aaccccgag ggccatctac acacaggag aactcaaaca 360
 ccagacacaa cagctccatc gcaaaaccaca gacaaacaca cagcaactgcc aaaaatcaacc 420
 aatgaacaga tcaccccgac aaccacagag aaaaagacaa ccagagaaac aacccaaaga 480
 agggaaaaag gaaaaagaaaa cacaaaccaa accacaagca cagctgcaac ccaaacaacc 540
 aacaccacca accaaatcg aaatgcaagc gagacaatca caacatccga cagacccaga 600
 actgactcca caaacccaaag cagcgaacag acaacccagg caacagaccc aagctccccca 660
 gcacaccatg cacagggaaag tgcaaaaaccc aaatgaacac aacacacaaa catccatcc 720
 aagtagttaa caaaaaatca agaccagaaa aacacacagac actatatgga aggtccgagc 780
 atatgcacccg atgaaaatggc atctgttcatttatcaatag caccaccattttaaggaa 840
 taagaagaggc aaaaattca a 861

<210> 123

<211> 860

<212> DNA

<213> Human metapneumo virus

<400> 123
atggaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaac 60
cgtataagaa gcagcagggtg ctatagaaaat gctacattga tccttattgg actaacagcg 120
ttaagcatgg cacttaatat ttccctgatc atcgatcatg caacattaag aaacatgatc 180
aaaacagaaa atttgctaa catgccaccg gcagaaccaa gcaaaaagac cccaatgacc 240
tccacagcg gcctaaacac taaacccaat ccacagcaag caacacagtg gaccacggag 300
aactcaacat ccccagcgc aaccccagag ggccatctac acacagggac aactcaaaca 360
ccagacacaa cagctcctca gcaaaccaca gacaagcaca cagcactgcc aaaatcaacc 420
aatgaacaga tcacccagac aaccacagag aaaaagacaa ccagagcaac aacccaaaga 480
aggaaaaaag gaaaagaaaa cacaaaccaa accacaagca cagctgcaac ccaaacaacc 540
aacaccacca accaaatcg aaatgcaagc gagacaatca caacatccga cagaccaga 600
actgactcca caacccaaag cagcgaacag acaacccggg caacagaccc aagctcccc 660
ccacaccatg cacagggaa tgcaaaaccc aaatgaacac aacacacaaa catccatcc 720
aagttagttaa caaaaaatca gacccagaaa aacatagaca ctatatggaa ggtccgagca 780
tatgcaccga tgaaatggca tctgttcatg tatcaatagc gccaccatta ttttaggaat 840
aagaagaggc aaaaattcaa 860

<210> 124
<211> 860
<212> DNA
<213> Human metapneumo virus

<400> 124
atggaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaac 60
cgtataagaa gcagcagggtg ctatagaaaat gctacactga tccttattgg actaacagcg 120
ttaagcatgg cacttaatat ttccctgatc atcgatcatg caacattaag aaacatgatc 180
aaaacagaaa atttgctaa catgccccgg gcagaaccaa gcaaaaagac cccaatgacc 240
tccacagcg gcccaaacac caaacccaat ccacagcaag caacacagtg gaccacggag 300
aactcaacat ccccagcgc aaccccagag ggccatctac acacagggac aactcaaaca 360
ccagacacaa cagctcctca gcaaaccaca gacaaacaca cagcactgcc aaaatcaacc 420
aatgaacaga tcacccagac aaccacagag aaaaagacaa ccagagcaac aacccaaaga 480
aggaaaaaag gaaaagaaaa cacaaaccaa accacaagca cagctgcaac ccaaacaacc 540
aacaccacca accaaatcg aaatgcaatt gagacaatca caacatccga cagaccaga 600
actgactcca caacccaaag cagcgaacag acaacccggg caacagaccc aagctcccc 660
ccacaccatg cacagggaa tgcaaaaccc aaatgaacac aacacacaaa catccatcc 720
aagttagttaa caaaaaatca gacccagaaa aacatagaca ctatatggaa ggtccgagca 780
tatgcaccga tgaaatggca tctgttcatg tatcaatagc gccaccatta ttttaggaat 840
aagaagaggc aagaattcaa 860

<210> 125
<211> 886
<212> DNA
<213> Human metapneumo virus

<400> 125
atggaagtaa gagtggagaa cattcgccca atagacatgt tcaaagcaaa aatgaaaaac 60
cgtataagaa gtagcaagtg ctatagaaaat gctacactga tccttattgg attaacagca 120
ttaagtatgg cacttaatat ttttttaatc attgattatg caatgtaaa aaacatgacc 180
aaagtggAAC actgtgttaa tatgccggc gtagaaccaa gcaagaagac cccaatgacc 240
tctcagtag acttaaacac caaacccaat ccacagcagg caacacagtgg ggccgcagag 300
gattcaacat ctctagcagc aacctcagag gaccatctac acacagggac aactccaaca 360
ccagatgcaa cagtctcctca gcaaaccaca gacgagtaca caacattgt gagatcaacc 420
aacagacaga ccacccaaac aaccacagag aaaaagccaa cggagcaac aaccaaaaaa 480
gaaaccacaa ctcgaactac aagcacagct gcaacccaaa cactcaacac taccaaccaa 540
actagctatg tgagagaggc aaccacaaca tccgcagat ccagaaacag tgccacaact 600
caaagcagcg accaaacaaac ccaggcagca gacccaaacct cccaaccaca ccatacacag 660
aaaagcacaa caacaacata caacacagac acatcctctc caagtagttt aaaaaaaaaac 720
tataaaataa tcatggaaaac cgaaaaacta gaaaagttaa tttgaactca gaaaagaaca 780
caaacactat atgaattgtt tgagcgtata tactaatgaa atagcatctg tttgtgcattc 840
aataataccca tcattattta agaaataaga agaagctaaa attcaa 886

<210> 126

<211> 889

<212> DNA

<213> Human metapneumo virus

<400> 126

atggaagtaa gagtggagaa cattcggaca atagacatgt tcaaagcaaa gataaaaaac 60
 cgtataagaa gcagcaagt ctatagaaat gctacactga tccttattgg actgacagca 120
 ttaagtatgg cacttaatat ttcttgatc atcgattatg caacattaa aaacatgacc 180
 aaagtggAAC actgtgtcaa tatgccgccc gtagaaccga gtaagaagac cccaatgacc 240
 tctacagttag actcaaggcac cgacccat ccacagcaga caacacagtg gaccacagag 300
 gattcaacat ctctagcagc aacctcgag gaccatctac acacagggac aactccaaca 360
 ctagatgcaa cagtttcata gcaaaacccc gacaaggaca caacaccgct gagatcaacc 420
 aatggacaga ccaccccgac aaccacagag aaaaagccaa ccagagcaat agccaaaaaa 480
 gaaaccacaa accaaaccac aagcacagct gcaacccaaa cattcaacac caccaatcaa 540
 accagaaaatg gaagagagac aaccataaca tctgcccAGAT ccagaaacga cgccacaact 600
 caaaggcgcg aacaaacaaa ccagacaaca gacccaaGCT cccaaaccaca tcatgcatag 660
 ataagcacaa taacaatatg aacacaacac agacacatct tctccaagta gttaacaaaa 720
 aactataaaa taaccatgaa aaccaaaaaa ctagaaaagt aaatttgaac tcagaaaaga 780
 acacaaacac taaatgatt gttgagcat atatactaata gaaatagcat ctgttcatgc 840
 atcaataata ccatcattac ttaagaaata agaagaagca aaaattcaa 889

<210> 127

<211> 885

<212> DNA

<213> Human metapneumo virus

<400> 127

atggaagtaa gagtggagaa cattcgggca atagacatgt tcaaagcaaa gataaaaaac 60
 cgtataagaa gtagcaagt ctatagaaat gctacactga tccttattgg attaacagca 120
 ttaagtatgg cacttaatat tttttaatc attgattatg caatgttaaa aaacatgacc 180
 aaagtggAAC actgtgttaa tatgccgccc gtagaaccaa gcaagaagac cccaatgacc 240
 tctgcagttag acttaaacac caaactcaat ccacagcagg caacacagt gaccacagag 300
 gattcaacat ctctagcagc aacctcgag gatcatttac tcacagggac aactccaaca 360
 ccagatgcaa cagttctca gcaaaaccaca gacgagcaca caacactgct gagatcaacc 420
 aacagacaga ccacccaaac aaccacagag aaaaagccaa ccggagcaac aaccaaaaaa 480
 gaaaccacaa ctcgaaccac aagcacagct gcaacccaaa cactcaacac caccaaccaa 540
 actagcaatg gaagagaggc aaccacaaca tccaccagat ccagaaacgg tgccacaact 600
 caaaacagcg atcaaacaa ctagacagca gacccaaGCT cccaaaccaca ccatacacag 660
 aaaagcacaa caacaacata caacacagac acatcttctc caagtagtta aaaaaaaaaact 720
 ataaaataac catgaaaact aaaaaacttag aaaaagttaat ttgaactcag aaaagaacac 780
 aaacactata tgaattgttt gagcgttat ataaatgaaa tagcatctgt ttgtgcatca 840
 ataataccat cattattaa gaaataagaa gaagctaaaa ttcaa 885

<210> 128

<211> 885

<212> DNA

<213> Human metapneumo virus

<400> 128

atggaagtaa gagtggagaa cattcgggca atagacatgt tcaaagcaaa gataaaaaac 60
 cgcataagaa gtagcaagt ctatagaaat gctacactga tccttattgg attaacagca 120
 ttaagtatgg cacttaatat tttttaatc attgattatg caacattaa aaacatgacc 180
 aaagtggAAC actgtgttaa tatgccgccc gtagaaccaa gcaagaagac cccaatgacc 240
 tctgcagttag acttaaacac caaactcaat ccacagcagg caacacagt gaccacagag 300
 gattcaacat ctctagcagc aacctcgag ggccatccac acacaggaac aactccaaca 360
 ccagacgcaa cagttctca gcaaaaccaca gacgagcaca caacactgct gagatcaacc 420
 aacagacaga ccacccaaac agccacagag aaaaagccaa ctggagcaac aaccaaaaaa 480
 gaaaccacaa cccgaactac aagtacagct gcaacccaaa cacccaaacac caccaaccaa 540
 accagcaatg gaagagaggc aaccacaaca tccgcccAGGT ccagaaacgg tgccacaact 600
 caaaacagcg atcaaataac ccaggcagca gactcaagct cccaaaccaca ccatacacag 660
 aaaagcacaa caacagcata caacacagac acatcttctc caagtagtta aaaaaaaaaact 720
 ataaaataac catgaaaacc aaaaaacttag aaaaagttaat ttgaactcag aaaagaacac 780

aaacactata tgaattgttt gagcgtatat actaatgaaa tagcatctgt ttgtgcata 840
ataataccat cattatttaa gaaataagaa gaagctaaaa ttcaa 885

<210> 129
<211> 886
<212> DNA
<213> Human metapneumo virus

<400> 129
atggaaagtaa gagtggagaa cattcggca atagacatgt tcaaagcaaa gatgaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttattgg attacatcgca 120
ctaagtatgg cacttaatat tttttatc attgattatg caacattaaa aaacatgacc 180
aaagtggAAC actgtgttaa tatgccggc gttagaaccAA gcaagaAGAC cccaatgacc 240
tctgcagtag actcaaACAC caaacCCAA ccacAGCAGG caacACAGTT gaccACAGAG 300
gattctacat cttagcAGC aaccCTAGAG gaccATCCAC acacAGGGAC aactCCAACA 360
ccagatgcaa cagtctctca gcaaACCACA gacgAGCACA caacACTGCT gagatCAACC 420
aacagacaga ccacCCAAAC aactGCAGAG AAAAGCCAA ccaggGCAAC aaccaAAAAAA 480
gaaaccacAA ctcgaaccAC aagcacAGCT gcaacCCAAA cactcaACAC caccaACAA 540
actagcaatg gaagAGAGGC aaccacaACA tctGCCAGAT ccagAAACAA tgccACAAct 600
caaAGCAGCG atcaaACAC ccaggCAGCA gaaccAAGCT cccaatcaca acataCACAG 660
aaaAGCATAA caacaACATA caacACAGAC acatCTTCTC taagttagtTA acaaaaaAAAC 720
tataAAATAA ccatggAAAAC caaaaaACTA gaaaAGTTA ttGAGACTCA gaaaAGAAAC 780
caaacactat atgaatttt tgagcgtata tactaatgaa atagcatctg ttGAGCTC 840
aataatacca tcattattta agaaATAAGA agaagctaaa attcaa 886

<210> 130
<211> 887
<212> DNA
<213> Human metapneumo virus

<400> 130
atggaaagtaa gagtggagaa cattcggca atagacatgt tcaaagcaaa gatgaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttattgg attatcagca 120
ctaagtatgg cacttaatat tttttatc attgattatg caaaatcaaa aaacatgacc 180
agagtggAAC actgtgtCAA tatGCCGGC gttagaaccAA gcaagaAGAC cccaatgacc 240
tctgcagtag acttaaACAC caaacCCAA ccacAGCAGG caacACAGTT gaccACAGAG 300
gattcaacat ctctAGCAGC aaccCTAGAG ggccatctac acacAGGGAC aactCCAACA 360
ccagatgtAA cagtctctca gcaaACCACA gacgAGCACA caacACTGCT gagatCAACC 420
aacagacaga ccacCCAAAC agccGAGAG AAAAGCCAA ccagAGTAAC aactAAACAA 480
gaaaccataA ctcgaaccAC aagcacAGCC gcaacCCAAA cactcaACAC caccaACAA 540
accaacaATG gaagAGAGGC aaccACAACA tctGCCAGAT ccagAAACAA tgccACAAct 600
caaAGCAGCG accaaACAC ccaggCAGCA gacccAAAGCT cccaatcaca acataCACAG 660
aaaAGCATAA caacaACATA caacACAGAC acatCTTCTC caagttagtTA acaaaaaAAAC 720
tataAAATAA ccatggAAAAC caaaaaACTA agaaaAGTTA attGAGACTC agaaaAGAAAC 780
acaaacactaT tatgaatttG ttGAGCTAT atactaatgA aatAGCATCT gtttGAGCT 840
caataatacc atcattatttA aagaATTAAAG aagaagctAA aattcaa 887

<210> 131
<211> 887
<212> DNA
<213> Human metapneumo virus

<400> 131
atggaaagtaa gagtggagaa cattcggca atagacatgt tcaaagcaaa gatgaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttattgg attatcagca 120
ctaagtatgg cacttaatat tttttatc attgattatg caaaatcaaa aaccatgacc 180
agagtggAAC actgtgttaa tatGCCGGC gttagaaccAA gcaagaAGAC cccaatgacc 240
tctgcagtag acttaaACAC caaacCCAA ccacAGCAGG caacACAGTT gaccACAGAG 300
gattcaacat ctccAGCAGC aaccCTAGAG ggccatctac acacAGGGAC aactCCAACA 360
ccagatgcaa cagtctctca gcaaACCACA gacgAGCACA caacACTGCT gagatCAACC 420
aacagacaga ccacCCAAAC aaccGAGAG AAAAGCCAA ccagAGTAAC aaccaAAAAAA 480
gaaaccataA ctcgaaccAC aagcacAGCT gcaacCCAAA cactcaACAC caccaACAA 540

accagcaatg gaagagagggc aaccacaaca tctgccagat ccagaaacaa tgccacaact 600
 caaaggcgcg accaaacaac ccaggcagca gacccaagct cccaatcaca acatacaaag 660
 aaaagcacaa caacaacata caacacagac acatcttctc caagtagtta aaaaaaaaaac 720
 tataaaataa ccatgaaaac caaaaaact agaaaaagttt atttgaactc agaaaagaac 780
 acaaacacta tatgaattgt ttgagcgtat atactaatga aatagcatct gtttgtcat 840
 caataatacc atcattattt aagaattaag aagaagctaa aattcaa 887

<210> 132
<211> 886
<212> DNA
<213> Human metapneumo virus

<400> 132
atgaaagttaa gagtggagaa cattcggca atagacatgt tcaaagcaaa gataaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttattgg attaacagca 120
ctaatgtatgg cacttaatat ttttttaatc attgattatg caacattaaa aaacatgacc 180
aaagtggAAC actgtgttaa tatgccggcgtt gtagaaccaa gcaagaagac cccaatgacc 240
tctgcagtag acttaaacac caaaccat ccacagcagg caacacagtt gaccacagag 300
gactctacat ctttagcagc aacccttagag gaccatccac acacaggac aactccaaca 360
ccagatgcaa cagtctctca gcaaaccaca gacgagcaca caacactgtc gagatcaacc 420
aacagacaga ccacccaaac aactgcagag aaaaagccaa ccagagcac acacccaaaa 480
gaaaccacaa ctcgaaccac aagcacagct gcaacccaaa cactcaacac caccaccaa 540
actagcaatg gaagagagggc aaccacaaca tctgccagat ccagaaacaa tgccacaact 600
caaagcagcg atcaaacaac ccaagcagca gaacccaaact cccaatcaca acatacag 660
aaaagcacaa caacaacata caacacagac acatcttctc taatgtta aaaaaaaaaac 720
tataaaataa ccatgaaaac caaaaaacta gaaaagttt tttgaactca gaaaggaaca 780
caaacactat atgaattatt tgagcgtata tactaatgaa atagcatctg ttttgtcatc 840
aataatacc tcattatttta agaaataaga agaagctaa attcaa 886

<210> 133
<211> 236
<212> PRT
<213> Human metapneumo virus

<400> 133
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65 70 75 80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Ser Ser
100 105 110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asn Arg Pro Pro
115 120 125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr
130 135 140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Thr Ser Ser Arg Thr
145 150 155 160
His Ser Pro Pro Arg Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr
165 170 175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
180 185 190
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Glu Ala Ser Pro Ala
195 200 205
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Ile Gln Arg Lys Ser Val

210	215	220
Glu Ala Asn Thr Ser	Thr Thr Tyr Asn Gln Thr	Ser
225	230	235

<210> 134
<211> 236
<212> PRT
<213> Human metapneumo virus

<400> 134

Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala			
1	5	10	15
Ser Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser			
20	25	30	
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr			
35	40	45	
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His			
50	55	60	
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val			
65	70	75	80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln			
85	90	95	
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Ser Ser			
100	105	110	
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asn Arg Pro Pro			
115	120	125	
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr			
130	135	140	
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Thr Ser Ser Arg Thr			
145	150	155	160
His Ser Pro Pro Arg Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr			
165	170	175	
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Val Gln			
180	185	190	
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Glu Ala Ser Pro Ala			
195	200	205	
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Ile Gln Arg Lys Ser Val			
210	215	220	
Glu Ala Asn Thr Ser Thr Thr Tyr Asn Gln Thr Ser			
225	230	235	

<210> 135
<211> 236
<212> PRT
<213> Human metapneumo virus

<400> 135

Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala			
1	5	10	15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser			
20	25	30	
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr			
35	40	45	
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His			
50	55	60	
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val			
65	70	75	80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln			
85	90	95	
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Asn Ser			

	100		105		110
Pro	Glu	Thr	Glu	Pro	Thr
Ser	Thr	Pro	Asp	Thr	Asn
115	120	125	Arg	Pro	Pro
Phe	Val	Asp	Thr	His	Thr
130	135	140	Pro	Pro	Ser
Ser	Pro	Ala	Val	His	Thr
145	150	155	Lys	Asn	Asn
His	Ser	Pro	Pro	Trp	Ala
165	170	175	Thr	Thr	Arg
Leu	Arg	Thr	Ser	Ser	Thr
180	185	190	Arg	Lys	Arg
Pro	Asp	Ile	Ser	Ala	Thr
195	200	205	Thr	His	Lys
Ser	Pro	Gln	Thr	Ser	Ala
210	215	220	Thr	Thr	Arg
Glu	Ala	Asn	Thr	Ser	Thr
225	230	235	Tyr	Asn	Gln

<210> 136

<211> 236

<212> PRT

<213> Human metapneumo virus

<400> 136

Met	Glu	Val	Lys	Val	Glu	Asn	Ile	Arg	Thr	Ile	Asp	Met	Leu	Lys	Ala
1				5					10			15			
Arg	Val	Lys	Asn	Arg	Val	Ala	Arg	Ser	Lys	Cys	Phe	Lys	Asn	Ala	Ser
				20				25				30			
Leu	Val	Leu	Ile	Gly	Ile	Thr	Thr	Leu	Ser	Ile	Ala	Leu	Asn	Ile	Tyr
				35				40				45			
Leu	Ile	Ile	Asn	Tyr	Lys	Met	Gln	Lys	Asn	Thr	Ser	Glu	Ser	Glu	His
			50		55				60						
His	Thr	Ser	Ser	Pro	Met	Glu	Ser	Ser	Arg	Glu	Thr	Pro	Thr	Val	
	65				70			75			80				
Pro	Thr	Asp	Asn	Ser	Asp	Thr	Asn	Ser	Ser	Pro	Gln	His	Pro	Thr	Gln
			85				90				95				
Gln	Ser	Thr	Glu	Gly	Ser	Thr	Leu	Tyr	Phe	Ala	Ala	Ser	Ala	Asn	Ser
			100				105				110				
Pro	Glu	Thr	Glu	Pro	Thr	Ser	Thr	Pro	Asp	Thr	Thr	Asp	Arg	Pro	Pro
			115				120			125					
Phe	Val	Asp	Thr	His	Thr	Thr	Pro	Pro	Ser	Ala	Ser	Arg	Thr	Lys	Thr
			130				135			140					
Ser	Pro	Ala	Val	His	Thr	Lys	Asn	Asn	Pro	Arg	Ile	Ser	Ser	Arg	Thr
	145				150			155			160				
His	Ser	Pro	Pro	Trp	Ala	Thr	Thr	Arg	Thr	Ala	Arg	Arg	Thr	Thr	Thr
				165			170			175					
Leu	Arg	Thr	Ser	Ser	Thr	Arg	Lys	Arg	Pro	Ser	Thr	Ala	Ser	Val	Gln
			180			185				190					
Pro	Asp	Ile	Ser	Ala	Thr	Thr	His	Lys	Asn	Glu	Ala	Ser	Pro	Ala	
			195			200			205						
Ser	Pro	Gln	Thr	Ser	Ala	Ser	Thr	Thr	Arg	Thr	Gln	Arg	Lys	Ser	Val
		210			215			220							
Glu	Ala	Asn	Thr	Ser	Thr	Thr	Tyr	Asn	Gln	Thr	Ser				
		225			230			235							

<210> 137

<211> 236

<212> PRT

<213> Human metapneumo virus

<400> 137
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65 70 75 80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Ser Ser
100 105 110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asp Arg Pro Pro
115 120 125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr
130 135 140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Ile Ser Ser Arg Thr
145 150 155 160
His Ser Pro Pro Trp Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr
165 170 175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
180 185 190
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Ala Ser Pro Ala
195 200 205
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Thr Gln Arg Lys Ser Val
210 215 220
Glu Ala Asn Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225 230 235

<210> 138
<211> 236
<212> PRT
<213> Human metapneumo virus

<400> 138
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Thr Met Gln Glu Asn Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65 70 75 80
Pro Ile Asp Asn Ser Asp Thr Asn Pro Gly Ser Gln Tyr Pro Thr Gln
85 90 95
Gln Ser Thr Glu Asp Ser Thr Leu His Ser Ala Ala Ser Ala Ser Ser
100 105 110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Ser Arg Pro Pro
115 120 125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Arg Thr
130 135 140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Val Ser Pro Arg Thr
145 150 155 160
His Ser Pro Pro Trp Ala Met Thr Arg Thr Val Arg Gly Thr Thr Thr
165 170 175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Leu Ser Thr Ala Ser Val Gln

	180	185	190												
Pro	Asp	Ser	Ser	Ala	Thr	Thr	His	Lys	His	Glu	Glu	Thr	Ser	Pro	Val
		195				200						205			
Ser	Pro	Gln	Thr	Ser	Ala	Ser	Thr	Ala	Arg	Pro	Gln	Arg	Lys	Gly	Met
		210				215						220			
Glu	Ala	Ala	Ser	Thr	Ser	Thr	Thr	Tyr	Asn	Gln	Thr	Ser			
		225				230						235			

<210> 139

<211> 236

<212> PRT

<213> Human metapneumo virus

<400> 139

Met	Glu	Val	Lys	Val	Glu	Asn	Ile	Arg	Thr	Ile	Asp	Met	Leu	Lys	Ala
							5			10			15		
Arg	Val	Lys	Asn	Arg	Val	Ala	Arg	Ser	Lys	Cys	Phe	Lys	Asn	Ala	Ser
							20			25			30		
Leu	Ile	Leu	Ile	Gly	Ile	Thr	Thr	Leu	Ser	Ile	Ala	Leu	Asn	Ile	Tyr
							35			40			45		
Leu	Ile	Ile	Asn	Tyr	Thr	Met	Gln	Glu	Asn	Thr	Ser	Glu	Ser	Glu	His
							50			55			60		
His	Thr	Ser	Ser	Ser	Pro	Met	Glu	Ser	Ser	Arg	Glu	Thr	Pro	Thr	Val
							65			70			75		80
Pro	Met	Asp	Asn	Ser	Asp	Thr	Asn	Pro	Gly	Ser	Gln	Tyr	Pro	Thr	Gln
							85			90			95		
Gln	Ser	Thr	Glu	Gly	Ser	Thr	Leu	His	Phe	Ala	Ala	Ser	Ala	Ser	Ser
							100			105			110		
Pro	Glu	Thr	Glu	Pro	Thr	Ser	Thr	Pro	Asp	Thr	Thr	Ser	Arg	Pro	Pro
							115			120			125		
Phe	Val	Asp	Thr	His	Thr	Thr	Pro	Ser	Ser	Ala	Ser	Arg	Thr	Lys	Thr
							130			135			140		
Ser	Pro	Ala	Val	His	Thr	Lys	Asn	Asn	Leu	Arg	Ile	Ser	Pro	Arg	Thr
							145			150			155		160
His	Ser	Pro	Pro	Trp	Ala	Met	Thr	Arg	Thr	Val	Arg	Gly	Thr	Thr	Thr
							165			170			175		
Leu	Arg	Thr	Ser	Ser	Ile	Arg	Lys	Arg	Pro	Ser	Thr	Ala	Ser	Val	Gln
							180			185			190		
Pro	Asp	Ser	Ser	Ala	Thr	Thr	His	Lys	His	Glu	Glu	Ala	Ser	Pro	Val
							195			200			205		
Ser	Pro	Gln	Ala	Ser	Ala	Ser	Thr	Ala	Arg	Pro	Gln	Arg	Lys	Gly	Met
							210			215			220		
Glu	Ala	Ala	Ser	Thr	Ser	Thr	Thr	Tyr	Asn	Gln	Thr	Ser			
							225			230			235		

<210> 140

<211> 236

<212> PRT

<213> Human metapneumo virus

<400> 140

Met	Glu	Val	Lys	Val	Glu	Asn	Ile	Arg	Thr	Ile	Asp	Met	Leu	Lys	Ala
							1			5			10		15
Arg	Val	Lys	Asn	Arg	Val	Ala	Arg	Ser	Lys	Cys	Phe	Lys	Asn	Ala	Ser
							20			25			30		
Leu	Ile	Leu	Ile	Gly	Ile	Thr	Thr	Leu	Ser	Ile	Ala	Leu	Asn	Ile	Tyr
							35			40			45		
Leu	Ile	Ile	Asn	Tyr	Thr	Met	Gln	Glu	Asn	Thr	Ser	Glu	Ser	Glu	His
							50			55			60		
His	Thr	Ser	Ser	Ser	Pro	Met	Glu	Ser	Ser	Arg	Glu	Thr	Pro	Thr	Val

65	70	75	80
Pro Met Asp Asn Ser Asp Thr Asn Pro Gly Ser Gln Tyr Pro Thr Gln			
85	90	95	
Gln Ser Thr Glu Gly Ser Thr Leu His Phe Ala Ala Ser Ala Ser Ser			
100	105	110	
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Ser Arg Pro Pro			
115	120	125	
Phe Val Asp Thr His Thr Pro Ser Ser Ala Ser Arg Ile Arg Thr			
130	135	140	
Ser Pro Ala Val His Thr Lys Asn Asn Leu Arg Ile Ser Pro Arg Thr			
145	150	155	160
His Ser Pro Pro Trp Ala Met Thr Arg Thr Val Arg Gly Thr Thr Thr			
165	170	175	
Leu Arg Thr Ser Ser Ile Arg Lys Arg Pro Ser Thr Ala Ser Val Gln			
180	185	190	
Pro Asp Ser Ser Ala Thr Thr His Lys His Glu Glu Ala Ser Pro Val			
195	200	205	
Ser Pro Gln Ala Ser Ala Ser Thr Ala Arg Pro Gln Arg Lys Gly Met			
210	215	220	
Glu Ala Ser Thr Ser Thr Tyr Asn Gln Thr Ser			
225	230	235	

<210> 141

<211> 228

<212> PRT

<213> Human metapneumovirus

<220>

<221> VARIANT

<222> 220

<223> Xaa = unknown amino acid or other

<400> 141

Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala			
1	5	10	15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser			
20	25	30	
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr			
35	40	45	
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His			
50	55	60	
His Thr Ser Ser Pro Pro Thr Glu Pro Asn Lys Glu Ala Ser Thr Ile			
65	70	75	80
Ser Thr Asp Asn Pro Asp Ile Asn Pro Ser Ser Gln His Pro Thr Gln			
85	90	95	
Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Ala Ser Pro			
100	105	110	
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser			
115	120	125	
Ser Val Asp Arg Ser Thr Ala Gln Pro Ser Glu Ser Arg Thr Lys Thr			
130	135	140	
Lys Pro Thr Val His Thr Ile Asn Asn Pro Asn Thr Ala Ser Ser Thr			
145	150	155	160
Gln Ser Pro Pro Arg Thr Thr Lys Ala Ile Arg Arg Ala Thr Thr			
165	170	175	
Phe Arg Met Ser Ser Thr Gly Lys Arg Pro Thr Thr Leu Val Gln			
180	185	190	
Ser Asp Ser Ser Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala			
195	200	205	
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Xaa His Thr Asn Asn			
210	215	220	

Ile Lys Pro Asn
225

<210> 142
<211> 228
<212> PRT
<213> Human metapneumo virus

<400> 142
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65 70 75 80
Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Ser Pro Thr Leu Asn Pro Ala Ala Ser Val Ser Pro
100 105 110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
115 120 125
Ser Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
130 135 140
Lys Pro Thr Val His Thr Lys Asn Asn Pro Ser Thr Val Ser Arg Thr
145 150 155 160
Gln Ser Pro Leu Arg Ala Thr Thr Lys Ala Val Leu Arg Ala Thr Ala
165 170 175
Phe Arg Thr Ser Ser Thr Arg Lys Arg Pro Thr Thr Thr Ser Val Gln
180 185 190
Ser Asp Ser Ser Thr Thr Gln Asn His Glu Glu Thr Ser Ser Ala
195 200 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Ser Gln His Thr Asn Asn
210 215 220
Ile Lys Pro Asn
225

<210> 143
<211> 228
<212> PRT
<213> Human metapneumo virus

<400> 143
Met Glu Val Lys Val Glu Asn Ile Arg Ala Val Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Val Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Val Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Ser Pro Thr Glu Ser Asn Lys Gly Thr Ser Thr Ile
65 70 75 80
Pro Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Ser Pro Thr Leu Asn Thr Ala Ala Ser Val Ser Pro
100 105 110

Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
 115 120 125
 Ser Ala Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
 130 135 140
 Lys Leu Thr Val His Thr Lys Asn Asn Leu Ser Thr Ala Ser Arg Thr
 145 150 155 160
 Gln Ser Pro Pro Arg Ala Thr Thr Lys Ala Val Leu Arg Asp Thr Ala
 165 170 175
 Phe His Thr Ser Ser Thr Gly Lys Arg Pro Thr Thr Ser Val Gln
 180 185 190
 Ser Gly Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Ser Ser Ser
 195 200 205
 Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asp Gln Asp Thr Asn Asn
 210 215 220
 Thr Lys Gln Asn
 225

<210> 144
 <211> 228
 <212> PRT
 <213> Human metapneumo virus

<220>
 <221> VARIANT
 <222> 81
 <223> Xaa = Any Amino Acid

<400> 144
 Met Glu Val Lys Val Glu Asn Ile Arg Ala Val Asp Met Leu Lys Ala
 1 5 10 15
 Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
 20 25 30
 Leu Ile Leu Val Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
 35 40 45
 Leu Ile Val Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
 50 55 60
 His Thr Ser Ser Ser Pro Thr Glu Ser Asn Lys Gly Thr Ser Thr Ile
 65 70 75 80
 Xaa Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
 85 90 95
 Gln Ser Thr Glu Ser Pro Thr Leu Asn Thr Ala Ala Ser Val Ser Pro
 100 105 110
 Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
 115 120 125
 Ser Ala Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
 130 135 140
 Lys Leu Thr Val His Thr Lys Asn Asn Leu Ser Thr Ala Ser Arg Thr
 145 150 155 160
 Gln Ser Pro Pro Arg Ala Thr Thr Lys Ala Val Leu Arg Asp Thr Ala
 165 170 175
 Phe His Thr Ser Ser Thr Gly Lys Arg Pro Thr Thr Ser Val Gln
 180 185 190
 Ser Gly Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Ser Ser Ser
 195 200 205
 Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asp Gln Asp Thr Asn Asn
 210 215 220
 Thr Lys Gln Asn
 225

<210> 145

<211> 228
<212> PRT
<213> Human metapneumovirus

<220>
<221> VARIANT
<222> 220
<223> Xaa = unknown amino acid or other

<400> 145
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Met Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65 70 75 80
Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Ser Leu Thr Leu Asn Pro Ala Ala Ser Val Ser Pro
100 105 110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
115 120 125
Ser Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
130 135 140
Lys Leu Thr Val His Lys Lys Asn Ile Pro Ser Thr Val Ser Arg Thr
145 150 155 160
Gln Ser Ser Ile Arg Ala Thr Thr Lys Ala Val Leu Arg Ala Thr Ala
165 170 175
Phe Arg Thr Ser Ser Thr Gly Glu Arg Pro Thr Thr Ser Val Gln
180 185 190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
195 200 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Xaa His Thr Asn Ile
210 215 220
Val Lys Pro Asn
225

<210> 146
<211> 228
<212> PRT
<213> Human metapneumovirus

<220>
<221> VARIANT
<222> 220
<223> Xaa = unknown amino acid or other

<400> 146
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile

65	70	75	80
Ser Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln			
85	90	95	
Gln Ser Thr Glu Ser Leu Thr Leu Ser Pro Thr Ala Ser Val Ser Pro			
100	105	110	
Ser Glu Thr Glu Pro Ala Ser Thr Ser Asp Thr Thr Ser Arg Leu Ser			
115	120	125	
Ser Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Ala Arg Thr			
130	135	140	
Lys Pro Thr Val His Lys Lys Asn Ile Pro Ser Thr Val Ser Arg Thr			
145	150	155	160
Gln Ser Pro Leu Arg Ala Thr Thr Lys Ala Val Leu Arg Ala Thr Ala			
165	170	175	
Phe Arg Thr Ser Ser Thr Gly Glu Gly Pro Thr Thr Thr Ser Val Gln			
180	185	190	
Ser Asp Ser Ser Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala			
195	200	205	
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Xaa His Thr Asn Ile			
210	215	220	
Val Lys Pro Asn			
225			

<210> 147

<211> 228

<212> PRT

<213> Human metapneumovirus

<220>

<221> VARIANT

<222> 220

<223> Xaa = unknown amino acid or other

<400> 147

Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala			
1	5	10	15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser			
20	25	30	
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr			
35	40	45	
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His			
50	55	60	
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Ala Ser Thr Ile			
65	70	75	80
Ser Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln			
85	90	95	
Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Val Ser Ser			
100	105	110	
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser			
115	120	125	
Ser Val Asp Arg Ser Thr Ala Gln Pro Ser Glu Ser Arg Thr Lys Thr			
130	135	140	
Lys Pro Thr Val His Thr Arg Asn Asn Pro Ser Thr Ala Ser Ser Thr			
145	150	155	160
Gln Ser Pro Pro Arg Val Thr Thr Lys Ala Ile Leu Arg Ala Thr Val			
165	170	175	
Phe Arg Met Ser Ser Thr Gly Lys Arg Pro Ala Thr Thr Leu Val Gln			
180	185	190	
Ser Asp Ser Ser Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala			
195	200	205	
Asn Ser Gln Ala Ser Ala Ser Thr Met Gln Asn Xaa His Ser Asn Asn			
210	215	220	

Ile Lys Pro Asn
225

<210> 148
<211> 228
<212> PRT
<213> Human metapneumo virus

<400> 148
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65 70 75 80
Ser Ile Asp Asn Ser Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Ser Leu Thr Leu Ser Pro Thr Ala Ser Val Ser Pro
100 105 110
Ser Glu Thr Glu Pro Ala Ser Thr Ser Asp Thr Thr Asn Arg Leu Ser
115 120 125
Ser Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Ala Arg Thr
130 135 140
Lys Pro Thr Val His Lys Lys Asn Ile Pro Ser Thr Val Ser Arg Thr
145 150 155 160
Gln Ser Pro Leu Arg Ala Thr Thr Lys Ala Val Leu Arg Ala Thr Ala
165 170 175
Phe Arg Met Ser Ser Thr Gly Glu Gly Pro Thr Thr Thr Ser Val Gln
180 185 190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
195 200 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Ile
210 215 220
Ala Lys Pro Asn
225

<210> 149
<211> 228
<212> PRT
<213> Human metapneumo virus

<400> 149
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65 70 75 80
Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Ser Leu Thr Leu Tyr Pro Thr Ser Ser Val Ser Ser
100 105 110

Ser Glu Thr Glu Pro Ala Ser Thr Pro Gly Ile Thr Asn His Leu Ser
 115 120 125
 Phe Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
 130 135 140
 Asn Arg Thr Val His Lys Lys Asn Ile Ser Ser Thr Val Ser Arg Thr
 145 150 155 160
 Gln Ser Pro Pro Arg Thr Thr Ala Lys Ala Val Pro Arg Ala Thr Ala
 165 170 175
 Leu Arg Thr Ser Ser Thr Gly Glu Arg Pro Thr Thr Pro Val Gln
 180 185 190
 Pro Asp Ser Ser Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
 195 200 205
 Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Ile
 210 215 220
 Ala Arg Pro Asn
 225

<210> 150
 <211> 228
 <212> PRT
 <213> Human metapneumo virus

<400> 150
 Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
 1 5 10 15
 Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
 20 25 30
 Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
 35 40 45
 Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
 50 55 60
 His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
 65 70 75 80
 Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
 85 90 95
 Gln Ser Ala Glu Ser Leu Thr Leu Tyr Pro Thr Ser Ser Val Ser Ser
 100 105 110
 Ser Glu Thr Glu Pro Ala Ser Thr Pro Gly Ile Thr Asn His Leu Ser
 115 120 125
 Phe Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
 130 135 140
 Asn Arg Thr Val His Lys Lys Asn Ile Ser Ser Thr Val Ser Arg Thr
 145 150 155 160
 Gln Ser Pro Pro Arg Thr Thr Ala Lys Ala Val Pro Arg Ala Thr Ala
 165 170 175
 Leu Arg Thr Ser Ser Thr Gly Glu Arg Pro Thr Thr Pro Val Gln
 180 185 190
 Pro Asp Ser Ser Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
 195 200 205
 Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Ile
 210 215 220
 Ala Arg Pro Asn
 225

<210> 151
 <211> 228
 <212> PRT
 <213> Human metapneumo virus

<400> 151

Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
 1 5 10 15
 Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
 20 25 30
 Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
 35 40 45
 Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Ser Glu Ser Glu His
 50 55 60
 His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
 65 70 75 80
 Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
 85 90 95
 Gln Ser Thr Glu Ser Leu Thr Leu Tyr Pro Thr Ser Ser Val Ser Ser
 100 105 110
 Ser Glu Thr Glu Pro Ala Ser Thr Pro Gly Ile Thr Asn His Leu Ser
 115 120 125
 Phe Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
 130 135 140
 Asn Arg Thr Val His Lys Lys Asn Ile Ser Ser Thr Val Ser Arg Thr
 145 150 155 160
 Gln Ser Pro Pro Arg Thr Thr Ala Lys Ala Val Pro Arg Ala Thr Ala
 165 170 175
 Leu Arg Thr Ser Ser Thr Gly Glu Arg Pro Thr Thr Pro Val Gln
 180 185 190
 Pro Asp Ser Ser Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
 195 200 205
 Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Ile
 210 215 220
 Ala Arg Pro Asn
 225

<210> 152
 <211> 228
 <212> PRT
 <213> Human metapneumo virus

<400> 152
 Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
 1 5 10 15
 Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
 20 25 30
 Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
 35 40 45
 Leu Ile Ile Asn Tyr Thr Ile Gln Gln Thr Thr Ser Glu Ser Glu His
 50 55 60
 His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Ala Ser Thr Ile
 65 70 75 80
 Ser Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
 85 90 95
 Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Ala Ser Pro
 100 105 110
 Ser Glu Thr Glu Ser Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
 115 120 125
 Ser Val Asp Arg Ser Thr Val Gln Pro Ser Glu Asn Arg Thr Lys Thr
 130 135 140
 Lys Leu Thr Val His Thr Arg Asn Asn Leu Ser Thr Ala Ser Ser Thr
 145 150 155 160
 Gln Ser Pro Pro Arg Ala Thr Thr Lys Ala Ile Arg Arg Ala Thr Thr
 165 170 175
 Leu Arg Met Ser Ser Thr Gly Arg Arg Pro Thr Thr Thr Leu Val Gln
 180 185 190

Ser Asp Ser Ser Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
 195 200 205
 Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Asn
 210 215 220
 Ile Lys Pro Asn
 225

<210> 153
<211> 228
<212> PRT
<213> Human metapneumo virus

<400> 153
 Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
 1 5 10 15
 Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
 20 25 30
 Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
 35 40 45
 Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
 50 55 60
 His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Ala Ser Thr Ile
 65 70 75 80
 Ser Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
 85 90 95
 Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Ala Ser Pro
 100 105 110
 Ser Glu Thr Glu Ser Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
 115 120 125
 Ser Val Asp Arg Ser Thr Val Gln Pro Ser Glu Asn Arg Thr Lys Thr
 130 135 140
 Lys Leu Thr Val His Thr Arg Asn Asn Leu Ser Thr Ala Ser Ser Thr
 145 150 155 160
 Gln Ser Pro Pro Arg Ala Thr Thr Lys Ala Ile Arg Arg Ala Thr Thr
 165 170 175
 Leu Arg Met Ser Ser Thr Gly Arg Arg Pro Thr Thr Thr Leu Val Gln
 180 185 190
 Ser Asp Ser Ser Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
 195 200 205
 Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Asn
 210 215 220
 Ile Lys Pro Asn
 225

<210> 154
<211> 231
<212> PRT
<213> Human metapneumovirus

<220>
<221> VARIANT
<222> 225
<223> Xaa = unknown amino acid or other

<400> 154
 Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
 1 5 10 15
 Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
 20 25 30
 Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe

35	40	45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn		
50	55	60
Cys Ala Asn Met Pro Ser Ala Glu Pro Ser Lys Lys Thr Pro Met Thr		
65	70	75
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln		
85	90	95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Val Ala Thr Pro Glu Gly His		
100	105	110
Pro Tyr Thr Gly Thr Thr Gln Thr Ser Asp Thr Thr Ala Pro Gln Gln		
115	120	125
Thr Thr Asp Lys His Thr Ala Pro Leu Lys Ser Thr Asn Glu Gln Ile		
130	135	140
Thr Gln Thr Thr Glu Lys Lys Thr Ile Arg Ala Thr Thr Gln Lys		
145	150	155
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala		
165	170	175
Thr Gln Thr Thr Asn Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr		
180	185	190
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Thr Thr Gln Ser Ser		
195	200	205
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro Pro His His Ala		
210	215	220
Xaa Arg Gly Ala Lys Leu Lys		
225	230	

<210> 155

<211> 231

<212> PRT

<213> Human metapneumo virus

<400> 155

Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala		
1	5	10
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr		
20	25	30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe		
35	40	45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn		
50	55	60
Cys Ala Asn Met Pro Ser Ala Glu Pro Ser Lys Lys Thr Pro Met Thr		
65	70	75
Ser Thr Ala Gly Pro Ser Thr Glu Pro Asn Pro Gln Gln Ala Thr Gln		
85	90	95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Ala Ala Thr Leu Glu Ser His		
100	105	110
Pro Tyr Thr Gly Thr Thr Gln Thr Pro Asp Ile Thr Ala Pro Gln Gln		
115	120	125
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile		
130	135	140
Thr Gln Thr Thr Glu Lys Lys Thr Thr Arg Ala Thr Thr Gln Lys		
145	150	155
Arg Glu Lys Glu Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala		
165	170	175
Thr Gln Thr Thr Asn Thr Asn Gln Thr Arg Asn Ala Ser Glu Thr		
180	185	190
Ile Thr Thr Ser Asp Arg Pro Arg Ile Asp Thr Thr Gln Ser Ser		
195	200	205
Asp Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro Pro His His Ala		
210	215	220
Gln Ser Gly Ala Lys Pro Lys		

225

230

<210> 156
<211> 231
<212> PRT
<213> Human metapneumo virus

<400> 156
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1 5 10 15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
20 25 30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
35 40 45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
50 55 60
Cys Ala Asn Met Pro Pro Ala Glu Pro Ser Lys Lys Thr Pro Met Thr
65 70 75 80
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
85 90 95
Trp Thr Thr Glu Asn Ser Thr Phe Pro Ala Ala Thr Ser Glu Gly His
100 105 110
Leu His Thr Gly Thr Thr Gln Thr Pro Asp Thr Thr Ala Pro Gln Gln
115 120 125
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile
130 135 140
Thr Gln Thr Thr Glu Lys Lys Thr Thr Arg Ala Thr Thr Gln Arg
145 150 155 160
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala
165 170 175
Thr Gln Thr Thr Asn Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr
180 185 190
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Ser Thr Thr Gln Ser Ser
195 200 205
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro Pro His His Ala
210 215 220
Gln Gly Ser Ala Lys Pro Lys
225 230

<210> 157
<211> 231
<212> PRT
<213> Human metapneumo virus

<400> 157
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1 5 10 15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
20 25 30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
35 40 45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
50 55 60
Cys Ala Asn Met Pro Pro Ala Glu Pro Ser Arg Lys Thr Pro Met Thr
65 70 75 80
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
85 90 95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Ala Ala Thr Pro Glu Gly His
100 105 110
Leu His Thr Gly Thr Thr Gln Thr Pro Asp Thr Thr Ala Pro Gln Gln

115	120	125
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile		
130	135	140
Thr Gln Ala Thr Thr Glu Lys Lys Thr Thr Arg Glu Thr Thr Gln Arg		
145	150	155
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala		
165	170	175
Thr Gln Thr Thr Asn Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr		
180	185	190
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Ser Thr Thr Gln Ser Ser		
195	200	205
Glu Gln Thr Thr Gln Ala Thr Asp Pro Ser Ser Pro Ala His His Ala		
210	215	220
Gln Gly Ser Ala Lys Pro Lys		
225	230	

<210> 158

<211> 231

<212> PRT

<213> Human metapneumo virus

<400> 158

Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala		
1	5	10
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr		
20	25	30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe		
35	40	45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn		
50	55	60
Cys Ala Asn Met Pro Pro Ala Glu Pro Ser Lys Lys Thr Pro Met Thr		
65	70	75
Ser Thr Ala Gly Leu Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln		
85	90	95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Ala Ala Thr Pro Glu Gly His		
100	105	110
Leu His Thr Gly Thr Thr Gln Thr Pro Asp Thr Thr Ala Pro Gln Gln		
115	120	125
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile		
130	135	140
Thr Gln Thr Thr Glu Lys Lys Thr Thr Arg Ala Thr Thr Gln Arg		
145	150	155
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala		
165	170	175
Thr Gln Thr Thr Asn Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr		
180	185	190
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Ser Thr Thr Gln Ser Ser		
195	200	205
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro Pro His His Ala		
210	215	220
Gln Gly Ser Ala Lys Pro Lys		
225	230	

<210> 159

<211> 231

<212> PRT

<213> Human metapneumo virus

<400> 159

Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala

1	5	10	15
Lys Ile Lys Asn Arg Ile Arg Ser Ser	Arg Cys Tyr Arg Asn Ala Thr		
20	25	30	
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe			
35	40	45	
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn			
50	55	60	
Cys Ala Asn Met Pro Pro Ala Glu Pro Ser Lys Lys Thr Pro Met Thr			
65	70	75	80
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln			
85	90	95	
Trp Thr Thr Glu Asn Ser Thr Ser Pro Ala Ala Thr Pro Glu Gly His			
100	105	110	
Leu His Thr Gly Thr Thr Gln Thr Pro Asp Thr Thr Ala Pro Gln Gln			
115	120	125	
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile			
130	135	140	
Thr Gln Thr Thr Glu Lys Lys Thr Thr Arg Ala Thr Thr Gln Arg			
145	150	155	160
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala			
165	170	175	
Thr Gln Thr Thr Asn Thr Thr Asn Gln Ile Arg Asn Ala Ile Glu Thr			
180	185	190	
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Ser Thr Thr Gln Ser Ser			
195	200	205	
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser His Pro His His Ala			
210	215	220	
Gln Gly Ser Ala Lys Pro Lys			
225	230		

<210> 160

<211> 236

<212> PRT

<213> Human metapneumo virus

<400> 160

Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala			
1	5	10	15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr			
20	25	30	
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe			
35	40	45	
Leu Ile Ile Asp Tyr Ala Met Leu Lys Asn Met Thr Lys Val Glu His			
50	55	60	
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr			
65	70	75	80
Ser Ala Val Asp Leu Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln			
85	90	95	
Leu Ala Ala Glu Asp Ser Thr Ser Leu Ala Ala Thr Ser Glu Asp His			
100	105	110	
Leu His Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln			
115	120	125	
Thr Thr Asp Glu Tyr Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr			
130	135	140	
Thr Gln Thr Thr Glu Lys Lys Pro Thr Gly Ala Thr Thr Lys Lys			
145	150	155	160
Glu Thr Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn			
165	170	175	
Thr Thr Asn Gln Thr Ser Tyr Val Arg Glu Ala Thr Thr Ser Ala			
180	185	190	
Arg Ser Arg Asn Ser Ala Thr Thr Gln Ser Ser Asp Gln Thr Thr Gln			

195	200	205
Ala Ala Asp Pro Ser Ser Gln Pro His His Thr Gln Lys Ser Thr Thr		
210	215	220
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Pro Ser Ser		
225	230	235

<210> 161
<211> 236
<212> PRT
<213> Human metapneumovirus

<220>
<221> VARIANT
<222> 220, 227
<223> Xaa = unknown amino acid or other

<400> 161			
Met Glu Val Arg Val Glu Asn Ile Arg Thr Ile Asp Met Phe Lys Ala			
1	5	10	15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr			
20	25	30	
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe			
35	40	45	
Leu Ile Ile Asp Tyr Ala Thr Phe Lys Asn Met Thr Lys Val Glu His			
50	55	60	
Cys Ala Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr			
65	70	75	80
Ser Thr Val Asp Ser Ser Thr Gly Pro Asn Pro Gln Gln Thr Thr Gln			
85	90	95	
Trp Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Ser Glu Asp His			
100	105	110	
Leu His Thr Gly Thr Thr Pro Thr Leu Asp Ala Thr Val Ser Gln Gln			
115	120	125	
Thr Pro Asp Lys His Thr Thr Pro Leu Arg Ser Thr Asn Gly Gln Thr			
130	135	140	
Thr Gln Thr Thr Glu Lys Lys Pro Thr Arg Ala Ile Ala Lys Lys			
145	150	155	160
Glu Thr Thr Asn Gln Thr Thr Ser Thr Ala Ala Thr Gln Thr Phe Asn			
165	170	175	
Thr Thr Asn Gln Thr Arg Asn Gly Arg Glu Thr Thr Ile Thr Ser Ala			
180	185	190	
Arg Ser Arg Asn Asp Ala Thr Thr Gln Ser Ser Glu Gln Thr Asn Gln			
195	200	205	
Thr Thr Asp Pro Ser Ser Gln Pro His His Ala Xaa Ile Ser Thr Ile			
210	215	220	
Thr Ile Xaa Thr Gln His Arg His Ile Phe Ser Lys			
225	230	235	

<210> 162
<211> 236
<212> PRT
<213> Human metapneumovirus

<220>
<221> VARIANT
<222> 208
<223> Xaa = unknown amino acid or other

<400> 162
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala

1	5	10	15
Lys Met Lys Asn Arg Ile Arg Ser Ser	Lys Cys Tyr Arg Asn Ala Thr		
20	25	30	
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe			
35	40	45	
Leu Ile Ile Asp Tyr Ala Met Leu Lys Asn Met Thr Lys Val Glu His			
50	55	60	
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr			
65	70	75	80
Ser Ala Val Asp Leu Asn Thr Lys Leu Asn Pro Gln Gln Ala Thr Gln			
85	90	95	
Leu Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Ser Glu Asp His			
100	105	110	
Leu Leu Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln			
115	120	125	
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr			
130	135	140	
Thr Gln Thr Thr Glu Lys Lys Pro Thr Gly Ala Thr Thr Lys Lys			
145	150	155	160
Glu Thr Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn			
165	170	175	
Thr Thr Asn Gln Thr Ser Asn Gly Arg Glu Ala Thr Thr Ser Thr			
180	185	190	
Arg Ser Arg Asn Gly Ala Thr Thr Gln Asn Ser Asp Gln Thr Thr Xaa			
195	200	205	
Thr Ala Asp Pro Ser Ser Gln Pro His His Thr Gln Lys Ser Thr Thr			
210	215	220	
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Pro Ser Ser			
225	230	235	

<210> 163

<211> 236

<212> PRT

<213> Human metapneumo virus

<400> 163

Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala			
1	5	10	15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr			
20	25	30	
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe			
35	40	45	
Leu Ile Ile Asp Tyr Ala Thr Leu Lys Asn Met Thr Lys Val Glu His			
50	55	60	
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr			
65	70	75	80
Ser Ala Val Asp Leu Asn Thr Lys Leu Asn Pro Gln Gln Ala Thr Gln			
85	90	95	
Leu Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Ser Glu Gly His			
100	105	110	
Pro His Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln			
115	120	125	
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr			
130	135	140	
Thr Gln Thr Ala Thr Glu Lys Lys Pro Thr Gly Ala Thr Thr Lys Lys			
145	150	155	160
Glu Thr Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Pro Asn			
165	170	175	
Thr Thr Asn Gln Thr Ser Asn Gly Arg Glu Ala Thr Thr Ser Ala			
180	185	190	
Arg Ser Arg Asn Gly Ala Thr Thr Gln Asn Ser Asp Gln Ile Thr Gln			

195	200	205
Ala Ala Asp Ser Ser Ser Gln Pro His His Thr Gln Lys Ser Thr Thr		
210	215	220
Thr Ala Tyr Asn Thr Asp Thr Ser Phe Pro Ser Ser		
225	230	235

<210> 164
<211> 236
<212> PRT
<213> Human metapneumo virus

<400> 164			
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala			
1	5	10	15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr			
20	25	30	
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe			
35	40	45	
Leu Ile Ile Asp Tyr Ala Thr Leu Lys Asn Met Thr Lys Val Glu His			
50	55	60	
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr			
65	70	75	80
Ser Ala Val Asp Ser Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln			
85	90	95	
Leu Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Leu Glu Asp His			
100	105	110	
Pro His Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln			
115	120	125	
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr			
130	135	140	
Thr Gln Thr Thr Ala Glu Lys Lys Pro Thr Arg Ala Thr Thr Lys Lys			
145	150	155	160
Glu Thr Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn			
165	170	175	
Thr Thr Asn Gln Thr Ser Asn Gly Arg Glu Ala Thr Thr Ser Ala			
180	185	190	
Arg Ser Arg Asn Asn Ala Thr Thr Gln Ser Ser Asp Gln Thr Thr Gln			
195	200	205	
Ala Ala Glu Pro Ser Ser Gln Ser Gln His Thr Gln Lys Ser Thr Thr			
210	215	220	
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Leu Ser Ser			
225	230	235	

<210> 165
<211> 236
<212> PRT
<213> Human metapneumo virus

<400> 165			
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala			
1	5	10	15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr			
20	25	30	
Leu Ile Leu Ile Gly Leu Ser Ala Leu Ser Met Ala Leu Asn Ile Phe			
35	40	45	
Leu Ile Ile Asp Tyr Ala Lys Ser Lys Asn Met Thr Arg Val Glu His			
50	55	60	
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr			
65	70	75	80
Ser Ala Val Asp Leu Asn Thr Lys Pro Asn Pro Gln Arg Ala Thr Gln			

85	90	95
Leu Thr Thr Glu Asp Ser Thr Ser	Leu Ala Ala Thr	Leu Glu Gly His
100	105	110
Leu His Thr Gly Thr Thr Pro	Thr Pro Asp Val Thr	Val Ser Gln Gln
115	120	125
Thr Thr Asp Glu His Thr Thr	Leu Leu Arg Ser Thr	Asn Arg Gln Thr
130	135	140
Thr Gln Thr Ala Ala Glu Lys	Lys Pro Thr Arg Val	Thr Thr Asn Lys
145	150	155
Glu Thr Ile Thr Arg Thr Thr	Ser Thr Ala Ala Thr	Gln Thr Leu Asn
165	170	175
Thr Thr Asn Gln Thr Asn Asn	Gly Arg Glu Ala Thr	Thr Thr Ser Ala
180	185	190
Arg Ser Arg Asn Asn Ala Thr	Thr Gln Ser Ser Asp	Gln Thr Thr Gln
195	200	205
Ala Ala Asp Pro Ser Ser Gln	Ser Gln His Thr	Gln Lys Ser Ile Thr
210	215	220
Thr Thr Tyr Asn Thr Asp Thr	Ser Ser Pro Ser	Ser
225	230	235

<210> 166
<211> 236
<212> PRT
<213> Human metapneumo virus

<400> 166																
Met	Glu	Val	Arg	Val	Glu	Asn	Ile	Arg	Ala	Ile	Asp	Met	Phe	Lys	Ala	
1																15
Lys	Met	Lys	Asn	Arg	Ile	Arg	Ser	Ser	Lys	Cys	Tyr	Arg	Asn	Ala	Thr	
																30
Leu	Ile	Leu	Ile	Gly	Leu	Ser	Ala	Leu	Ser	Met	Ala	Leu	Asn	Ile	Phe	
																45
Leu	Ile	Ile	Asp	Tyr	Ala	Lys	Ser	Lys	Thr	Met	Thr	Arg	Val	Glu	His	
																50
Cys	Val	Asn	Met	Pro	Pro	Val	Glu	Pro	Ser	Lys	Lys	Thr	Pro	Met	Thr	
65																80
Ser	Ala	Val	Asp	Leu	Asn	Thr	Lys	Pro	Asn	Pro	Gln	Gln	Ala	Thr	Gln	
																85
Leu	Thr	Thr	Glu	Asp	Ser	Thr	Ser	Pro	Ala	Ala	Thr	Leu	Glu	Gly	His	
																100
Leu	His	Thr	Gly	Thr	Thr	Pro	Thr	Pro	Asp	Ala	Thr	Val	Ser	Gln	Gln	
																115
Thr	Thr	Asp	Glu	His	Thr	Thr	Leu	Leu	Arg	Ser	Thr	Asn	Arg	Gln	Thr	
																130
Thr	Gln	Thr	Thr	Ala	Glu	Lys	Lys	Pro	Thr	Arg	Ala	Thr	Thr	Lys	Lys	
145																150
Glu	Thr	Ile	Thr	Arg	Thr	Thr	Ser	Thr	Ala	Ala	Thr	Gln	Thr	Leu	Asn	
																165
Thr	Thr	Asn	Gln	Thr	Ser	Asn	Gly	Arg	Glu	Ala	Thr	Thr	Thr	Ser	Ala	
																180
Arg	Ser	Arg	Asn	Asn	Ala	Thr	Thr	Gln	Ser	Ser	Asp	Gln	Thr	Thr	Gln	
																195
Ala	Ala	Asp	Pro	Ser	Ser	Gln	Ser	Gln	His	Thr	Lys	Lys	Ser	Thr	Thr	
																210
Thr	Thr	Tyr	Asn	Thr	Asp	Thr	Ser	Ser	Pro	Ser	Ser					
																225
																230
																235

<210> 167
<211> 236
<212> PRT

<213> Human metapneumo virus

<400> 167

Met	Glu	Val	Arg	Val	Glu	Asn	Ile	Arg	Ala	Ile	Asp	Met	Phe	Lys	Ala	
1					5				10					15		
Lys	Met	Lys	Asn	Arg	Ile	Arg	Ser	Ser	Lys	Cys	Tyr	Arg	Asn	Ala	Thr	
					20				25					30		
Leu	Ile	Leu	Ile	Gly	Leu	Thr	Ala	Leu	Ser	Met	Ala	Leu	Asn	Ile	Phe	
					35				40					45		
Leu	Ile	Ile	Asp	Tyr	Ala	Thr	Leu	Lys	Asn	Met	Thr	Lys	Val	Glu	His	
					50				55					60		
Cys	Val	Asn	Met	Pro	Pro	Val	Glu	Pro	Ser	Lys	Lys	Thr	Pro	Met	Thr	
					65				70					80		
Ser	Ala	Val	Asp	Leu	Asn	Thr	Lys	Pro	Asn	Pro	Gln	Gln	Ala	Thr	Gln	
					85				90					95		
Leu	Thr	Thr	Glu	Asp	Ser	Thr	Ser	Leu	Ala	Ala	Thr	Leu	Glu	Asp	His	
					100				105					110		
Pro	His	Thr	Gly	Thr	Thr	Pro	Thr	Pro	Asp	Ala	Thr	Val	Ser	Gln	Gln	
					115				120					125		
Thr	Thr	Asp	Glu	His	Thr	Thr	Leu	Leu	Arg	Ser	Thr	Asn	Arg	Gln	Thr	
					130				135					140		
Thr	Gln	Thr	Thr	Ala	Glu	Lys	Lys	Pro	Thr	Arg	Ala	Thr	Thr	Lys	Lys	
					145				150					155		160
Glu	Thr	Thr	Arg	Thr	Thr	Ser	Thr	Ala	Ala	Thr	Gln	Thr	Leu	Asn		
					165				170					175		
Thr	Thr	Asn	Gln	Thr	Ser	Asn	Gly	Arg	Glu	Ala	Thr	Thr	Thr	Ser	Ala	
					180				185					190		
Arg	Ser	Arg	Asn	Asn	Ala	Thr	Thr	Gln	Ser	Ser	Asp	Gln	Thr	Thr	Gln	
					195				200					205		
Ala	Ala	Glu	Pro	Asn	Ser	Gln	Ser	Gln	His	Thr	Gln	Lys	Ser	Thr	Thr	
					210				215					220		
Thr	Thr	Tyr	Asn	Thr	Asp	Thr	Ser	Ser	Leu	Ser	Ser					
					225				230					235		

<210> 168

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 168

ataggagttt	acggaagctc	cgttatattac	atggtgcaac	tgccaatctt	tggggttata	60
gacacgcctt	gctggatagt	aaaagcagcc	ccttcggatgtt	cagaaaaaaaaa	gggaaactat	120
gcttcctctt	taagagaaga	ccaaggatgg	tattgtcaaa	atgcagggtc	aactgtttac	180
tacccaaatg	aaaaagactg	tgaaacaaga	ggagaccatg	tctttgcga	cacagcagca	240
ggaatcaatg	ttgctgagca	gtcaaaggag	tgcaacatca	acatatctac	tactaattac	300
ccatgcaaag	ttagcacagg	aagacatcct	atcgttatgg	ttgcactatc	tcctcttggg	360
gctttggttt	cttgcataaa	gggagtgagc	tgttccattt	gcagcaacag	agtagggatc	420
atcaagcaac	tgaacaaagg	ctgtcttta				449

<210> 169

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 169

ataggagttt	acggaagctc	cgttatattac	atggtgcaac	tgccaatctt	tggggttata	60
gacacgcctt	gctggatagt	aaaagcagcc	ccttcggatgtt	cagaaaaaaaaa	gggaaactat	120
gcttcctctt	taagagaaga	tcaaggatgg	tattgtcaga	atgcagggtc	aactgtttac	180
tacccaaatg	aaaaagactg	cgaacaaga	ggagaccatg	tctttgcga	cacagcagca	240
ggaatcaatg	ttgctgagca	gtcaaaggag	tgcaacatca	acatatccac	tactaattac	300
ccatgcaaag	ttagcacagg	aagacatcct	atcgttatgg	ttgcactatc	tcctcttggg	360

gctttgggtt cttgctacaa gggagtgagc tgccatcg gcagcaac agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449

<210> 170
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 170
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccatctt tggggttata 60
gacacgcctt gctggatagt aaaagcagcc ctttcttgc cagaaaaaaaa gggaaactat 120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagattg cggaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttgggtt cttgctacaa gggagtgagc tgccatcg gcagcaac agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449

<210> 171
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 171
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccatctt tggggttata 60
gacacgcctt gctggatagt aaaagcagcc ctttcttgc cagaaaaaaaa gggaaactat 120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cggaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttgggtt cttgctacaa gggagtgagc tgccatcg gcagcaac agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449

<210> 172
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 172
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccatctt tggggttata 60
gacacgcctt gctggatagt aaaagcagcc ctttcttgc cagaaaaaaaa gggaaactat 120
gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagattg cggaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttgggtt cttgctacaa gggagtgagc tgccatcg gcagcaac agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449

<210> 173
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 173
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccatctt tggggttata 60
gacacgcctt gctggatagt aaaagcagcc ctttcttgc cagaaaaaaaa gggaaactat 120
gcttgcctct taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg tggaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatctac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttgggtt cttgctacaa gggagtgagc tgccatcg gcagcaac agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449

<210> 174
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 174
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata 60
gacacgcctt gctggatagt aaaagcagcc ccttcttgc t cagaaaaaaaaa gggaaaactat 120
gcttcctct taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg tgaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac 300
ccatgcaaag ttagcacagg aagacatctt atcagtatgg ttgcaactgtc tcctcttggg 360
gcttgggtg cttgctacaa gggagtgagc tgccatttgc gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgcttta 449

<210> 175
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 175
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata 60
gacacgcctt gctggatagt aaaagcagcc ccttcttgc t cagaaaaaaaaa gggaaaactat 120
gcttcctct taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg tgaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac 300
ccatgcaaag ttagcacagg aagacatctt atcagtatgg ttgcaactgtc tcctcttggg 360
gcttgggtg cttgctacaa gggagtgagc tgccatttgc gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgcttta 449

<210> 176
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 176
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata 60
gacacgcctt gctggatagt aaaagcagcc ccttcttgc t cagaaaaaaaaa gggaaaactat 120
gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg tgaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatctt atcagtatgg ttgcaactgtc tcctcttggg 360
gcttgggtg cttgctacaa gggagtgagc tgccatttgc gcagcaacag agtaggaatc 420
atcaagcaac tgaacaaagg ctgcttta 449

<210> 177
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 177
ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggagttata 60
gacacgcctt gctggatagt aaaagcagcc ccttcttgc t cagaaaaaaaaa gggaaaactat 120
gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatctt atcagtatgg ttgcaactgtc tcctcttggg 360
gcttgggtg cttgctacaa gggagtgagc tgccatttgc gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgcttta 449

<210> 178
<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 178

```
ataggagttt acggaagctc cgtaattac atggtgcaac tgccaatctt tgggttata 60
gacacgcctt gttggatagt aaaagcagcc cttcttgct cagaaaaaaaa gggaaactat 120
gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtciaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gcttgggtt cttgctacaa gggagtgagc tgccatttgcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgcttta 449
```

<210> 179

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 179

```
ataggagttt acggaagctc cgtaattac atggtgcaac tgccaatctt tggagtata 60
gacacgcctt gttggatagt aaaagcggcc cttcttgct cagaaaaaaaa gggaaactat 120
gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtciaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gcttgggtt cttgctacaa gggagtgagc tgccatttgcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgcttta 449
```

<210> 180

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 180

```
ataggagttt acggaagctc cgtaattac atggtgcaac tgccaatctt tgggttata 60
gacacgcctt gttggatagt aaaagcagcc cttcttgct cagaaaaaaaa gggaaactat 120
gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtciaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gcttgggtt cttgctacaa gggagtgagc tgccatttgcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgcttta 449
```

<210> 181

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 181

```
ataggagttt acggaagctc cgtaattac atggtgcaac tgccaatctt tggagttata 60
gacacgcctt gttggatagt aaaagcggcc cttcttgct cgaaaaaaaa gggaaactat 120
gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtciaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gcttgggtt cttgctacaa gggagtgagc tgccatttgcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgcttta 449
```

<210> 182

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 182
ataggagttt atggaagctc cgtaattac atggtgcaac tgccaatctt tggagttata 60
gacaacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaaaa gggaaactat 120
gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gcttgggtg ctgctacaa gggagtgagc tgccatttgcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgcttta 449

<210> 183
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 183
ataggagttt atggaagctc cgtaattac atggtgcaac tgccaatctt tggagttata 60
gacaacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaaaa gggaaactat 120
gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gcttgggtg ctgctacaa gggagtgagc tgccatttgcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgcttta 449

<210> 184
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 184
ataggagttt acggaagctc cgtaattac atggtgcaac tgccaatctt tggagttata 60
gacaacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaaaa gggaaactat 120
gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gcttgggtg ctgctacaa gggagtgagc tgccatttgcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgcttta 449

<210> 185
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 185
ataggagttt atggaagctc cgtaattac atggtgcaac tgccaatctt tggagttata 60
gacaacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaaaa gggaaactat 120
gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gcttgggtg ctgctacaa gggagtgagc tgccatttgcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgcttta 449

<210> 186
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 186
ataggagttt atggaagctc cgtaattac atggtgcaac tgccaatctt tggagttata 60

gacacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaaa gggaaactat 120
 gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
 tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
 ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
 ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
 gcttgggtt cttgctacaa gggagtgagc tgccatttgcga acatatccac tactaattac 420
 atcaagcaac tgaacaaagg ctgcttta 449

<210> 187
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 187
 ataggagttt atggaagctc cgtaatttac atggtgcaac tgccaatctt tggagttata 60
 gacacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaaa gggaaactat 120
 gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
 tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
 ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
 ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
 gcttgggtt cttgctacaa gggagtgagc tgccatttgcga acatatccac tactaattac 420
 atcaagcaac tgaacaaagg ctgcttta 449

<210> 188
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 188
 ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata 60
 gacacgcctt gctggatagt aaaagcagcc ccttcttggtt cagggaaaaaaa gggaaactat 120
 gcttcctct taagagaaga ccaaggatgg tattgtcaaa atgcagggtc aactgtttac 180
 tacccaaatg aaaaagactg tgaacaaaga ggagaccatg tctttgcga cacagcagca 240
 ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac 300
 ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactatc tcctcttggg 360
 gcttgggtt cttgctacaa gggagtgagc tgccatttgcga acatatccac tactaattac 420
 atcaagcaac tgaacaaagg ctgcttta 449

<210> 189
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 189
 ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata 60
 gacacgcctt gctggatagt aaaagcagcc ccttcttggtt cagggaaaaaaa gggaaactat 120
 gcttcctct taagagaaga ccaaggatgg tattgtcaaa atgcagggtc aactgtttac 180
 tacccaaatg aaaaagactg tgaacaaaga ggagaccatg tctttgcga cacagcagca 240
 ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac 300
 ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactatc tcctcttggg 360
 gcttgggtt cttgctacaa gggagtgagc tgccatttgcga acatatccac tactaattac 420
 atcaagcaac tgaacaaagg ctgcttta 449

<210> 190
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 190
 ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggagttata 60
 gacacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaaa gggaaactat 120
 gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180

tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
 ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac cactaattac 300
 ccatgcaaag ttagcacagg aagacatct atcagtatgg ttgcaactgtc tcctcttggg 360
 gcttgggttg ctgtacaa gggagtgagc tgccatttgcga cagcaacag agtagggatc 420
 atcaagcaac tgaacaaagg ctgcttta 449

<210> 191
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 191
ataggagttt acggaagctc cgtaatttac atgggtcaac tgccaatctt tggggttata 60
gacacgcctt gctggatagt aaaagcagcc ccttcttgct cagaaaaaaaaa gggaaaactat 120
gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatct atcagtatgg ttgcaactgtc tcctcttggg 360
gcttgggttg ctgtacaa gggagtgagc tgccatttgcga cagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgcttta 449

<210> 192
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 192
ataggagttt acggaagctc cgtaatttac atgggtcaac tgccaatctt tggagttata 60
gacacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaaaa gggaaaactat 120
gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatct atcagtatgg ttgcaactgtc tcctcttggg 360
gcttgggttg ctgtacaa gggagtgagc tgccatttgcga cagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgcttta 449

<210> 193
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 193
ataggagttt acggaagctc cgtaatttac atgggtcaac tgccaatctt tggagttata 60
gacacgcctt gctggatagt aaaagcggcc ccttcttgct cagaaaaaaaaa gggaaaactat 120
gcttcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatct atcagtatgg ttgcaactgtc tcctcttggg 360
gcttgggttg ctgtacaa gggagtgagc tgccatttgcga cagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgcttta 449

<210> 194
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 194
ataggagttt acggaagctc cgtaatttac atgggtcaac tgccaatctt tggggttata 60
gacacgcctt gctggatagt aaaagcagcc ccttcttgct cagaaaaaaaaa gggaaaactat 120
gcttcctct taagagaaga ccaaggatgg tattgtcaaa atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg tgaacaaaga ggagaccatg tctttgcga cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatctac tactaattac 300

ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactata tcctcttggg 360
 gcttggttg cttgtacaa gggagtgagc tgccatttgc acagcaacag agtagggatc 420
 atcaagcaac tgaacaaagg ctgctctta 449

<210> 195
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 195
 ataggagttt atggaagctc cgtaatttac atggtgcaac tgccaatctt tggagttata 60
 gacacgcctt gctggatagt aaaagcggcc ccctcttgc cagaaaaaaa gggaaactat 120
 gcttgcctct taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
 tacccaaattg aaaaagactg cgaaacaaga ggagaccatg tctttgcga cacagcagca 240
 ggaatcaatg ttgctgagca gtccaaaggag tgcaacatca acatatccac tactaattac 300
 ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
 gcttggttg cttgtacaa gggagtgagc tgccatttgc acagcaacag agtagggatc 420
 atcaagcaac tgaacaaagg ctgctctta 449

<210> 196
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 196
 ataggagttt acggaagctc cgtaatttac atggtgcaac tgccaatctt tggggttata 60
 gacacgcctt gctggatagt aaaagcagcc ccctcttgc cagaaaaaaa gggaaactat 120
 gcttgcctct taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac 180
 tacccaaattg aaaaagactg taaaacaaga ggagaccatg tctttgcga cacagcagca 240
 ggaatcaatg ttgctgagca gtccaaaggag tgcaacatca acatatctac tactaattac 300
 ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactata tcctcttggg 360
 gcttggttg cttgtacaa gggagtgagc tgccatttgc acagcaacag agtagggatc 420
 atcaagcaac tgaacaaagg ctgctctta 449

<210> 197
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 197
 ataggggtct acgggagctc tggatattac atggtgcaac tgccaatctt tggcggtata 60
 gacacgcctt gctggatagt aaaagcagcc ccctcttgc cggaaaaaaa gggaaactat 120
 gcttgcctct taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
 tacccaaattg agaaagactg taaaacaaga ggagaccatg tctttgcga cacagcagca 240
 ggaattaatg ttgctgagca atcaaaaggag tgcaacatca acatatccac tacaattac 300
 ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgcactgtc ccctcttggg 360
 gctctgggtt cttgtacaa aggagtaagc tgccatttgc acagcaatag agtagggatt 420
 atcaagcagc tgaacaaagg ttgctctta 449

<210> 198
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 198
 ataggggtct acgggagctc cgtaatttac atggtgcaac tgccaatctt tggcggtata 60
 gacacgcctt gctggatagt aaaagcagcc ccctcttgc cggaaaaaaa gggaaactat 120
 gcttgcctt taagagaaga tcaagggtgg tattgtcaga atgcagggtc aactgtttac 180
 tacccaaattg agaaagactg taaaacaaga ggagaccatg tctttgcga cacagcagca 240
 ggaattaatg ttgctgagca atcaaaaggag tgcaacatca acatatccac tacaattac 300
 ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgcactgtc ccctcttggg 360
 gctctgggtt cttgtacaa aggagtaagc tgccatttgc acagcaatag agtagggatt 420

atcaaggcagc tgaacaaagg ttgctccta

449

<210> 199

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 199

ataggggct acgggagctc cgtaatttac atgggtcagc tgccaatctt tggcgctata 60
 gacacgcctt gctggatagt aaaagcagcc ccctttgtt ccgaaaaaaaaa gggaaactat 120
 gcttcctt taagagaaga tcaagggtgg tattgtcaga atgcagggtc aactgtttac 180
 tacccaaatg agaaagactg tgaacaaga ggagaccatg tctttgcga cacagtagca 240
 ggaattaatg ttgctgagca atcaaaaagag tgcaacatca acatatccac tacaattac 300
 ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgcaactgtc ccctttggg 360
 gctctagttg ctgtacaa aggagtaagc tttccattt gcagcaatag agtagggatc 420
 atcaaggcagc tgaacaaagg ttgctccta 449

<210> 200

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 200

ataggggct acgggagctc cgtaatttac atgggtcagc tgccaatctt tggcgctata 60
 gacacgcctt gctggatagt aaaagcagcc ccctttgtt ccgaaaaaaaaa gggaaactat 120
 gcttcctt taagagaaga tcaagggtgg tattgtcaga atgcagggtc aactgtttac 180
 tacccaaatg agaaagactg tgaacaaga ggagaccatg tctttgcga cacagcagca 240
 ggaattaatg ttgctgagca atcaaaaagag tgcaacatca acatatccac tacaattac 300
 ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgcaactgtc ccctttggg 360
 gctctagttg ctgtacaa aggagtaagc tttccattt gcagcaatag agtagggatc 420
 atcaaggcagc tgaacaaagg ttgctccta 449

<210> 201

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 201

ataggggct acgggagctc cgtaatttac atgggtcagc tgccaatctt tggcgttata 60
 gacacgcctt gctggatagt aaaagcagcc ccctttgtt ccgaaaaaaaaa gggaaactat 120
 gcttcctt taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
 tacccaaatg agaaagactg tgaacaaga ggagaccatg tctttgcga cacagcagca 240
 ggaattaatg ttgctgagca atcaaaaaggag tgcaacatca acatatccac cacaattac 300
 ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgcaactgtc ccctttggg 360
 gctctgggtg ctgtacaa aggagtaagc tttccattt gcagcaatag agtagggatc 420
 atcaaggcagc tgaacaaagg ttgctccta 449

<210> 202

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 202

ataggggct acgggagctc cgtaatttac atgggtcagc tgccaatctt tggcgttata 60
 gacacgcctt gctggatagt aaaagcagcc ccctttgtt ccgaaaaaaaaa gggaaactat 120
 gcttcctt taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
 tacccaaatg agaaagactg tgaacaaga ggagaccatg tctttgcga cacagcagca 240
 ggaattaatg ttgctgagca atcaaaaaggag tgcaacatca acatatccac tacaattac 300
 ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgcaactgtc ccctttggg 360
 gctctagttg ctgtacaa aggagtaagc tttccattt gcagcaacag agtagggatc 420
 atcaaggcagc tgaacaaagg ttgctccta 449

<210> 203
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 203
ataggggtct acgggagctc cgtaatttac atgggcagc tgccaatctt tggcggtata 60
gacacgcctt gctggatagt aaaagcagcc ccttcttggtt ccggaaaaaaa gggaaactat 120
gcttccttc taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg agaaagactg tgaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac cacaattac 300
ccatgcaaag tcagcacagg aaggcatcct atcagtatgg ttgcactgtc ccctcttggg 360
gctctgggtt cttgtacaa aggagtaagc tggccatttgcagcaatag agtagggatc 420
atcaaggcagc tgaacaaagg ttgctctta 449

<210> 204
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 204
ataggggtct acgggagctc cgtaatttac atgggcagc tgccaatctt tggcggtata 60
gacacgcctt gctggatagt aaaagcagcc ccttcttggtt ccggaaaaaaa gggaaactat 120
gcttccttc taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg agaaagactg tgaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac tacaattac 300
ccatgcaaag tcagcacagg aaggcatcct atcagtatgg ttgcactgtc ccctcttggg 360
gctctgggtt cttgtacaa aggagtaagc tggccatttgcagcaacag agtagggatc 420
atcaaggcagc tgaacaaagg ttgctctta 449

<210> 205
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 205
ataggggtct acgggagctc cgtaatttac atgggcagc tgccaatctt tggcggtata 60
gacacgcctt gctggatagt aaaagcagcc ccttcttggtt ccggaaaaaaa gggaaactat 120
gcttccttc taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg agaaagactg tgaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac tacaattac 300
ccatgcaaag tcagcacagg aaggcatcct atcagtatgg ttgcactgtc ccctcttggg 360
gctctgggtt cttgtacaa aggagtaagc tggccatttgcagcaacag agtagggatc 420
atcaaggcagc tgaacaaagg ttgctctta 449

<210> 206
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 206
ataggggtct acgggagctc cgtaatttac atgggcagc tgccaatctt tggcggtata 60
gacacgcctt gctggatagt aaaagcagcc ccttcttggtt ccggaaaaaaa gggaaactat 120
gcttccttc taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg agaaagactg tgaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac cacaattac 300
ccatgcaaag tcagcacagg aaggcatcct atcagtatgg ttgcactgtc ccctcttggg 360
gctctgggtt cttgtacaa aggagtaagc tggccatttgcagcaatag agtagggatc 420
atcaaggcagc tgaacaaagg ttgctctta 449

<210> 207
<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 207

ataggggtct acgggagctc cgtaattac atgggcagc tgccaatctt tggcggtata 60
 gacacgcctt gctggatagt aaaagcagcc ccttcgttt ccgaaaaaaaaa gggaaactat 120
 gcttcctct taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
 tacccaaatg agaaagactg tgaacaaga ggagaccatg tctttgcga cacagcagca 240
 ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac tacaattac 300
 ccatgcaaag tcagcacagg aagacatctt atcagtatgg ttgcactgtc ccctctggg 360
 gctcggttg cttgtacaa aggataagc tgccatttgcga acagcaacag agtagggatc 420
 ataaagcagc tgaacaaagg ttgctcta 449

<210> 208

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 208

ataggggtct acgggagctc cgtaattac atgggcagc tgccaatctt tggcggtata 60
 gacacgcctt gctggatagt aaaagcagcc ccttcgttt ccgaaaaaaaaa gggaaactat 120
 gcttcctct taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac 180
 tacccaaatg agaaagactg tgaacaaga ggagaccatg tctttgcga cacagcagca 240
 ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac cacaattac 300
 ccatgcaaag tcagcacagg aagacatctt atcagtatgg ttgcactgtc ccctctggg 360
 gctcggttg cttgtacaa aggataagt tgccatttgcga acagcaatag agtagggatc 420
 atcaagcagc tgaacaaagg ttgctcta 449

<210> 209

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 209

ataggggtct acgggagctc cgtaattac atgggcagc tgccaatctt tggcggtata 60
 gacacacctt gctggatagt aaaagcagcc ccttcgttt ccgaaaaaaaaa gggaaattat 120
 gcttcctct taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
 tacccaaatg agaaagactg tgaacaaga ggagaccatg tctttgcga cacagcagca 240
 ggaattaatg ttgctgagca atcaaaggaa tgcaacatca acatatccac tacaattac 300
 ccatgcaaag tcagcacagg aagacatctt atcagtatgg ttgcactgtc ccctctggg 360
 gctcggttg cttgtacaa aggataagc tgccatttgcga acagcaacag agtagggatc 420
 atcaagcagc tgaacaaagg ttgctcta 449

<210> 210

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 210

ataggggtct acgggagctc cgtaattac atgggcagc tgccaatctt tggcggtata 60
 gacacgcctt gctggatagt aaaagcagcc ccttcgttt ccgaaaaaaaaa gggaaactat 120
 gcttcctct taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac 180
 tacccaaatg agaaagactg tgaacaaga ggagaccatg tctttgcga cacagcagca 240
 ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac cacaattac 300
 ccatgcaaag tcagcacagg aagacatctt atcagtatgg ttgcactgtc ccctctggg 360
 gctcggttg cttgtacaa aggataagt tgccatttgcga acagcaatag agtagggatc 420
 atcaagcagc tgaacaaagg ttgctcta 449

<210> 211

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 211
ataggggtct acggagctc cgtaattac atgggcagc tgccaatctt tggcggtata 60
gacacgcctt gctggatagt aaaagcagcc ctttctgtt ccgaaaaaaaaa gggaaactat 120
gcttcctct taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg agaaagactg taaaacaaga ggagaccatg tctttgcga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac tacaaattac 300
ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgcactgtc tcctctggg 360
gctctgggtg cttgctacaa aggagtaagc tggccattt gcagcaacag agtagggatc 420
ataaaggcagc tgaacaaagg ttgctccta 449

<210> 212

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 212

ataggggtct acggagctc cgtgatttac atggttcaat tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaaaa cgggaattat 120
gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagcagca 240
ggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttgggtg cttgctataa agggttaagc tgctcgattt gcagcaatcg ggttggaaatc 420
ataaaacaat tacctaaagg ctgctcata 449

<210> 213

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 213

ataggggtct acggagctc tggatattac atggttcaat tgccgatctt tgggtgtcata 60
gatacacctt gttggatcat caaggcagct ccctcttgct cagaaaaaaaaa cgggaattat 120
gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc tactgtttac 180
tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagcagca 240
ggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttgggtg cttgctataa agggttaagc tgctcgattt gcagcaattt ggttggaaatc 420
ataaaacaat tacccaaagg ctgctcata 449

<210> 214

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 214

ataggggtct acggagctc tggatattac atggttcaat tgccgatctt tgggtgtcata 60
gatacacctt gttggatcat caaggcagct ccctcttgct cagaaaaaaaaa cgggaattat 120
gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc tactgtttac 180
tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagcagca 240
ggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttgggtg cttgctataa agggttaagc tgctcgattt gcagcaatcg ggttggaaatc 420
ataaaacaat tacccaaagg ctgctcata 449

<210> 215

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 215

ataggggtct acggagctc tggatattac atggttcaat tgccgatctt tgggtgtcata 60

gatacacctt gttggatcat caaggcagct ccctcttgc taaaaaaa cgggaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc tactgtttac 180
 tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
 ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcaactatc acctctcggt 360
 gcttgggtgg cttgctataa agggtaagc tgctcgattg gcagcaatcg gtttggaaatc 420
 atcaaacaat tacccaaagg ctgctcataa 449

<210> 216
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 216
 ataggggtct acggaagctc tggatttac atggttcaat tgccgatctt tgggtgtcata 60
 gatacacctt gttggataat caaggcagct ccctcttgc taaaaaaa cgggaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
 ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcaactatc acctctcggt 360
 gcttgggtgg cttgctataa agggtaagc tgctcgattg gcagcaatcg gtttggaaatc 420
 atcaaacaat tacctaaagg ctgctcataa 449

<210> 217
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 217
 ataggggtct acggaagctc cgtgatttac atggttcaat tgccgatctt tgggtgtcata 60
 gatacacctt gttggataat caaggcagct ccctcttgc taaaaaaa cgggaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
 ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcaactatc acctctcggt 360
 gcttgggtgg cttgctataa agggtaagc tgctcgattg gcagcaatcg gtttggaaatc 420
 atcaaacaat tacctaaagg ctgctcataa 449

<210> 218
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 218
 ataggggtct acggaagctc tgtaatttac atggttcaat tgccgatctt tgggtgtcata 60
 gatacacctt gttggataat caaggcagct ccctcttgc taaaaaaa cgggaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
 ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcaactatc acctctcggt 360
 gcttgggtgg cttgctataa agggtaagc tgctcgattg gcagcaatcg gtttggaaatc 420
 atcaaacaat tacctaaagg ctgctcataa 449

<210> 219
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 219
 ataggggtct acggaagctc cgtgatttac atggttcaat tgccgatctt tgggtgtcata 60
 gatacacctt gttggataat caaggcagct ccctcttgc taaaaaaa cgggaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180

tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacactct ataagcatgg ttgcactatac acctctcggt 360
gcttggtgg cttgctataa agggtaagc tgctcgattg gcagcaatcg gggttgaatc 420
atcaaacaat tacctaaagg ctgctcata 449

<210> 220
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 220
ataggggtct acggaagctc cgtgattac atggttcaat tgccgatctt tgggtgcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaaaa cgaaaaattat 120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatac acctctcggt 360
gcttggtgg cttgctataa agggtaagc tgctcgattg gcagcaatcg gggttgaatc 420
atcaaacaat tacctaaagg ctgctcata 449

<210> 221
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 221
ataggggtct acggaagctc tggattac atggttcaat tgccgatctt tgggtgcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaaaa cgaaaaattat 120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg tggaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatac acctctcggt 360
gcttggtgg cttgctataa agggtaagc tgctcgattg gcagcaatcg gggttgaatc 420
atcaaacaat tacctaaagg ctgctcata 449

<210> 222
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 222
ataggggtct acggaagctc cgtgattac atggttcaat tgccgatctt tgggtgcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaaaa cgaaaaattat 120
gcttgcctcc taagagagga tcaagggtgg tactgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatac acctctcggt 360
gcttggtgg cttgctataa agggtaagc tgctcgattg gcagcaatcg gggttgaatc 420
atcaaacaat tacctaaagg ctgctcata 449

<210> 223
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 223
ataggggtct acggaagctc tggattac atggttcaat tgccgatctt tgggtgcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaaaa cgaaaaattat 120
gcttgcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga tacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300

ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
 gcttggtgg cttgtataaa agggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
 atcaaacaat tacccaaagg ctgctcata 449

<210> 224
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 224
 ataggggtct acggaagctc tgtgatttac atggttcaat tgccgatctt tgggtgcata 60
 gatacacctt gttggataat caaggcagcc ccctcttgct cagaaaaaaa cgaaaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgttac 180
 tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tggtttgtga cacagcagca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
 ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
 gcttggtgg cttgtataaa agggtaagc tgctcgattg gcagcaatcg ggttggaatt 420
 atcaaacaat tacctaaagg ctgctcata 449

<210> 225
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 225
 ataggggtct acggaagctc tgtgatttac atggttcaat tgccgatctt tgggtgcata 60
 gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgaaaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgttac 180
 tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tggtttgtga cacagcagca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
 ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
 gcttggtgg cttgtataaa agggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
 atcaaacaat tacctaaagg ctgctcata 449

<210> 226
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 226
 ataggggtct acggaagctc tgtgatttac atggttcaat tgccgatctt tgggtgcata 60
 gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgaaaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgttac 180
 tacccaaatg aaaaagactg tgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
 ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
 gcttggtgg cttgtataaa agggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
 atcaaacaat tacctaaagg ctgctcata 449

<210> 227
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 227
 ataggggtct acggaagctc cgtgatttac atggttcaat tgccgatctt tgggtgcata 60
 gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgaaaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgttac 180
 tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
 ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
 gcttggtgg cttgtataaa agggtaagc tgctcgattg gcagcaatcg ggttggaatc 420

atcaaacaat tacctaaagg ctgctcata

449

<210> 228

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 228

ataggggtct acggaagctc tgtgatttac atggttcaat tgccgatctt tgggtgcata 60
 gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgggaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagcagca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac tbeccaactac 300
 ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
 gcttgggtgg cttgctataa agggtaagc tgctcgattt gcagcaatcg ggttggaaatc 420
 atcaaacaat tacctaaagg ctgctcata 449

<210> 229

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 229

ataggggtct acggaagctc tgtgatttac atggttcaat tgccgatctt tgggtgcata 60
 gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgggaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga tacagcagca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac tbeccaactac 300
 ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
 gcttgggtgg cttgctataa agggtaagc tgctcgattt gcagcaatcg ggttggaaatc 420
 atcaaacaat tacccaaagg ctgctcata 449

<210> 230

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 230

ataggggtct acggaagctc cgtgatttac atggttcaat tgccgatctt tgggtgcata 60
 gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgggaattat 120
 gcttcctcc taagagagga tcaagggtgg tactgtaaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagcagca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac tbeccaactac 300
 ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
 gcttgggtgg cttgctataa agggtaagc tgctcgattt gcagcaatcg ggttggaaatc 420
 atcaaacaat tacctaaagg ctgctcata 449

<210> 231

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 231

ataggggtct acggaagctc tgtgatttac atggccagc tgccgatctt tgggtgcata 60
 gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaga tggaaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgcaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagcagca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac caccactac 300
 ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
 gcttggtag cttgctacaa gggggtagc tgctcgattt gcagtaatcg ggttggaaata 420
 atcaaacaac tacctaaagg ctgctcata 449

<210> 232
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 232
ataggggtct acggaagctc tgtgatttac atgggccagc tgccgatctt tgggtgcata 60
gatacacctt gttggataat caaggcagct ccctcttgg tggaaaattat 120
gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac caccaactac 300
ccatgcaaag tcagcacagg aagacacccc atcagcatgg ttgactatc acctctcggt 360
gcttggttag cttgctacaa aggggttagc tgctcgattg gcagtaatcg gtttggata 420
atcaaacaac tacctaaagg ctgctcata 449

<210> 233
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 233
ataggggtct acggaagctc tgtgatttac atgggccagc tgccgatctt tgggtgcata 60
gatacacctt gttggataat caaggcagct ccctcttgg tggaaaattat 120
gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac caccaactac 300
ccatgcaaag tcagcacagg aagacacccc atcagcatgg ttgactatc acctctcggt 360
gcttggttag cttgctacaa aggggttagc tgctcgattg gcagtaatcg gtttggata 420
atcaaacaac tacctaaagg ctgctcata 449

<210> 234
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 234
ataggggtct acggaagctc cgtgatttac atgggccagc tgccgatctt tgggtgcata 60
gatacacctt gttggataat caaggcagct ccctcttgg tggaaaattat 120
gcttcctcc taagagagga ccaagggtgg tattgtaaaa atgcgggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacacccc atcagcatgg ttgactatc acctctcggt 360
gcttggttag cttgctacaa aggggttagc tgctcgattg gcagtaatcg gtttggata 420
atcaaacaac tacctaaagg ctgctcata 449

<210> 235
<211> 449
<212> DNA
<213> Human metapneumo virus

<400> 235
ataggggtct acggaagctc cgtgatttac atgggccagc taccgatctt tgggtgcata 60
gatacacctt gttggataat caaggcagct ccctcttgg tggaaaattat 120
gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagctgca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatccac aaccaactac 300
ccatgcaaag tcagcacagg aagacacccc atcagcatgg ttgactatc acctctcggt 360
gcttggttag cttgctacaa aggggttagc tgctcgattg gcagtaatcg gtttggata 420
atcaaacaac tacctaaagg ctgctcata 449

<210> 236
<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 236

ataggggct acggaagctc cgtgattac atggccagc tgccgatctt tgggtcata 60
gatacacctt gttggataat caaggcagct ccctcttgc taaaaaaga tggaaattat 120
gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgttac 180
tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gcttggtag ctgtacaa aggggttagc tgccgattt gcagtaatcg gggttggata 420
atcaaacaac tacctaaagg ctgctcata 449

<210> 237

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 237

ataggggct acggaagctc cgtgattac atggccagc tgccgatctt tgggtcata 60
gatacacctt gttggataat caaggcagct ccctcttgc taaaaaaga tggaaattat 120
gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgttac 180
tacccaaatg aaaaagactg tggaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gcttggtag ctgtacaa aggggttagc tgccgattt gcagtaatcg gggttggata 420
atcaaacaac tacctaaagg ctgctcata 449

<210> 238

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 238

ataggggct acggaagctc cgtgattac atggccagc tgccgatctt tgggtcata 60
gatacacctt gttggataat caaggcagct ccctcttgc taaaaaaga tggaaattat 120
gcttcctcc taagagagga ccaagggtgg tattgtaaaa atgcgggatc cactgttac 180
tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gcttggtag ctgtacaa aggggttagc tgccgattt gcagtaatcg gggttggata 420
atcaaacaac tacctaaagg ctgctcata 449

<210> 239

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 239

ataggggct acggaagctc cgtgattac atggccagc tgccgatctt tgggtcata 60
gatacacctt gttggataat caaggcagct ccctcttgc taaaaaaga tggaaattat 120
gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgttac 180
tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gcttggtag ctgtacaa aggggttagc tgccgattt gcagtaatcg gggttggata 420
atcaaacaac tacctaaagg ctgctcata 449

<210> 240

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 240
 ataggggtct acggaagctc cgtgattac atggtccagc tgccgatctt tgggtgcata 60
 gatacacctt gttggataat caaggcagct ccctcttgg tggaaaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg taaaaacaaga ggtgatcatg tttttgtga cacagcagca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
 ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcaactatc acctctcggt 360
 gcttggtag cttgctacaa aggggttagc tggtcgattg gcagtaatcg gggttggaaata 420
 atcaaacaac tacctaaagg ctgctcata 449

<210> 241
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 241
 ataggggtct acggaagctc cgtgattac atggtccagc tgccgatctt tgggtgcata 60
 gatacacctt gttggataat caaggcagct ccctcttgg tggaaaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagctgca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
 ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcaactatc acctctcggt 360
 gcttggtag cttgctacaa aggggttagc tggtcaatttgcagtaatcg gggttggaaata 420
 atcaaacaac tacctaaagg ctgctcata 449

<210> 242
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 242
 ataggggtct acggaagctc cgtgattac atggtccagc tgccgatctt tgggtgcata 60
 gatacacctt gttggataat caaggcagct ccctcttgg tggaaaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagctgca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
 ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcaactatc acctctcggt 360
 gcttggtag cttgctacaa aggggttagc tggtcaatttgcagtaatcg gggttggaaata 420
 atcaaacaac tacctaaagg ctgctcata 449

<210> 243
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 243
 ataggggtct acggaagctc cgtgattac atggtccagc tgccgatctt tgggtgcata 60
 gatacacctt gttggataat caaggcagct ccctcttgg tggaaaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg cggaaacaaga ggtgatcatg tttttgtga cacagctgca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
 ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcaactatc acctctcggt 360
 gcttggtag cttgctacaa aggggttagc tggtcaatttgcagtaatcg gggttggaaata 420
 atcaaacaac tacctaaagg ctgctcata 449

<210> 244
 <211> 449
 <212> DNA
 <213> Human metapneumo virus

<400> 244
 ataggggtct acggaagctc tgtgattac atggtccagc tgccgatctt tgggtgcata 60

gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagctgca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatccac aaccaactac 300
 ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactgtc acctctcggt 360
 gcttggttag cttgctacaa aggggttagc tgtcgattg gcagtaatcg gggttggaaata 420
 atcaaacaac tacctaaagg ctgctcata 449

<210> 245

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 245

ataggggtct acggaagctc tggatattac atggccagc tgccgatctt tgggtgtcata 60
 gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
 gggatcaacg ttgctgagca atcaagagaa tgcaacatca acatatctac caccacat 300
 ccgtgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
 gcttggttag cttgctacaa aggggttagc tgtcgattg gcagtaatcg gggttggaaata 420
 atcaaacaac tacctaaagg ctgctcata 449

<210> 246

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 246

ataggggtct acggaagctc cgtgatattac atggccagc tgccgatctt tgggtgtcata 60
 gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagctgca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
 ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
 gcttggttag cttgctacaa aggggttagc tgtcgattg gcagtaatcg gggttggaaata 420
 atcaaacaac tacctaaagg ctgctcata 449

<210> 247

<211> 449

<212> DNA

<213> Human metapneumo virus

<400> 247

ataggggtct acggaagctc cgtgatattac atggccagc tgccgatctt tgggtgtcata 60
 gatacacctt gttggataat caaggcagct ccctcttgtt cagaaaaaga tggaaattat 120
 gcttcctcc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
 tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
 gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
 ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
 gcttggttag cttgctacaa aggggttagc tgtcgattg gcagtaatcg gggttggaaata 420
 atcaaacaac tacctaaagg ctgctcata 449

<210> 248

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 248

Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser

20	25	30
Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln		
35	40	45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu		
50	55	60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala		
65	70	75
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser		
85	90	95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser		
100	105	110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly		
115	120	125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu		
130	135	140
Asn Lys Gly Cys Ser		
145		

<210> 249

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 249

Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile		
1	5	10
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser		
20	25	30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln		
35	40	45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu		
50	55	60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala		
65	70	75
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser		
85	90	95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser		
100	105	110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly		
115	120	125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu		
130	135	140
Asn Lys Gly Cys Ser		
145		

<210> 250

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 250

Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile		
1	5	10
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser		
20	25	30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln		
35	40	45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu		
50	55	60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala		

65	70	75	80
Gly Ile Asn Val Ala Glu Gln Ser Lys	Glu Cys Asn Ile Asn Ile Ser		
85	90		95
Thr Thr Asn Tyr Pro Cys Lys Val Ser	Thr Gly Arg His Pro Ile Ser		
100	105		110
Met Val Ala Leu Ser Pro Leu Gly	Ala Leu Val Ala Cys Tyr Lys Gly		
115	120		125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val	Gly Ile Ile Lys Gln Leu		
130	135		140
Asn Lys Gly Cys Ser			
145			

<210> 251
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 251	251		
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile			
1	5	10	15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser			
20	25		30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln			
35	40	45	
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu			
50	55	60	
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala			
65	70	75	80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser			
85	90	95	
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser			
100	105	110	
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly			
115	120	125	
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu			
130	135	140	
Asn Lys Gly Cys Ser			
145			

<210> 252
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 252	252		
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile			
1	5	10	15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser			
20	25	30	
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln			
35	40	45	
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu			
50	55	60	
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala			
65	70	75	80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser			
85	90	95	
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser			
100	105	110	
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly			

115	120	125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu		
130	135	140
Asn Lys Gly Cys Ser		
145		

<210> 253
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 253			
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile			
1	5	10	15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser			
20	25	30	
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln			
35	40	45	
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu			
50	55	60	
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala			
65	70	75	80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser			
85	90	95	
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser			
100	105	110	
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly			
115	120	125	
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu			
130	135	140	
Asn Lys Gly Cys Ser			
145			

<210> 254
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 254			
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile			
1	5	10	15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser			
20	25	30	
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln			
35	40	45	
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu			
50	55	60	
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala			
65	70	75	80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser			
85	90	95	
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser			
100	105	110	
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly			
115	120	125	
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu			
130	135	140	
Asn Lys Gly Cys Ser			
145			

<210> 255
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 255
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 256
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 256
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 257
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 257

Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Asn Lys Gly Cys Ser
 145

<210> 258

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 258

Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Asn Lys Gly Cys Ser
 145

<210> 259

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 259

Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45

Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Asn Lys Gly Cys Ser
 145

<210> 260
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 260
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
Asn Lys Gly Cys Ser
 145

<210> 261
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 261
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
Arg Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95

Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Asn Lys Gly Cys Ser
 145

<210> 262
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 262
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Asn Lys Gly Cys Ser
 145

<210> 263
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 263
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140

Asn Lys Gly Cys Ser
145

<210> 264
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 264
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 265
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 265
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 266
<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 266

Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	Leu	Pro	Ile
1					5					10					15
Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala	Ala	Pro	Ser
					20					25					30
Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	Glu	Asp	Gln
					35					40					45
Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	Pro	Asn	Glu
					50					55					60
Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	Thr	Ala	Ala
					65					70					80
Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile	Asn	Ile	Ser
					85					90					95
Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	Pro	Ile	Ser
					100					105					110
Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	Tyr	Lys	Gly
					115					120					125
Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	Lys	Gln	Leu
					130					135					140
Asn	Lys	Gly	Cys	Ser											
					145										

<210> 267

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 267

Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	Leu	Pro	Ile
1					5					10					15
Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala	Ala	Pro	Ser
					20					25					30
Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	Glu	Asp	Gln
					35					40					45
Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	Pro	Asn	Glu
					50					55					60
Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	Thr	Ala	Ala
					65					70					80
Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile	Asn	Ile	Ser
					85					90					95
Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	Pro	Ile	Ser
					100					105					110
Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	Tyr	Lys	Gly
					115					120					125
Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	Lys	Gln	Leu
					130					135					140
Asn	Lys	Gly	Cys	Ser											
					145										

<210> 268

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 268

Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	Leu	Pro	Ile
1					5					10					15

Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Asn Lys Gly Cys Ser
 145

<210> 269

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 269
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Asn Lys Gly Cys Ser
 145

<210> 270

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 270
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60

Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Asn Lys Gly Cys Ser
 145

<210> 271
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 271
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
Asn Lys Gly Cys Ser
 145

<210> 272
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 272
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110

Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Asn Lys Gly Cys Ser
 145

<210> 273
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 273
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
Asn Lys Gly Cys Ser
 145

<210> 274
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 274
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
Asn Lys Gly Cys Ser
 145

<210> 275
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 275
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 276
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 276
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 277
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 277
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Asn Lys Gly Cys Ser
 145

<210> 278
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 278
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Asn Lys Gly Cys Ser
 145

<210> 279
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 279
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln

35	40	45
Gly Trp Tyr Cys Gln Asn Ala	Gly Ser Thr Val Tyr Tyr Pro Asn Glu	
50	55	60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Val Ala		
65	70	75
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser		80
85	90	95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser		
100	105	110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly		
115	120	125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu		
130	135	140
Asn Lys Gly Cys Ser		
145		

<210> 280

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 280

Ile Gly Val Tyr Gly Ser Ser Val Ile	Tyr Met Val Gln Leu Pro Ile	
1	5	10
Phe Gly Val Ile Asp Thr Pro Cys Trp	Ile Val Lys Ala Ala Pro Ser	
20	25	30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln		
35	40	45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu		
50	55	60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala		
65	70	75
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser		80
85	90	95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser		
100	105	110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly		
115	120	125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu		
130	135	140
Asn Lys Gly Cys Ser		
145		

<210> 281

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 281

Ile Gly Val Tyr Gly Ser Ser Val Ile	Tyr Met Val Gln Leu Pro Ile	
1	5	10
Phe Gly Val Ile Asp Thr Pro Cys Trp	Ile Val Lys Ala Ala Pro Ser	
20	25	30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln		
35	40	45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu		
50	55	60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala		
65	70	75
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser		80

85	90	95
Thr Thr Asn Tyr Pro Cys Lys Val Ser	Thr Gly Arg His Pro Ile Ser	
100	105	110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly		
115	120	125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu		
130	135	140
Asn Lys Gly Cys Ser		
145		

<210> 282
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 282			
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile			
1	5	10	15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser			
20	25	30	
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln			
35	40	45	
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu			
50	55	60	
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala			
65	70	75	80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser			
85	90	95	
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser			
100	105	110	
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly			
115	120	125	
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu			
130	135	140	
Asn Lys Gly Cys Ser			
145			

<210> 283
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 283			
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile			
1	5	10	15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser			
20	25	30	
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln			
35	40	45	
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu			
50	55	60	
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala			
65	70	75	80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser			
85	90	95	
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser			
100	105	110	
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly			
115	120	125	
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu			

130
Asn Lys Gly Cys Ser
145

135

140

<210> 284
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 284
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 285
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 285
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 286

<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 286
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 287
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 287
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 288
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 288
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile

1	5	10	15												
Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala	Ala	Pro	Ser
20	25	30													
Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	Glu	Asp	Gln
35	40	45													
Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	Pro	Asn	Glu
50	55	60													
Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	Thr	Ala	Ala
65	70	75	80												
Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile	Asn	Ile	Ser
85	90	95													
Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	Pro	Ile	Ser
100	105	110													
Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	Tyr	Lys	Gly
115	120	125													
Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	Lys	Gln	Leu
130	135	140													
Asn	Lys	Gly	Cys	Ser											
145															

<210> 289

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 289

Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	Leu	Pro	Ile
1	5	10	15												
Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala	Ala	Pro	Ser
20	25	30													
Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	Glu	Asp	Gln
35	40	45													
Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	Pro	Asn	Glu
50	55	60													
Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	Thr	Ala	Ala
65	70	75	80												
Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile	Asn	Ile	Ser
85	90	95													
Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	Pro	Ile	Ser
100	105	110													
Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	Tyr	Lys	Gly
115	120	125													
Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	Lys	Gln	Leu
130	135	140													
Asn	Lys	Gly	Cys	Ser											
145															

<210> 290

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 290

Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	Leu	Pro	Ile
1	5	10	15												
Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala	Ala	Pro	Ser
20	25	30													
Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	Glu	Asp	Gln
35	40	45													
Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	Pro	Asn	Glu

50	55	60
Lys Asp Cys Glu Thr Arg	Gly Asp His Val Phe Cys Asp Thr Ala Ala	
65	70	75
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser		80
85	90	95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser		
100	105	110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly		
115	120	125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu		
130	135	140
Asn Lys Gly Cys Ser		
145		

<210> 291

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 291

Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile		
1	5	10
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser		
20	25	30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln		
35	40	45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu		
50	55	60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala		
65	70	75
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser		80
85	90	95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser		
100	105	110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly		
115	120	125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu		
130	135	140
Asn Lys Gly Cys Ser		
145		

<210> 292

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 292

Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile		
1	5	10
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser		
20	25	30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln		
35	40	45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu		
50	55	60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala		
65	70	75
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser		80
85	90	95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser		

100	105	110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly		
115	120	125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu		
130	135	140
Pro Lys Gly Cys Ser		
145		

<210> 293
<211> 149
<212> PRT
<213> Human metapneumo virus

100	105	110	
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile			
1	5	10	15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser			
20	25	30	
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln			
35	40	45	
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu			
50	55	60	
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala			
65	70	75	80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser			
85	90	95	
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser			
100	105	110	
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly			
115	120	125	
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu			
130	135	140	
Pro Lys Gly Cys Ser			
145			

<210> 294
<211> 149
<212> PRT
<213> Human metapneumo virus

100	105	110	
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile			
1	5	10	15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser			
20	25	30	
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln			
35	40	45	
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu			
50	55	60	
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala			
65	70	75	80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser			
85	90	95	
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser			
100	105	110	
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly			
115	120	125	
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu			
130	135	140	
Pro Lys Gly Cys Ser			

145

<210> 295
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 295
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Pro Lys Gly Cys Ser
145

<210> 296
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 296
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Pro Lys Gly Cys Ser
145

<210> 297
<211> 149
<212> PRT

<213> Human metapneumo virus

<400> 297

Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	Leu	Pro	Ile
1					5					10					15
Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Ile	Lys	Ala	Ala	Pro	Ser
					20					25					30
Cys	Ser	Glu	Lys	Asn	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	Glu	Asp	Gln
					35					40					45
Gly	Trp	Tyr	Cys	Lys	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	Pro	Asn	Glu
					50					55					60
Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	Thr	Ala	Ala
					65					70					80
Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Arg	Glu	Cys	Asn	Ile	Asn	Ile	Ser
					85					90					95
Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	Pro	Ile	Ser
					100					105					110
Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	Tyr	Lys	Gly
					115					120					125
Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	Lys	Gln	Leu
					130					135					140
Pro	Lys	Gly	Cys	Ser											
					145										

<210> 298

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 298

Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	Leu	Pro	Ile
1					5					10					15
Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Ile	Lys	Ala	Ala	Pro	Ser
					20					25					30
Cys	Ser	Glu	Lys	Asn	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	Glu	Asp	Gln
					35					40					45
Gly	Trp	Tyr	Cys	Lys	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	Pro	Asn	Glu
					50					55					60
Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	Thr	Ala	Ala
					65					70					80
Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Arg	Glu	Cys	Asn	Ile	Asn	Ile	Ser
					85					90					95
Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	Pro	Ile	Ser
					100					105					110
Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	Tyr	Lys	Gly
					115					120					125
Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	Lys	Gln	Leu
					130					135					140
Pro	Lys	Gly	Cys	Ser											
					145										

<210> 299

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 299

Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	Leu	Pro	Ile
1					5					10					15
Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Ile	Lys	Ala	Ala	Pro	Ser

20	25	30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln		
35	40	45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu		
50	55	60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala		
65	70	75
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser		
85	90	95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Ser Ile Ser		
100	105	110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly		
115	120	125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu		
130	135	140
Pro Lys Gly Cys Ser		
145		

<210> 300

<211> 149

<212> PRT

<213> Human metapneumo virus

400	300	
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile		
1	5	10
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser		
20	25	30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln		
35	40	45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu		
50	55	60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala		
65	70	75
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser		
85	90	95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser		
100	105	110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly		
115	120	125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu		
130	135	140
Pro Lys Gly Cys Ser		
145		

<210> 301

<211> 149

<212> PRT

<213> Human metapneumo virus

400	301	
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile		
1	5	10
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser		
20	25	30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln		
35	40	45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu		
50	55	60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala		

65	70	75	80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser			
85	90	95	
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser			
100	105	110	
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly			
115	120	125	
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu			
130	135	140	
Pro Lys Gly Cys Ser			
145			

<210> 302
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 302			
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile			
1	5	10	15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser			
20	25	30	
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln			
35	40	45	
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu			
50	55	60	
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala			
65	70	75	80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser			
85	90	95	
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser			
100	105	110	
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly			
115	120	125	
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu			
130	135	140	
Pro Lys Gly Cys Ser			
145			

<210> 303
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 303			
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile			
1	5	10	15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser			
20	25	30	
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln			
35	40	45	
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu			
50	55	60	
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala			
65	70	75	80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser			
85	90	95	
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser			
100	105	110	
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly			

115	120	125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu		
130	135	140
Pro Lys Gly Cys Ser		
145		

<210> 304
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 304			
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile			
1	5	10	15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser			
20	25	30	
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln			
35	40	45	
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu			
50	55	60	
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala			
65	70	75	80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser			
85	90	95	
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser			
100	105	110	
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly			
115	120	125	
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu			
130	135	140	
Pro Lys Gly Cys Ser			
145			

<210> 305
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 305			
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile			
1	5	10	15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser			
20	25	30	
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln			
35	40	45	
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu			
50	55	60	
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala			
65	70	75	80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser			
85	90	95	
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser			
100	105	110	
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly			
115	120	125	
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu			
130	135	140	
Pro Lys Gly Cys Ser			
145			

<210> 306
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 306
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Pro Lys Gly Cys Ser
145

<210> 307
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 307
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Pro Lys Gly Cys Ser
145

<210> 308
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 308

Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Pro Lys Gly Cys Ser
 145

<210> 309
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 309
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Pro Lys Gly Cys Ser
 145

<210> 310
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 310
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45

Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Pro Lys Gly Cys Ser
 145

<210> 311

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 311
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Pro Lys Gly Cys Ser
 145

<210> 312

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 312
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95

Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Pro Lys Gly Cys Ser
 145

<210> 313
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 313
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Pro Lys Gly Cys Ser
 145

<210> 314
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 314
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140

Pro Lys Gly Cys Ser
145

<210> 315
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 315

Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	Leu	Pro	Ile
1					5					10				15	
Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Ile	Lys	Ala	Ala	Pro	Ser
					20				25				30		
Cys	Ser	Glu	Lys	Asp	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	Glu	Asp	Gln
		35				40				45					
Gly	Trp	Tyr	Cys	Lys	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	Pro	Asn	Glu
	50					55				60					
Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	Thr	Ala	Ala
65			70					75				80			
Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Arg	Glu	Cys	Asn	Ile	Asn	Ile	Ser
		85					90				95				
Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	Pro	Ile	Ser
	100					105				110					
Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	Tyr	Lys	Gly
	115					120				125					
Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	Lys	Gln	Leu
	130					135				140					
Pro	Lys	Gly	Cys	Ser											
145															

<210> 316
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 316

Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	Leu	Pro	Ile
1					5					10			15		
Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Ile	Lys	Ala	Ala	Pro	Ser
					20				25			30			
Cys	Ser	Glu	Lys	Asp	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	Glu	Asp	Gln
		35				40				45					
Gly	Trp	Tyr	Cys	Lys	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	Pro	Asn	Glu
	50					55				60					
Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	Thr	Ala	Ala
65				70				75				80			
Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Arg	Glu	Cys	Asn	Ile	Asn	Ile	Ser
		85					90				95				
Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	Pro	Ile	Ser
	100					105				110					
Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	Tyr	Lys	Gly
	115					120				125					
Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	Lys	Gln	Leu
	130					135				140					
Pro	Lys	Gly	Cys	Ser											
145															

<210> 317
<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 317

Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	Leu	Pro	Ile
1				5					10						15
Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Ile	Lys	Ala	Ala	Pro	Ser
				20					25						30
Cys	Ser	Glu	Lys	Asp	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	Glu	Asp	Gln
				35					40						45
Gly	Trp	Tyr	Cys	Lys	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	Pro	Asn	Glu
				50					55						60
Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	Thr	Ala	Ala
				65					70						80
Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Arg	Glu	Cys	Asn	Ile	Asn	Ile	Ser
				85					90						95
Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	Pro	Ile	Ser
				100					105						110
Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	Tyr	Lys	Gly
				115					120						125
Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	Lys	Gln	Leu
				130					135						140
Pro	Lys	Gly	Cys	Ser											
				145											

<210> 318

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 318

Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	Leu	Pro	Ile
1				5					10						15
Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Ile	Lys	Ala	Ala	Pro	Ser
				20					25						30
Cys	Ser	Glu	Lys	Asp	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	Glu	Asp	Gln
				35					40						45
Gly	Trp	Tyr	Cys	Lys	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	Pro	Asn	Glu
				50					55						60
Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	Thr	Ala	Ala
				65					70						80
Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Arg	Glu	Cys	Asn	Ile	Asn	Ile	Ser
				85					90						95
Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	Pro	Ile	Ser
				100					105						110
Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	Tyr	Lys	Gly
				115					120						125
Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	Lys	Gln	Leu
				130					135						140
Pro	Lys	Gly	Cys	Ser											
				145											

<210> 319

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 319

Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	Leu	Pro	Ile
1				5					10						15

Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Pro Lys Gly Cys Ser
 145

<210> 320

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 320
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Pro Lys Gly Cys Ser
 145

<210> 321

<211> 149

<212> PRT

<213> Human metapneumo virus

<400> 321
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60

Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Pro Lys Gly Cys Ser
 145

<210> 322
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 322
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
Pro Lys Gly Cys Ser
 145

<210> 323
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 323
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110

Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Pro Lys Gly Cys Ser
 145

<210> 324
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 324
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
Pro Lys Gly Cys Ser
 145

<210> 325
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 325
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
Pro Lys Gly Cys Ser
 145

<210> 326
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 326
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Pro Lys Gly Cys Ser
145

<210> 327
<211> 149
<212> PRT
<213> Human metapneumo virus

<400> 327
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Pro Lys Gly Cys Ser
145

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
4 September 2003 (04.09.2003)

PCT

(10) International Publication Number
WO 2003/072720 A3

(51) International Patent Classification⁷: C12N 7/00. (74) Agents: CORUZZI, Laura, A. et al.; Pennie & Edmonds LLP, 1155 Avenue of the Americas, New York, NY 10036 (US).

(21) International Application Number:
PCT/US2003/005276

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(22) International Filing Date: 21 February 2003 (21.02.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/358,934 21 February 2002 (21.02.2002) US

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

(71) Applicants (*for all designated States except US*): MED-IMMUNE VACCINES, INC. [US/US]; 35 W. Watkins Mill Road, Gaithersburg, MD 20878 (US). VIRONOVATIVIVE BV [NL/NL]; P.O. Box 1738, NL-3000 DR Rotterdam (NL).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): HALLER, Aurelia [AT/US]; 313 Hillview Avenue, Redwood City, CA 94062 (US). TANG, Roderick [MY/US]; 730 Chestnut Street, #3, San Carlos, CA 94070 (US). FOUCHIER, Ronaldus, Adrianus, Maria [NL/NL]; Essenburgsingel 44a, NL-3021 AR Rotterdam (NL). VAN DEN HOGEN, Bernadetta, Gerarda [NL/NL]; Essenburgsingel 44a, NL-3021 AR Rotterdam (NL). OSTERHAUS, Albertus, Dominicus, Marcellinus, Erasmus [NL/NL]; Dr. Breveestraat 16, NL-3981 CH Bunnik (NL).

Published:

- with international search report
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

(88) Date of publication of the international search report:
19 August 2004

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 2003/072720 A3

(54) Title: RECOMBINANT PARAINFLUENZA VIRUS EXPRESSION SYSTEMS AND VACCINES COMPRISING HETEROLOGOUS ANTIGENS DERIVED FROM METAPNEUMOVIRUS

(57) Abstract: The present invention relates to recombinant bovine parainfluenza virus (bPIV) cDNA or RNA which may be used to express heterologous gene products in appropriate host cell systems and/or to rescue negative strand RNA recombinant viruses that express, package, and/or present the heterologous gene product. In particular, the heterologous gene products include gene product of another species of PIV or from another negative strand RNA virus, including but not limited to, influenza virus, respiratory syncytial virus, human metapneumovirus and avian pneumovirus. The chimeric viruses and expression products may advantageously be used in vaccine formulations including vaccines against a broad range of pathogens and antigens.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US03/05276

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12N 7/00; A61K 39/12, 39/15
 US CL : 435/ 235.1, 236, 320.1; 424199.1, 202.1, 204.1, 211.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/ 235.1, 236, 320.1; 424199.1, 202.1, 204.1, 211.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
 Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 98/53078 (THE GOVERNMENT OF THE UNITED STATES OF AMERICA) 26 November 1998 (26.11.98), see pages 6- 10 and examples XII and XIII.	1- 3, 22, 27- 44
Y	NISSEN, M.D. et al., Evidence of human metapneumovirus in Australian children. The Medical Journal of Australia 18 February 2002, Vol. 176, No. 4, page 188, see entire document.	1- 3, 22, 27- 44
A	SKIADAPOULOS, M.H. et al., A Chimeric Human-Bovine Parainfluenza Virus Type 3 Expressing Measles Virus Hemagglutinin Is Attenuated for Replication but Is Still Immunogenic in Rhesus Monkeys. Journal of Virology 2001 Vol. 75, pages 10498-10504.	
A	SCHMIDT, A. C. et al., Mucosal Immunization of Rhesus Monkeys against Respiratory Syncytial Virus Subgroups A and B and Human Parainfluenza Virus Type 3 by Using a Live cDNA-Derived Vaccine Based on a Host Range-Attenuated Bovine Parainfluenza Virus Type 3 Vector Backbone. Journal of Virology 2002 Vol. 76, pages 1089-1099.	
A	WO 03/043587 (THE GOVERNMENT OF THE UNITED STATES OF AMERICA) 30 May 2003 (30.05.2003).	1- 48

Further documents are listed in the continuation of Box C.

See patent family annex.

* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier application or patent published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T"

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X"

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y"

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&"

document member of the same patent family

Date of the actual completion of the international search

12 December 2003 (12.12.2003)

Date of mailing of the international search report

01 JUL 2004

Name and mailing address of the ISA/US
 Mail Stop PCT, Attn: ISA/US
 Commissioner for Patents
 P.O. Box 1450
 Alexandria, Virginia 22313-1450
 Facsimile No. (703) 305-3230

Authorized officer

Myron G. Hill

Telephone No. 703-308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

PCT/US03/05276

Continuation of B. FIELDS SEARCHED Item 3:
WEST and MEDLINE STN
parainfluenza, bovine, chimeric, metapneumovirus, recombinant, vaccine, leukemia, lymphoma, asthma